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(54) Title: CRYSTAL OF GLUCOKINASE PROTEIN, AND METHOD FOR DRUG DESIGN USING THE CRYSTAL

(54) 発明の名称: グルコキナーゼタンパク質の結晶、及びその結晶を用いたドラッグデザイン方法

(57) Abstract: Glucokinase is crystallized, the three-dimensional structure thereof is analyzed, and then a compound to be bonded to glucokinase is designed on the basis of the coordinate for the resulting three-dimensional structure. Specifically, glucokinase is freed of a part of amino acid residues being on the N-terminal side thereof, to thereby crystallize it, and the three-dimensional structure of the resulting crystal is elucidated through the X-ray crystallographic analysis thereof.

(57) 要約: 本発明は、グルコキナーゼを結晶化し、その三次元構造を解析し、得られる三次元構造座標に基づいてグルコキナーゼに結合する化合物を設計する。具体的には、グルコキナーゼのN末端側のアミノ酸残基の一部を欠失させることによってグルコキナーゼを結晶化し、この結晶についてX線結晶構造解析によってその三次元構造を解明することによって達成される。

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## 明細書

グルコキナーゼタンパク質の結晶、及びその結晶を用いたドラッグデザイン方法

## 5 技術分野

本発明は、新規なグルコキナーゼタンパク質（以下、「GKタンパク質」ともいう）の結晶、その結晶を用いて得られる三次元構造座標を用いたドラッグデザイン方法などに関する。

## 10 背景技術

グルコキナーゼ（ATP : D-hexose 6-phosphotransferase, EC 2. 7. 1. 1）は、哺乳類の4種のヘキソキナーゼアイソザイムのうちのひとつ（ヘキソキナーゼI V）である。これらのアイソザイムは同じ反応を触媒するが、グルコースに対する  $K_m$  値に差がある。すなわち、  
15 ヘキソキナーゼI、II、IIIの  $K_m$  値は  $10^{-6} \sim 10^{-4} M$  であるのに対し、グルコキナーゼともよばれるヘキソキナーゼI Vのグルコースに対する  $K_m$  値はずっと大きく、約  $10^{-2} M$  である。ヘキソキナーゼは、解糖系の初期段階に関与する酵素であり、グルコースからグルコース6リン酸への反応を触媒する。

グルコキナーゼは、主に肝臓と膵臓ベータ細胞に発現が限局しており、それ  
20 らの細胞におけるグルコース代謝の律速段階を制御することで、体全体の糖代謝に重要な役割を果たしている。肝臓と膵臓ベータ細胞のグルコキナーゼは、それぞれスプライシングの違いによりN末端の15アミノ酸の配列が異なっているが、酵素学的性質は同一である。

10年ほど前から、グルコキナーゼは膵臓ベータ細胞や肝臓のグルコースセ  
25 ンサーとして働くという仮説が提唱されている（Garfinkel D, et al: Am J Physiol 247 (3Pt2):R527-536, 1984）。最近のグルコキナーゼ遺伝子操作マウスの結果から、実際にグルコキナーゼは全身のグルコース恒常性に重要な役割を担うことが明らかになっている。

グルコキナーゼ遺伝子を破壊したマウスは、生後まもなく糖尿病で死亡する

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(Grupe A, et al: Cell 83:69-78, 1995)。一方、グルコキナーゼを過剰発現させたマウスは血糖値が低くなる (Ferre T, et al: Proc Natl Acad Sci U S A 93:7225-7230, 1996)。グルコース濃度上昇によってグルコキナーゼ活性が上昇すると、膵臓ベータ細胞と肝細胞の反応は異なるが、いずれも血糖を低下させる方向に作用する。膵臓ベータ細胞は、より多くのインスリンを分泌するようになり、肝臓は糖を取り込みグリコーゲンとして貯蔵すると同時に糖放出を低下させる。

このようにグルコキナーゼ酵素活性の変動は、肝臓および膵臓ベータ細胞を介した哺乳類のグルコースホメオスタシスにおいて重要な役割を果たしている。

10 MODY2 (maturity-onset diabetes of the young) と呼ばれる若年に糖尿病を発症する症例においてグルコキナーゼ遺伝子の突然変異が発見され、グルコキナーゼ活性の低下が血糖上昇の原因となっている (Vionnet N, et al: Nature 356:721-722, 1992)。一方グルコキナーゼ活性を上昇させる突然変異をもつ家系も見つかっており、このよう

15 な人たちは低血糖症状を示す (Glaser B, et al: N Engl J Med 338: 226-230, 1998)。

以上より、グルコキナーゼはヒトにおいてもグルコースセンサーとして働き、グルコース恒常性に重要な役割を果たしている。一方、多くの I I 型糖尿病患者のグルコキナーゼは変位を受けていないので、グルコキナーゼセンサーシステムを利用した血糖調節は可能と考えられる。グルコキナーゼ活性化物質には膵臓ベータ細胞のインスリン分泌促進作用と肝臓の糖取り込み亢進および糖放出抑制作用が期待できるので、I I 型糖尿病患者の治療薬として有用と考えられる。

近年、膵臓ベータ細胞型グルコキナーゼが、ラット脳、なかでも特に摂食中枢である視床下部腹内側核 (Ventr o m e d i a l h y p o t h a l a m u s, VMH) に限局して発現していることが明らかにされた。VMHの約2割の神経細胞は、グルコースレスポンスニューロンと呼ばれ、従来から体重コントロールに重要な役割を果たすと考えられてきた。ラットの脳内へグルコースを投与すると摂食量が低下するのに対して、グルコース類縁体のグルコ

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サミンの脳内投与によってグルコース代謝を抑制すると過食となる。電気生理学的実験からグルコースレスポンスニューロンは生理的なグルコース濃度変化（5 - 20 mM）に呼応して活性化されるがグルコサミン等でグルコース代謝を抑制すると活性抑制が認められる。VMHのグルコース濃度感知システム  
5 には膵臓ベータ細胞のインスリン分泌と同様なグルコキナーゼを介したメカニズムが想定されている。従って肝臓、膵臓ベータ細胞に加えVHMのグルコキナーゼ活性化を行う物質には血糖是正効果のみならず、多くのI I型糖尿病患者で問題となっている肥満をも是正できる可能性がある。

一方、DIABETES, vol. 48, 1698-1705, September 1999 にはヘキソキナー  
10 ゼI からグルコキナーゼの立体構造を予測した旨が記載されているが、実際に結晶化はされていないし、実用的なものではなかった。

以上より、グルコキナーゼの三次元立体構造を明らかにし、グルコキナーゼと相互作用する化合物を効率的に見いだすことを可能にすることは、例えば、糖尿病の治療剤、又は予防剤；網膜症、腎症、神経症、虚血性心疾患、動脈硬  
15 化等の糖尿病の慢性合併症の治療剤、又は予防剤；肥満の治療剤、又は予防剤の開発に大きな進展をもたらすと考えられる。

現在ではタンパク質の活性中心の解析や反応機作の予測といった作業にコンピュータを利用したCARD D (Computer Aided Rational Drug Design) が実用的なレベルで活用されるようになっている。

CARD Dによる創薬システムにおいては、ターゲットとなるタンパク質の  
20 3次元構造解析データに基づき、タンパク質の活性部位の構造が予測される。そして、その活性部位の構造と結合し得る化合物の候補に関する情報が化合物データベースから取得される。その後、ターゲットとなるタンパク質の活性部位と候補化合物の3次元構造や物理的性質を考慮し、ターゲットとなるタンパク質に結合しうる化合物の候補を選択する。これらの工程が、いわゆるインシリ  
25 コスクリーニング工程である。

インシリコスクリーニング工程で選択された化合物が、ターゲットとなるタンパク質と結合し、その活性を変化させるかどうかは、実際の試験（ウェット実験）により調べられる。そして、実際にターゲットとなるタンパク質の活性



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を変化させる化合物が医薬の有効成分となる。これにより、実験室で無数の化合物を標的タンパク質に一つ一つ作用させて相互作用を確認するという操作を行うことなく、標的タンパク質と相互作用する化合物を効率よく探し出される。

- 5 インシリコスクリーニングは、ターゲットとなるタンパク質と結合する化合物の候補を大幅に絞ることができるため医薬品開発に有効な手段であるといえる。

- CARDDによる創薬システムにおいては、ターゲットとなるタンパク質のX線構造解析による3次元構造解析データが重要な情報となる。X線構造解析による3次元構造解析には、解析試料としてターゲットとなるタンパク質の結晶10 が必要である。したがってCARDDによる創薬システムに基づいてGKに関連する創薬の開発を進めるためには、GKの結晶が必要である。しかしながら、前述のとおりGKは結晶化が困難で、CARDDに必要な情報を与えるものではなかった。

- 15 本発明は、上記従来技術の有する課題に鑑みてなされたものであり、グルコキナーゼの結晶を得ること、及び、当該結晶から得られた情報に基づいてグルコキナーゼに結合する化合物を設計することを目的とする。

#### 発明の開示

- 20 上記目的の少なくともひとつ以上は、以下の発明により解決される。

[1] 結晶化に用いることを特徴とする、グルコキナーゼタンパク質。

[2] 配列番号5に記載のアミノ酸配列からなることを特徴とする、前記[1]に記載のタンパク質。

- [3] 配列番号5に記載のアミノ酸配列又はそのアミノ酸配列と実質的に25 同一のアミノ酸配列からなることを特徴とするタンパク質の結晶。

[4] 前記タンパク質がグルコキナーゼタンパク質である、前記[3]に記載の結晶。

[5] 配列番号5に記載のアミノ酸配列を有するタンパク質の結晶である、前記[3]に記載の結晶。

- 5 -

[6] 格子定数が、下記式 (1) ~ (4)

$$a=b=79.9\pm4\text{オングストローム} \quad \dots (1)$$

$$c=322.2\pm15\text{オングストローム} \quad \dots (2)$$

$$\alpha=\beta=90^\circ \quad \dots (3)$$

5  $\gamma=120^\circ \quad \dots (4)$

を満たす、前記[3]に記載の結晶。

[7] 空間群が $P6_322$ である、前記[6]に記載の結晶。

[8] 表1に記載の三次元構造座標データによって特定されるタンパク質の結晶。

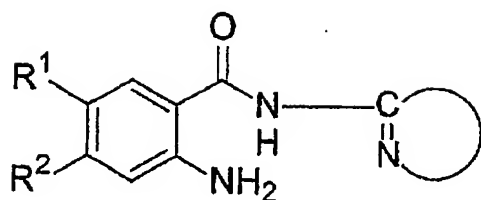
10 [9] 表1に記載の三次元構造座標データの少なくとも一つのデータを変更した三次元構造座標データにおいて、表1に記載の三次元構造座標データで示されるアミノ酸の主鎖の原子 ( $C\alpha$  原子) と、該  $C\alpha$  原子と対応する前記変更した三次元構造座標データで示される  $C\alpha$  原子との平均二乗偏差が、0.6オングストローム以下である結晶。

15 [10] 化合物結合部位が、配列番号5に示すアミノ酸配列における、チロシン61~セリン69、グルタミン酸96~グルタミン98、イソロイシン159、メチオニン210~チロシン215、ヒスチジン218~グルタミン酸221、メチオニン235、アルギニン250、ロイシン451~リジン459のアミノ酸残基の少なくともひとつによって構成される、[3]~[9]のいずれかに記載の結晶。

20 [11] 配列番号5に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同一のアミノ酸配列からなるタンパク質と該タンパク質に結合可能な化合物との複合体を含む結晶。

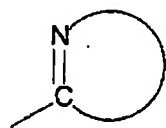
[12] 前記化合物が、式(I)で表される、前記[11]に記載の結晶。

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(I)

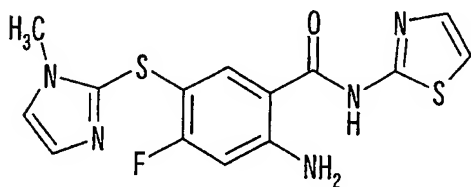
- [式中、 $R^1$ は、ハロゲン原子、 $-S-(O)_p-A$ 、 $-S-(O)_q-B$ 又は $-O-B$ を示し（ここで、 $p$ 及び $q$ は同一又は異なって、 $0 \sim 2$ の整数を示し、 $A$ は置換されていてもよい直鎖の $C_1-C_6$ アルキル基を示し、 $B$ は置換されてい
- 5   てもよい五員環又は六員環のアリール基又はヘテロアリール基を示し、  
 $R^2$ は水素原子又はハロゲン原子を示し、



(II)

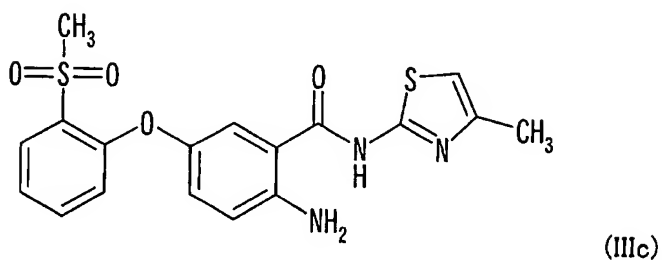
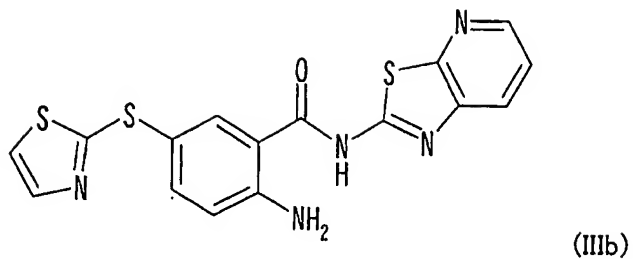
- は、アミド基に結合した炭素原子の隣に窒素原子を有する、置換されていても
- 10   よい単環の又は双環のヘテロアリール基を示す]

[13] 前記化合物が、式(IIIa)～式(IIIc)で表されるいずれかの化合物である前記[12]に記載の結晶。



(IIIa)

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5

[14] 配列番号 8 に記載のアミノ酸配列からなることを特徴とする、前記 [1] に記載のタンパク質。

[15] 配列番号 8 に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同一のアミノ酸配列からなることを特徴とするタンパク質の結晶。

10 [16] 前記タンパク質がグルコキナーゼタンパク質である、前記 [15] に記載の結晶。

[17] 配列番号 8 に記載のアミノ酸配列を有するタンパク質の結晶である、前記 [15] に記載の結晶。

[18] 格子定数が、下記式

15  $a=b=103.2 \pm 5$  オングストローム … (5)

$c=281.0 \pm 7$  オングストローム … (6)

$\alpha=\beta=90^\circ$  … (7)

$\gamma=120^\circ$  … (8)

を満たす、前記 [15] に記載の結晶。

20 [19] 空間群が  $P6_522$  である、前記 [18] に記載の結晶。

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〔20〕 表2に記載の三次元構造座標データによって特定されるタンパク質の結晶。

〔21〕 表2に記載の三次元構造座標データの少なくとも一つのデータを変更した三次元構造座標データにおいて、表2に記載の三次元構造座標データで示されるアミノ酸の主鎖の原子（C $\alpha$ 原子）と、該C $\alpha$ 原子と対応する前記変更した三次元構造座標データで示されるC $\alpha$ 原子との平均二乗偏差が、0.6  
5    オングストローム以下である結晶。

〔22〕 配列番号2に記載のアミノ酸配列を有するタンパク質のN末端、C  
末端のいずれかまたは両方から、1～50個のアミノ酸残基を欠損したアミノ  
10    酸配列を有するタンパク質を製造するタンパク質製造工程と、

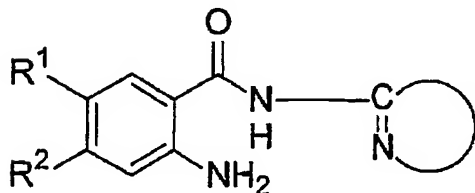
前記タンパク質製造工程で得られたタンパク質と結合する化合物と、前記タンパク質製造工程で得られたタンパク質とを反応させるタンパク質反応工程とを含む、

タンパク質及びそのタンパク質と結合する化合物の複合体を含む結晶の製造  
15    方法。

〔23〕 タンパク質の結晶を製造する方法であって、

配列番号5に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同一のアミノ酸配列を含みグルコキナーゼ活性を有するタンパク質、及び該タンパク質に結合可能な化合物を用いることを特徴とする、結晶の製造方法。

20    〔24〕 前記タンパク質に結合可能な化合物が、式（I）で表される化合物であることを特徴とする、前記〔23〕に記載のタンパク質の結晶の製造方法。

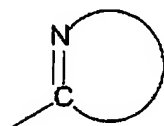


(I)

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[式中、 $R^1$ は、ハロゲン原子、 $-S-(O)_p-A$ 、 $-S-(O)_q-B$ 又は $-O-B$ を示し（ここで、 $p$ 及び $q$ は同一又は異なって、 $0 \sim 2$ の整数を示し、 $A$ は置換されていてもよい直鎖の $C_1-C_6$ アルキル基を示し、 $B$ は置換されていてもよい五員環又は六員環のアリール基又はヘテロアリール基を示し、

- 5  $R^2$ は水素原子又はハロゲン原子を示し、



(III)

は、アミド基に結合した炭素原子の隣に窒素原子を有する、置換されていてもよい単環の又は双環のヘテロアリール基を示す)

- 10 [25] 共結晶法又はソーキング法による、前記[23]、又は[24]に記載の結晶の製造方法。

[26] タンパク質の立体構造情報に基づいて該タンパク質に結合する化合物の構造をデザインするドラッグデザイン方法であって、

- 15 該タンパク質の立体構造情報が、前記[3]～[13]、又は[15]～[21]のうちのいずれか一項に記載の結晶を解析することによって得られる情報であることを特徴とする、ドラッグデザイン方法。

[27] 前記立体構造情報に基づいて、前記タンパク質の化合物結合部位を推測する結合部位推測工程と、

- 20 前記結合部位推測工程で推測された化合物結合部位に適合する化合物を、化合物ライブラリより選択する選択工程と、

を含むことを特徴とする、前記[26]に記載のドラッグデザイン方法。

[28] 前記立体構造情報に基づいて、前記タンパク質の化合物結合部位を推測する結合部位推測工程と、

- 25 前記結合部位推測工程で推測された化合物結合部位に適合する化合物の構造を構築する化合物構造構築工程と、

を含むことを特徴とする、前記[26]に記載のドラッグデザイン方法。

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〔29〕 前記立体構造情報に基づいて、前記タンパク質の化合物結合部位を推測する結合部位推測工程と、

前記結合部位推測工程で推測された化合物結合部位と該化合物結合部位に適合する化合物とが相互作用するように化合物の構造を目視によりデザインするデザイン工程と、

5

を含むことを特徴とする、前記〔26〕に記載のドラッグデザイン方法。

〔30〕 前記化合物結合部位が、配列番号5に示すアミノ酸配列における、チロシン61～セリン69、グルタミン酸96～グルタミン98、イソロイシン159、メチオニン210～チロシン215、ヒスチジン218～グルタミン酸221、メチオニン235、アルギニン250、ロイシン451～リジン459のアミノ酸残基の少なくともひとつによって構成されている、前記〔26〕～〔29〕のうちのいずれか一項に記載のドラッグデザイン方法。

10

15

〔31〕 さらに、前記化合物結合部位に適合すると推定される候補化合物の生理活性を測定する工程を含む、前記〔26〕～〔30〕のいずれか一項に記載のドラッグデザイン方法。

20

〔32〕 さらに、前記化合物結合部位に適合すると推定される候補化合物と、配列番号5に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同一のアミノ酸配列を含むタンパク質とを接触させ、その候補化合物が該タンパク質に結合するか否かを判定する結合判定工程を含む、前記〔26〕～〔30〕のいずれか一項に記載のドラッグデザイン方法。

〔33〕 前記〔26〕～〔30〕のいずれか一項に記載のドラッグデザイン方法によって選択された化合物群を化合物アレイとして組み合わせることを含む化合物アレイの製造方法。

25

図面の簡単な説明

図1は、グルコキナーゼの三次元構造を示すリボン図である。

(図1aは、グルコキナーゼ( $\Delta 1-11$ )/グルコース/化合物1(式IIIaの化合物)の構造を示すリボン図である。また、右図は、左図を回転した図である。)

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(図1 bは、グルコキナーゼ( $\Delta 1-15$ )単体の構造を示すリボン図である。また、右図は、左図を回転した図である。)

図2は、グルコキナーゼ( $\Delta 1-11$ )の結合部位に対する化合物1 (式 IIIa の化合物) の結合様式を示す図である。

5 図3は、グルコキナーゼ( $\Delta 1-11$ )の結合部位の構造を示す図である。

発明を実施するための最良の形態

本明細書において、アミノ酸、ペプチド、蛋白質は下記に示す IUPAC-IUB 生化学命名委員会 (CBN) で採用された略号を用いて表される。また、  
10 特に明示しない限りペプチド及び蛋白質のアミノ酸残基の配列は、左端から右端にかけてN末端からC末端となるように、またN末端が1番になるように表される。

以下、本発明の各実施態様について詳細に説明する。

15 (グルコキナーゼタンパク質)

まず、本発明は、結晶化に用いることを特徴とする、グルコキナーゼタンパク質を提供する。グルコキナーゼタンパク質 (GKタンパク質) は、上述のように、生体内で極めて重要な糖の代謝に関与している。したがって、GKタンパク質の三次元構造を明らかにし、GKタンパク質の活性部位を解明すること  
20 によって、GKタンパク質に結合する化合物 (すなわち、活性化剤又は阻害剤) を探索することができる。よって、GKタンパク質の三次元構造を明らかにすることは重要である。

タンパク質の3次元構造を明らかにする手法として、X線結晶構造解析が良く知られている。即ち、タンパク質を結晶化し、その結晶に単色化されたX線をあて、得られたX線の回折像をもとに、該タンパク質の3次元構造を解明する (Blundell, T. L. 及び Johnson, L. N., PROTEIN CRYSTALLOGRAPHY, 1-565頁, (1976) Academic Press, New York)。GKタンパク質のX線結晶  
25 構造解析に供するために、まず、GKタンパク質を結晶化する必要がある。



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ここで、本発明の「GKタンパク質」とは、配列番号2に示すアミノ酸配列を有するヒト由来の肝臓型グルコキナーゼと、配列番号2と実質的に同一のアミノ酸配列を含有するタンパク質をいう。ここで当該実質的に同一のアミノ酸配列を含有するタンパク質としては、グルコキナーゼ活性を有するものが好ましい。したがって、本明細書では、GKタンパク質は、ヒト由来の肝臓型グルコキナーゼのみならず、ヒト由来の膵臓型グルコキナーゼ、マウス、ラット、サル等の非ヒト由来GKタンパク質をも含む。本発明では、ヒト肝臓型グルコキナーゼが好ましく用いられる。ヒト由来のグルコキナーゼにおいて、肝臓型と膵臓型ではN末端の15アミノ酸残基が相違する。ここで、「グルコキナーゼ活性」とは、グルコースからグルコース6リン酸への反応を触媒する活性をいう。

タンパク質の結晶化が一般的に困難なことは良く知られており、GKタンパク質をそのまま結晶化することはできなかった。本発明者らは、種々、試行錯誤による実験の結果、GKタンパク質のN末端側のアミノ酸を11個、又は15個を欠失させることによって、始めてGKタンパク質の結晶化に成功した。欠失させた領域は、結晶化を試みた際に球状のGKタンパク質分子より突出し、その結果、結晶内で隣接するGKタンパク質分子との間で立体的な障害となりGKタンパク質が結晶となるのを妨げていたと考えられる。すなわち、本発明では、アミノ酸配列が既知でありながら結晶化には成功していなかったグルコキナーゼにおいて、N末端側の11個のアミノ酸残基を欠失させたGKタンパク質（配列番号5）、又はN末端側の15個のアミノ酸残基を欠失させたGKタンパク質（配列番号8）を用いることにより、GKタンパク質の結晶を得た。ただし、欠失させるアミノ酸は、隣接する結晶との間で立体的な障害がなくなる範囲であればその数は限定されない。具体的には、例えば、配列番号2で表されるアミノ酸配列において、N末端側の1～50個、好ましくは3～30個、より好ましくは5～25個、さらに好ましくは8～18個、特に好ましくは11～15個のアミノ酸残基を欠失させたアミノ酸配列などが本発明において用いられる。また、C末端側の1～8個、好ましくは1～7個、より好ましくは2～6個のアミノ酸残基を欠失させたアミノ酸配列などが本発明において用い

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られる。

(グルコキナーゼタンパク質の結晶及びその製造方法)

- 次に、本発明においては、配列番号 5、及び配列番号 8 に記載のアミノ酸配  
5 列又はそのアミノ酸配列と実質的に同一のアミノ酸配列を含むタンパク質を含  
む結晶を提供する。

上述したように、結晶化に供する GK タンパク質としては、配列番号 5、及び  
／又は配列番号 8 で表されるアミノ酸配列又はそれと実質的に同一のアミノ酸  
配列を含むタンパク質などが用いられる。

- 10 配列番号 5、及び／又は配列番号 8 で表されるアミノ酸配列又はそれと実質  
的に同一のアミノ酸配列を含むタンパク質（以下、配列番号 2 で表されるアミ  
ノ酸配列又はそれと実質的に同一のアミノ酸配列を有するタンパク質と併せて  
「GK タンパク質」と略すこともある）は、結晶化が可能であればよく、その  
アミノ酸配列は特に制限されない。ここで、配列番号 5、及び／又は配列番号  
15 8 に記載のアミノ酸配列と実質的に同一のアミノ酸配列を含むタンパク質は、  
グルコキナーゼ活性を有している必要はなく、ドラッグデザインに必要な情報  
を得ることができる結晶構造を有するものであれば、不活性な変異体（例えば、  
ATP の結合部位に変異を有することにより不活性化した変異体）であってもよ  
い。ここで、配列番号 2 又は 5 で表されるアミノ酸配列と実質的に同一のアミ  
20 ノ酸配列を含むタンパク質としては、配列番号 2 又は 5 で表わされるアミノ酸  
配列と約 60 % 以上、好ましくは約 70 % 以上、さらに好ましくは約 80 % 以  
上、なかでも好ましくは約 90 % 以上、最も好ましくは約 95 % 以上の相同性  
を有するアミノ酸配列などが挙げられる。また、配列番号 2 又は 5 で表される  
アミノ酸配列と実質的に同一のアミノ酸配列を含むタンパク質として、例えば、  
25 配列番号 2 又は 5 に記載のアミノ酸配列において 1 ～ 10 個、好ましくは 1 ～  
5 個、さらに好ましくは 1 ～ 3 個、さらに好ましくは 1 ～ 2 個のアミノ酸残基  
が置換、欠失、付加および／または挿入されたアミノ酸配列が例示される。

GK タンパク質の 3 次元構造解析は、例えば、次のようにして行う。まず、  
タンパク質を精製する。そして、結晶化、X 線回折強度データ収集、各回折斑

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点の位相決定、電子密度計算、分子モデル作成、構造の精密化などの一連の工程を行う。タンパク質構造解析を行うための主要な設備として、結晶化用インキュベーター、双眼顕微鏡、X線回折計、3次元コンピュータグラフィックス装置などが用いられる。具体的にタンパク質の結晶を作製する実験過程は、タンパク質を大量に（数mg以上が好ましい。）精製する段階、結晶が得られる条件を広く検索する段階、X線解析に適した良質の結晶を得る段階に分けられる。以下、各工程について具体的に説明する。

結晶化に際しては、GKタンパク質を、高純度に精製する。精製方法としては、公知のものが利用でき、例えば、カラムクロマトグラフィー、塩析、遠心分離などが用いられる。

精製されたGKタンパク質は、結晶化し、X線結晶構造解析のための試料とする。結晶化は、蒸気拡散法や透析法等の公知の方法に基づいて行われる。タンパク質の結晶を得る際に、タンパク質の純度・濃度、温度、pH、使用する沈殿剤濃度等多くの要素を検討する必要がある。結晶化条件の検討は、市販のスクリーニング試薬を使用して広い範囲で行うことができ、1つの条件に1～2%濃度のタンパク質溶液を1～2  $\mu$ Lずつ使用して検索することが好ましい。こうして微結晶などが得られた場合には、さらに条件を精密化することが好ましい。

なお、GKタンパク質の結晶を得るためには非常に多くの条件を検索しなければならない。従って、結晶化条件の検討のためにも、タンパク質の大量発現系を構築することが好ましい。一般にタンパク質のうち、結晶になるものの多くは、溶液状態で単分散であり、多分散のものは大体において結晶化しない。そこで、GKタンパク質のN末端を順次切除し、得られたタンパク質について、光散乱装置を用いてタンパク質溶液の単分散性を判定し、試料が結晶化に適しているかどうかを検討しても良い。

次に、得られたGKタンパク質の結晶を用いて、X線回折強度測定を行う。最近では、結晶を細い糸の輪などですくって液体窒素温度に急速冷却してそのまま低温で測定する方法も利用されている。回折X線の強度測定は、通常、イメージングプレートなどの2次元検出器によって行う。X線を当てながら結晶

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を回転させることで発生する多くの回折線をイメージングプレートに記録し、記録された回折強度をレーザーを当てることにより読み取る。

- 次に、重原子ソーキング法や共結晶化法により重原子同型置換体を調製することが好ましい。これを使用して多重同型置換法（MIR法）によりタンパク質結晶の位相を決定することができる。重原子を導入する代わりに、複雑な波長のX線による回折強度データに基づいて位相を決定する多波長異常散乱法（MAD法）も利用できる。類似構造を有する分子が既に解析されている場合には、その分子構造を結晶中にあてはめて初期構造を得ることができ、これをもとにフーリエ合成図を描き、残りの部分の構造を解明して全構造を決定する分子置換法（MR法）も知られている。

- 位相が上記の方法で決定したならば、これより電子密度を求める。この精度は、反射の数（分解能）と使用した反射の精度による。分解能は使用する反射の最小面間隔で表す。この電子密度図から分子モデルを組み立てる。分子モデルを組み立てると原子座標が得られるので、これより構造因子の計算値を求め、この大きさを観測値に近づける最小自乗法により原子パラメータの精密化を行う。このようにしてできるだけ妥当な構造情報を取得する。

本発明においては、配列番号5に示すGKタンパク質の結晶を調製することに成功している（後述の実施例参照）。そしてこのようにして得られたGKタンパク質の結晶は、格子定数が、下記式（1）～（4）：

$$a=b=79.9\pm4\text{オングストローム} \quad \dots (1)$$

$$c=322.2\pm15\text{オングストローム} \quad \dots (2)$$

$$\alpha=\beta=90^\circ \quad \dots (3)$$

$$\gamma=120^\circ \quad \dots (4)$$

- を満たすものであった。また、この結晶は、空間群が $P6_522$ であることが解明された。ここで、前記 $a=b$ は $79.9\pm3$ オングストロームであることが好ましく、 $79.9\pm2$ オングストロームであることがより好ましく、 $79.9\pm1$ オングストロームであることがさらに好ましい。また、前記 $c$ は $322.2\pm10$ オングストロームであることが好ましく、 $322.2\pm8$ オングストロームであることがより好ましく、 $322.2\pm5$ オングストロームであることがさらに好ましい。

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このようにして得られたG Kタンパク質結晶の3次元構造座標を表1に示す。

表1

	ATOM	1	CB	THR	14	25.972	-34.025	76.567	1.00	51.12
5	ATOM	2	OG1	THR	14	27.398	-34.012	76.715	1.00	51.49
	ATOM	3	CG2	THR	14	25.626	-34.173	75.095	1.00	49.96
	ATOM	4	C	THR	14	24.138	-32.317	76.374	1.00	50.95
	ATOM	5	O	THR	14	24.246	-31.685	75.330	1.00	52.42
	ATOM	6	N	THR	14	25.108	-32.861	78.611	1.00	51.41
10	ATOM	7	CA	THR	14	25.384	-32.717	77.154	1.00	50.49
	ATOM	8	N	LEU	15	22.957	-32.673	76.871	1.00	49.75
	ATOM	9	CA	LEU	15	21.733	-32.307	76.167	1.00	49.25
	ATOM	10	CB	LEU	15	20.496	-32.824	76.904	1.00	52.56
	ATOM	11	CG	LEU	15	20.439	-34.307	77.291	1.00	55.08
15	ATOM	12	CD1	LEU	15	21.186	-34.524	78.610	1.00	53.67
	ATOM	13	CD2	LEU	15	18.980	-34.742	77.438	1.00	54.84
	ATOM	14	C	LEU	15	21.676	-30.781	76.078	1.00	48.68
	ATOM	15	O	LEU	15	21.397	-30.208	75.023	1.00	47.52
	ATOM	16	N	VAL	16	21.955	-30.128	77.201	1.00	47.07
20	ATOM	17	CA	VAL	16	21.950	-28.677	77.265	1.00	44.96
	ATOM	18	CB	VAL	16	21.988	-28.188	78.733	1.00	46.09
	ATOM	19	CG1	VAL	16	22.239	-26.684	78.784	1.00	44.09
	ATOM	20	CG2	VAL	16	20.670	-28.523	79.418	1.00	45.38
	ATOM	21	C	VAL	16	23.142	-28.097	76.512	1.00	43.58
25	ATOM	22	O	VAL	16	23.004	-27.110	75.790	1.00	41.54
	ATOM	23	N	GLU	17	24.310	-28.712	76.672	1.00	43.48
	ATOM	24	CA	GLU	17	25.507	-28.223	75.998	1.00	45.62
	ATOM	25	CB	GLU	17	26.759	-28.931	76.532	1.00	46.30
	ATOM	26	CG	GLU	17	27.140	-28.571	77.984	1.00	49.19

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	ATOM	27	CD	GLU	17	27.467	-27.087	78.191	1.00	50.74
	ATOM	28	OE1	GLU	17	28.238	-26.520	77.386	1.00	50.39
	ATOM	29	OE2	GLU	17	26.966	-26.488	79.170	1.00	50.85
	ATOM	30	C	GLU	17	25.417	-28.378	74.479	1.00	45.93
5	ATOM	31	O	GLU	17	26.097	-27.666	73.735	1.00	44.10
	ATOM	32	N	GLN	18	24.577	-29.303	74.020	1.00	45.41
	ATOM	33	CA	GLN	18	24.400	-29.513	72.588	1.00	46.37
	ATOM	34	CB	GLN	18	23.643	-30.818	72.307	1.00	49.99
	ATOM	35	CG	GLN	18	24.488	-32.086	72.423	1.00	55.59
10	ATOM	36	CD	GLN	18	23.701	-33.352	72.088	1.00	58.40
	ATOM	37	OE1	GLN	18	23.158	-33.489	70.988	1.00	60.78
	ATOM	38	NE2	GLN	18	23.638	-34.280	73.037	1.00	56.40
	ATOM	39	C	GLN	18	23.617	-28.338	72.014	1.00	44.35
	ATOM	40	O	GLN	18	23.849	-27.912	70.885	1.00	43.20
15	ATOM	41	N	ILE	19	22.677	-27.821	72.791	1.00	41.97
	ATOM	42	CA	ILE	19	21.895	-26.689	72.327	1.00	40.37
	ATOM	43	CB	ILE	19	20.631	-26.500	73.193	1.00	39.71
	ATOM	44	CG2	ILE	19	19.976	-25.166	72.894	1.00	39.42
	ATOM	45	CG1	ILE	19	19.653	-27.653	72.915	1.00	40.83
20	ATOM	46	CD1	ILE	19	18.356	-27.599	73.719	1.00	38.38
	ATOM	47	C	ILE	19	22.764	-25.431	72.344	1.00	39.01
	ATOM	48	O	ILE	19	22.746	-24.644	71.394	1.00	40.12
	ATOM	49	N	LEU	20	23.550	-25.267	73.404	1.00	35.38
	ATOM	50	CA	LEU	20	24.423	-24.109	73.537	1.00	34.35
25	ATOM	51	CB	LEU	20	25.026	-24.050	74.944	1.00	32.09
	ATOM	52	CG	LEU	20	24.050	-23.887	76.106	1.00	30.92
	ATOM	53	CD1	LEU	20	24.813	-23.722	77.420	1.00	27.61
	ATOM	54	CD2	LEU	20	23.171	-22.689	75.843	1.00	29.31
	ATOM	55	C	LEU	20	25.555	-24.135	72.518	1.00	34.62

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	ATOM	56	O	LEU	20	26.066	-23.087	72.112	1.00	34.19
	ATOM	57	N	ALA	21	25.946	-25.336	72.116	1.00	33.16
	ATOM	58	CA	ALA	21	27.030	-25.509	71.163	1.00	34.30
	ATOM	59	CB	ALA	21	27.344	-26.992	70.993	1.00	34.49
5	ATOM	60	C	ALA	21	26.696	-24.886	69.814	1.00	35.20
	ATOM	61	O	ALA	21	27.587	-24.619	69.007	1.00	35.57
	ATOM	62	N	GLU	22	25.412	-24.652	69.578	1.00	36.75
	ATOM	63	CA	GLU	22	24.961	-24.053	68.329	1.00	37.80
	ATOM	64	CB	GLU	22	23.435	-24.102	68.256	1.00	41.47
10	ATOM	65	CG	GLU	22	22.878	-23.851	66.867	1.00	47.91
	ATOM	66	CD	GLU	22	21.384	-24.128	66.767	1.00	49.95
	ATOM	67	OE1	GLU	22	20.857	-24.163	65.630	1.00	50.84
	ATOM	68	OE2	GLU	22	20.741	-24.307	67.822	1.00	50.26
	ATOM	69	C	GLU	22	25.444	-22.605	68.177	1.00	37.38
15	ATOM	70	O	GLU	22	25.380	-22.039	67.088	1.00	38.34
	ATOM	71	N	PHE	23	25.928	-22.012	69.268	1.00	35.41
	ATOM	72	CA	PHE	23	26.426	-20.636	69.249	1.00	33.38
	ATOM	73	CB	PHE	23	26.224	-19.962	70.614	1.00	31.59
	ATOM	74	CG	PHE	23	24.826	-19.470	70.843	1.00	29.81
20	ATOM	75	CD1	PHE	23	23.836	-20.328	71.310	1.00	26.48
	ATOM	76	CD2	PHE	23	24.489	-18.151	70.555	1.00	28.79
	ATOM	77	CE1	PHE	23	22.520	-19.882	71.487	1.00	29.30
	ATOM	78	CE2	PHE	23	23.177	-17.691	70.727	1.00	31.65
	ATOM	79	CZ	PHE	23	22.189	-18.563	71.195	1.00	28.91
25	ATOM	80	C	PHE	23	27.899	-20.542	68.877	1.00	33.33
	ATOM	81	O	PHE	23	28.396	-19.467	68.549	1.00	34.12
	ATOM	82	N	GLN	24	28.596	-21.670	68.940	1.00	32.75
	ATOM	83	CA	GLN	24	30.016	-21.716	68.620	1.00	32.56
	ATOM	84	CB	GLN	24	30.543	-23.147	68.778	1.00	35.53

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	ATOM	85	CG	GLN	24	30.817	-23.603	70.210	1.00	37.84
	ATOM	86	CD	GLN	24	31.214	-25.074	70.266	1.00	42.36
	ATOM	87	OE1	GLN	24	31.802	-25.601	69.320	1.00	43.06
	ATOM	88	NE2	GLN	24	30.902	-25.739	71.375	1.00	40.61
5	ATOM	89	C	GLN	24	30.335	-21.233	67.208	1.00	31.93
	ATOM	90	O	GLN	24	29.508	-21.320	66.299	1.00	30.32
	ATOM	91	N	LEU	25	31.548	-20.717	67.043	1.00	31.64
	ATOM	92	CA	LEU	25	32.029	-20.257	65.751	1.00	31.85
	ATOM	93	CB	LEU	25	31.876	-18.742	65.615	1.00	31.24
10	ATOM	94	CG	LEU	25	30.441	-18.211	65.563	1.00	29.93
	ATOM	95	CD1	LEU	25	30.436	-16.690	65.710	1.00	28.63
	ATOM	96	CD2	LEU	25	29.801	-18.640	64.262	1.00	27.61
	ATOM	97	C	LEU	25	33.502	-20.635	65.667	1.00	33.30
	ATOM	98	O	LEU	25	34.298	-20.218	66.502	1.00	33.97
15	ATOM	99	N	GLN	26	33.856	-21.450	64.679	1.00	34.57
	ATOM	100	CA	GLN	26	35.244	-21.860	64.496	1.00	36.87
	ATOM	101	CB	GLN	26	35.330	-23.053	63.540	1.00	40.20
	ATOM	102	CG	GLN	26	35.105	-24.414	64.182	1.00	46.34
	ATOM	103	CD	GLN	26	33.863	-24.462	65.041	1.00	48.48
20	ATOM	104	OE1	GLN	26	33.918	-24.229	66.253	1.00	49.27
	ATOM	105	NE2	GLN	26	32.725	-24.757	64.417	1.00	51.72
	ATOM	106	C	GLN	26	36.024	-20.688	63.910	1.00	36.49
	ATOM	107	O	GLN	26	35.430	-19.735	63.403	1.00	35.76
	ATOM	108	N	GLU	27	37.347	-20.761	63.981	1.00	35.17
25	ATOM	109	CA	GLU	27	38.181	-19.705	63.441	1.00	37.77
	ATOM	110	CB	GLU	27	39.658	-20.047	63.627	1.00	40.11
	ATOM	111	CG	GLU	27	40.596	-19.156	62.831	1.00	47.14
	ATOM	112	CD	GLU	27	41.754	-18.639	63.662	1.00	52.56
	ATOM	113	OE1	GLU	27	41.507	-17.808	64.567	1.00	54.72



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	ATOM 114	OE2	GLU 27	42.906	-19.067	63.415	1.00	54.43
	ATOM 115	C	GLU 27	37.878	-19.511	61.961	1.00	37.80
	ATOM 116	O	GLU 27	37.915	-18.392	61.446	1.00	37.09
	ATOM 117	N	GLU 28	37.557	-20.605	61.282	1.00	36.94
5	ATOM 118	CA	GLU 28	37.261	-20.535	59.862	1.00	36.18
	ATOM 119	CB	GLU 28	37.175	-21.939	59.267	1.00	37.83
	ATOM 120	CG	GLU 28	37.826	-22.039	57.902	1.00	41.72
	ATOM 121	CD	GLU 28	39.154	-21.287	57.843	1.00	44.57
	ATOM 122	OE1	GLU 28	40.033	-21.531	58.706	1.00	46.91
10	ATOM 123	OE2	GLU 28	39.313	-20.446	56.933	1.00	44.10
	ATOM 124	C	GLU 28	35.973	-19.779	59.588	1.00	34.66
	ATOM 125	O	GLU 28	35.860	-19.089	58.575	1.00	33.91
	ATOM 126	N	ASP 29	34.994	-19.926	60.472	1.00	32.44
	ATOM 127	CA	ASP 29	33.738	-19.219	60.301	1.00	32.41
15	ATOM 128	CB	ASP 29	32.713	-19.625	61.370	1.00	34.13
	ATOM 129	CG	ASP 29	32.302	-21.091	61.285	1.00	34.13
	ATOM 130	OD1	ASP 29	32.012	-21.580	60.173	1.00	34.03
	ATOM 131	OD2	ASP 29	32.246	-21.749	62.347	1.00	35.16
	ATOM 132	C	ASP 29	34.054	-17.728	60.456	1.00	31.21
20	ATOM 133	O	ASP 29	33.542	-16.895	59.717	1.00	29.93
	ATOM 134	N	LEU 30	34.912	-17.403	61.419	1.00	29.60
	ATOM 135	CA	LEU 30	35.274	-16.016	61.674	1.00	28.38
	ATOM 136	CB	LEU 30	36.101	-15.901	62.964	1.00	23.67
	ATOM 137	CG	LEU 30	35.435	-16.298	64.289	1.00	23.54
25	ATOM 138	CD1	LEU 30	36.314	-15.823	65.433	1.00	22.55
	ATOM 139	CD2	LEU 30	34.038	-15.674	64.418	1.00	24.55
	ATOM 140	C	LEU 30	36.032	-15.390	60.499	1.00	29.80
	ATOM 141	O	LEU 30	35.775	-14.242	60.139	1.00	29.56
	ATOM 142	N	LYS 31	36.963	-16.131	59.906	1.00	29.13

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	ATOM 143	CA	LYS 31	37.704	-15.609	58.770	1.00	30.46
	ATOM 144	CB	LYS 31	38.823	-16.574	58.365	1.00	32.24
	ATOM 145	CG	LYS 31	39.970	-16.653	59.374	1.00	36.80
	ATOM 146	CD	LYS 31	41.091	-17.577	58.885	1.00	40.49
5	ATOM 147	CE	LYS 31	42.291	-17.534	59.829	1.00	44.52
	ATOM 148	NZ	LYS 31	43.443	-18.369	59.363	1.00	47.22
	ATOM 149	C	LYS 31	36.746	-15.391	57.599	1.00	31.28
	ATOM 150	O	LYS 31	36.918	-14.464	56.816	1.00	32.79
	ATOM 151	N	LYS 32	35.730	-16.243	57.486	1.00	30.96
10	ATOM 152	CA	LYS 32	34.758	-16.116	56.406	1.00	32.66
	ATOM 153	CB	LYS 32	33.868	-17.364	56.324	1.00	32.27
	ATOM 154	CG	LYS 32	32.921	-17.362	55.135	1.00	34.72
	ATOM 155	CD	LYS 32	32.203	-18.701	54.965	1.00	39.55
	ATOM 156	CE	LYS 32	31.272	-18.678	53.745	1.00	42.65
15	ATOM 157	NZ	LYS 32	30.699	-20.026	53.417	1.00	42.72
	ATOM 158	C	LYS 32	33.890	-14.868	56.609	1.00	32.63
	ATOM 159	O	LYS 32	33.607	-14.140	55.652	1.00	32.25
	ATOM 160	N	VAL 33	33.463	-14.629	57.847	1.00	30.17
	ATOM 161	CA	VAL 33	32.654	-13.451	58.149	1.00	29.03
20	ATOM 162	CB	VAL 33	32.154	-13.460	59.626	1.00	30.49
	ATOM 163	CG1	VAL 33	31.519	-12.123	59.985	1.00	31.03
	ATOM 164	CG2	VAL 33	31.130	-14.562	59.815	1.00	32.03
	ATOM 165	C	VAL 33	33.538	-12.226	57.908	1.00	26.62
	ATOM 166	O	VAL 33	33.091	-11.237	57.338	1.00	22.25
25	ATOM 167	N	MET 34	34.802	-12.321	58.317	1.00	25.50
	ATOM 168	CA	MET 34	35.750	-11.226	58.142	1.00	27.22
	ATOM 169	CB	MET 34	37.108	-11.583	58.748	1.00	24.41
	ATOM 170	CG	MET 34	38.150	-10.512	58.537	1.00	26.32
	ATOM 171	SD	MET 34	39.793	-11.040	59.074	1.00	32.95

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	ATOM 172	CE	MET 34	40.162	-12.313	57.821	1.00	30.64
	ATOM 173	C	MET 34	35.927	-10.879	56.665	1.00	29.30
	ATOM 174	O	MET 34	35.850	-9.717	56.286	1.00	29.01
	ATOM 175	N	ARG 35	36.164	-11.883	55.827	1.00	30.96
5	ATOM 176	CA	ARG 35	36.340	-11.621	54.403	1.00	32.99
	ATOM 177	CB	ARG 35	36.664	-12.913	53.641	1.00	34.85
	ATOM 178	CG	ARG 35	37.948	-13.585	54.081	1.00	38.82
	ATOM 179	CD	ARG 35	38.377	-14.682	53.126	1.00	43.22
	ATOM 180	NE	ARG 35	38.963	-15.791	53.869	1.00	47.35
10	ATOM 181	CZ	ARG 35	38.260	-16.801	54.366	1.00	47.12
	ATOM 182	NH1	ARG 35	36.946	-16.850	54.186	1.00	48.27
	ATOM 183	NH2	ARG 35	38.868	-17.746	55.064	1.00	50.91
	ATOM 184	C	ARG 35	35.090	-10.997	53.797	1.00	33.31
	ATOM 185	O	ARG 35	35.178	-10.089	52.966	1.00	33.49
15	ATOM 186	N	ARG 36	33.926	-11.493	54.206	1.00	32.00
	ATOM 187	CA	ARG 36	32.673	-10.982	53.675	1.00	31.76
	ATOM 188	CB	ARG 36	31.511	-11.857	54.158	1.00	29.95
	ATOM 189	CG	ARG 36	30.191	-11.607	53.441	1.00	31.90
	ATOM 190	CD	ARG 36	30.386	-11.434	51.929	1.00	33.67
20	ATOM 191	NE	ARG 36	29.114	-11.263	51.230	1.00	38.02
	ATOM 192	CZ	ARG 36	28.229	-12.238	51.018	1.00	40.67
	ATOM 193	NH1	ARG 36	28.477	-13.471	51.447	1.00	40.50
	ATOM 194	NH2	ARG 36	27.087	-11.979	50.382	1.00	41.02
	ATOM 195	C	ARG 36	32.459	-9.510	54.060	1.00	31.54
25	ATOM 196	O	ARG 36	31.959	-8.718	53.260	1.00	30.75
	ATOM 197	N	MET 37	32.856	-9.147	55.276	1.00	30.98
	ATOM 198	CA	MET 37	32.720	-7.774	55.742	1.00	30.21
	ATOM 199	CB	MET 37	33.134	-7.663	57.208	1.00	27.60
	ATOM 200	CG	MET 37	33.102	-6.240	57.761	1.00	27.98

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	ATOM 201	SD	MET 37	31.418	-5.613	57.981	1.00	30.18
	ATOM 202	CE	MET 37	31.115	-6.153	59.683	1.00	28.30
	ATOM 203	C	MET 37	33.598	-6.852	54.892	1.00	30.32
	ATOM 204	O	MET 37	33.162	-5.782	54.479	1.00	31.66
5	ATOM 205	N	GLN 38	34.835	-7.272	54.642	1.00	30.60
	ATOM 206	CA	GLN 38	35.774	-6.500	53.829	1.00	31.68
	ATOM 207	CB	GLN 38	37.126	-7.206	53.750	1.00	32.18
	ATOM 208	CG	GLN 38	38.051	-6.918	54.898	1.00	36.36
	ATOM 209	CD	GLN 38	39.318	-7.743	54.831	1.00	37.65
10	ATOM 210	OE1	GLN 38	39.352	-8.890	55.275	1.00	41.25
	ATOM 211	NE2	GLN 38	40.362	-7.170	54.258	1.00	39.99
	ATOM 212	C	GLN 38	35.241	-6.337	52.419	1.00	32.20
	ATOM 213	O	GLN 38	35.471	-5.318	51.769	1.00	32.83
	ATOM 214	N	LYS 39	34.541	-7.360	51.947	1.00	31.94
15	ATOM 215	CA	LYS 39	33.965	-7.343	50.611	1.00	33.33
	ATOM 216	CB	LYS 39	33.515	-8.754	50.220	1.00	34.32
	ATOM 217	CG	LYS 39	33.757	-9.105	48.756	1.00	41.05
	ATOM 218	CD	LYS 39	32.994	-8.183	47.799	1.00	43.55
	ATOM 219	CE	LYS 39	33.319	-8.502	46.336	1.00	47.30
20	ATOM 220	NZ	LYS 39	32.587	-7.625	45.363	1.00	48.42
	ATOM 221	C	LYS 39	32.774	-6.378	50.555	1.00	32.37
	ATOM 222	O	LYS 39	32.578	-5.676	49.564	1.00	33.02
	ATOM 223	N	GLU 40	31.975	-6.342	51.613	1.00	31.82
	ATOM 224	CA	GLU 40	30.831	-5.442	51.632	1.00	33.50
25	ATOM 225	CB	GLU 40	29.845	-5.831	52.737	1.00	34.39
	ATOM 226	CG	GLU 40	29.159	-7.167	52.507	1.00	36.32
	ATOM 227	CD	GLU 40	28.562	-7.293	51.112	1.00	38.53
	ATOM 228	OE1	GLU 40	27.878	-6.350	50.660	1.00	39.61
	ATOM 229	OE2	GLU 40	28.770	-8.342	50.469	1.00	38.22

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	ATOM 230	C	GLU 40	31.309	-4.009	51.833	1.00	33.20
	ATOM 231	O	GLU 40	30.691	-3.072	51.345	1.00	33.12
	ATOM 232	N	MET 41	32.409	-3.844	52.556	1.00	33.18
	ATOM 233	CA	MET 41	32.957	-2.515	52.783	1.00	34.90
5	ATOM 234	CB	MET 41	34.173	-2.585	53.706	1.00	32.91
	ATOM 235	CG	MET 41	33.838	-2.927	55.154	1.00	34.83
	ATOM 236	SD	MET 41	35.327	-2.987	56.170	1.00	34.41
	ATOM 237	CE	MET 41	35.747	-1.216	56.267	1.00	36.69
	ATOM 238	C	MET 41	33.368	-1.941	51.430	1.00	36.56
10	ATOM 239	O	MET 41	33.058	-0.792	51.108	1.00	34.98
	ATOM 240	N	ASP 42	34.054	-2.758	50.639	1.00	36.46
	ATOM 241	CA	ASP 42	34.508	-2.346	49.317	1.00	38.91
	ATOM 242	CB	ASP 42	35.318	-3.470	48.674	1.00	42.09
	ATOM 243	CG	ASP 42	36.130	-2.999	47.490	1.00	43.40
15	ATOM 244	OD1	ASP 42	37.081	-2.216	47.705	1.00	45.67
	ATOM 245	OD2	ASP 42	35.817	-3.411	46.350	1.00	42.51
	ATOM 246	C	ASP 42	33.311	-1.990	48.433	1.00	38.61
	ATOM 247	O	ASP 42	33.366	-1.036	47.656	1.00	39.03
	ATOM 248	N	ARG 43	32.232	-2.761	48.559	1.00	36.74
20	ATOM 249	CA	ARG 43	31.012	-2.524	47.788	1.00	33.90
	ATOM 250	CB	ARG 43	30.037	-3.688	47.967	1.00	33.80
	ATOM 251	CG	ARG 43	30.324	-4.890	47.080	1.00	34.68
	ATOM 252	CD	ARG 43	29.654	-6.163	47.614	1.00	34.89
	ATOM 253	NE	ARG 43	28.232	-5.997	47.906	1.00	35.11
25	ATOM 254	CZ	ARG 43	27.296	-5.729	46.998	1.00	37.42
	ATOM 255	NH1	ARG 43	27.620	-5.589	45.719	1.00	39.98
	ATOM 256	NH2	ARG 43	26.028	-5.615	47.366	1.00	36.46
	ATOM 257	C	ARG 43	30.313	-1.229	48.193	1.00	34.64
	ATOM 258	O	ARG 43	29.712	-0.550	47.357	1.00	35.89

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	ATOM 259	N	GLY 44	30.382	-0.892	49.475	1.00	31.21
	ATOM 260	CA	GLY 44	29.744	0.318	49.940	1.00	31.87
	ATOM 261	C	GLY 44	30.463	1.579	49.490	1.00	33.29
	ATOM 262	O	GLY 44	29.854	2.645	49.397	1.00	31.49
5	ATOM 263	N	LEU 45	31.756	1.455	49.200	1.00	31.44
	ATOM 264	CA	LEU 45	32.563	2.595	48.778	1.00	32.24
	ATOM 265	CB	LEU 45	34.033	2.358	49.129	1.00	27.43
	ATOM 266	CG	LEU 45	34.415	2.487	50.601	1.00	29.59
	ATOM 267	CD1	LEU 45	35.832	1.992	50.827	1.00	30.31
10	ATOM 268	CD2	LEU 45	34.281	3.941	51.022	1.00	30.45
	ATOM 269	C	LEU 45	32.455	2.933	47.294	1.00	33.00
	ATOM 270	O	LEU 45	32.537	4.098	46.924	1.00	32.78
	ATOM 271	N	ARG 46	32.277	1.911	46.460	1.00	34.18
	ATOM 272	CA	ARG 46	32.179	2.074	45.009	1.00	34.76
15	ATOM 273	CB	ARG 46	32.320	0.714	44.312	1.00	36.33
	ATOM 274	CG	ARG 46	33.519	-0.119	44.756	1.00	39.02
	ATOM 275	CD	ARG 46	34.794	0.267	44.035	1.00	43.71
	ATOM 276	NE	ARG 46	35.913	-0.593	44.431	1.00	48.60
	ATOM 277	CZ	ARG 46	37.142	-0.527	43.915	1.00	49.59
20	ATOM 278	NH1	ARG 46	37.429	0.359	42.969	1.00	49.57
	ATOM 279	NH2	ARG 46	38.091	-1.344	44.354	1.00	50.09
	ATOM 280	C	ARG 46	30.856	2.710	44.587	1.00	34.95
	ATOM 281	O	ARG 46	29.785	2.361	45.091	1.00	32.49
	ATOM 282	N	LEU 47	30.935	3.638	43.644	1.00	34.90
25	ATOM 283	CA	LEU 47	29.741	4.311	43.162	1.00	34.40
	ATOM 284	CB	LEU 47	30.100	5.297	42.049	1.00	34.27
	ATOM 285	CG	LEU 47	28.929	6.085	41.447	1.00	33.85
	ATOM 286	CD1	LEU 47	28.445	7.144	42.442	1.00	31.01
	ATOM 287	CD2	LEU 47	29.381	6.741	40.144	1.00	31.08

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	ATOM 288	C	LEU 47	28.727	3.316	42.625	1.00	34.52
	ATOM 289	O	LEU 47	27.535	3.411	42.922	1.00	32.39
	ATOM 290	N	GLU 48	29.202	2.353	41.841	1.00	34.67
	ATOM 291	CA	GLU 48	28.301	1.378	41.242	1.00	36.59
5	ATOM 292	CB	GLU 48	29.010	0.589	40.134	1.00	38.07
	ATOM 293	CG	GLU 48	30.205	-0.248	40.562	1.00	39.26
	ATOM 294	CD	GLU 48	31.499	0.534	40.580	1.00	40.85
	ATOM 295	OE1	GLU 48	32.571	-0.106	40.497	1.00	44.46
	ATOM 296	OE2	GLU 48	31.454	1.779	40.682	1.00	38.21
10	ATOM 297	C	GLU 48	27.600	0.406	42.188	1.00	37.46
	ATOM 298	O	GLU 48	26.654	-0.268	41.778	1.00	37.82
	ATOM 299	N	THR 49	28.037	0.321	43.441	1.00	36.85
	ATOM 300	CA	THR 49	27.371	-0.591	44.370	1.00	36.40
	ATOM 301	CB	THR 49	28.212	-1.855	44.645	1.00	34.37
15	ATOM 302	OG1	THR 49	29.554	-1.480	44.969	1.00	33.33
	ATOM 303	CG2	THR 49	28.215	-2.770	43.437	1.00	32.44
	ATOM 304	C	THR 49	27.032	0.037	45.703	1.00	38.54
	ATOM 305	O	THR 49	26.536	-0.647	46.599	1.00	40.86
	ATOM 306	N	HIS 50	27.272	1.335	45.842	1.00	38.89
20	ATOM 307	CA	HIS 50	26.994	1.990	47.115	1.00	41.74
	ATOM 308	CB	HIS 50	27.548	3.422	47.130	1.00	44.04
	ATOM 309	CG	HIS 50	26.666	4.426	46.451	1.00	46.35
	ATOM 310	CD2	HIS 50	25.795	5.331	46.959	1.00	48.65
	ATOM 311	ND1	HIS 50	26.607	4.565	45.081	1.00	47.18
25	ATOM 312	CE1	HIS 50	25.738	5.512	44.772	1.00	48.13
	ATOM 313	NE2	HIS 50	25.231	5.993	45.894	1.00	49.20
	ATOM 314	C	HIS 50	25.512	2.030	47.466	1.00	42.66
	ATOM 315	O	HIS 50	25.153	2.046	48.642	1.00	42.85
	ATOM 316	N	GLU 51	24.657	2.034	46.447	1.00	43.12

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	ATOM 317	CA	GLU 51	23.213	2.120	46.645	1.00	44.07
	ATOM 318	CB	GLU 51	22.555	2.574	45.329	1.00	44.83
	ATOM 319	CG	GLU 51	21.051	2.824	45.399	1.00	46.43
	ATOM 320	CD	GLU 51	20.531	3.691	44.243	1.00	48.89
5	ATOM 321	OE1	GLU 51	20.822	3.385	43.064	1.00	46.31
	ATOM 322	OE2	GLU 51	19.821	4.683	44.522	1.00	50.83
	ATOM 323	C	GLU 51	22.543	0.848	47.179	1.00	44.27
	ATOM 324	O	GLU 51	21.630	0.925	48.000	1.00	45.14
	ATOM 325	N	GLU 52	22.991	-0.317	46.723	1.00	44.47
10	ATOM 326	CA	GLU 52	22.422	-1.585	47.178	1.00	44.81
	ATOM 327	CB	GLU 52	22.199	-2.521	45.988	1.00	47.15
	ATOM 328	CG	GLU 52	23.485	-2.920	45.264	1.00	53.66
	ATOM 329	CD	GLU 52	23.698	-2.164	43.951	1.00	57.63
	ATOM 330	OE1	GLU 52	23.646	-0.909	43.953	1.00	55.90
15	ATOM 331	OE2	GLU 52	23.925	-2.835	42.917	1.00	57.72
	ATOM 332	C	GLU 52	23.313	-2.297	48.206	1.00	42.49
	ATOM 333	O	GLU 52	23.052	-3.441	48.575	1.00	43.45
	ATOM 334	N	ALA 53	24.362	-1.626	48.666	1.00	39.72
	ATOM 335	CA	ALA 53	25.285	-2.224	49.628	1.00	37.01
20	ATOM 336	CB	ALA 53	26.589	-1.438	49.645	1.00	35.23
	ATOM 337	C	ALA 53	24.700	-2.291	51.038	1.00	35.27
	ATOM 338	O	ALA 53	24.125	-1.321	51.528	1.00	34.63
	ATOM 339	N	SER 54	24.845	-3.439	51.689	1.00	32.88
	ATOM 340	CA	SER 54	24.339	-3.594	53.052	1.00	32.06
25	ATOM 341	CB	SER 54	24.397	-5.062	53.476	1.00	30.23
	ATOM 342	OG	SER 54	25.694	-5.576	53.261	1.00	35.67
	ATOM 343	C	SER 54	25.188	-2.741	53.990	1.00	28.49
	ATOM 344	O	SER 54	24.682	-2.147	54.934	1.00	29.57
	ATOM 345	N	VAL 55	26.485	-2.684	53.724	1.00	28.44



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	ATOM 346	CA	VAL 55	27.386	-1.876	54.535	1.00	28.63
	ATOM 347	CB	VAL 55	28.737	-2.594	54.726	1.00	27.89
	ATOM 348	CG1	VAL 55	29.660	-1.766	55.599	1.00	26.89
	ATOM 349	CG2	VAL 55	28.497	-3.957	55.365	1.00	27.94
5	ATOM 350	C	VAL 55	27.559	-0.551	53.788	1.00	29.80
	ATOM 351	O	VAL 55	28.367	-0.430	52.868	1.00	28.14
	ATOM 352	N	LYS 56	26.787	0.446	54.205	1.00	31.68
	ATOM 353	CA	LYS 56	26.788	1.750	53.550	1.00	30.06
	ATOM 354	CB	LYS 56	25.727	2.628	54.203	1.00	29.96
10	ATOM 355	CG	LYS 56	24.312	2.124	53.933	1.00	29.47
	ATOM 356	CD	LYS 56	23.279	2.935	54.689	1.00	31.68
	ATOM 357	CE	LYS 56	23.417	2.767	56.196	1.00	30.78
	ATOM 358	NZ	LYS 56	22.911	1.428	56.648	1.00	36.66
	ATOM 359	C	LYS 56	28.087	2.535	53.374	1.00	28.33
15	ATOM 360	O	LYS 56	28.222	3.256	52.388	1.00	30.83
	ATOM 361	N	MET 57	29.044	2.410	54.287	1.00	25.97
	ATOM 362	CA	MET 57	30.299	3.149	54.137	1.00	23.92
	ATOM 363	CB	MET 57	31.098	2.577	52.964	1.00	24.05
	ATOM 364	CG	MET 57	31.383	1.078	53.075	1.00	27.54
20	ATOM 365	SD	MET 57	32.303	0.659	54.580	1.00	26.48
	ATOM 366	CE	MET 57	33.991	1.127	54.113	1.00	21.76
	ATOM 367	C	MET 57	30.006	4.643	53.887	1.00	26.44
	ATOM 368	O	MET 57	30.460	5.237	52.903	1.00	24.39
	ATOM 369	N	LEU 58	29.250	5.235	54.803	1.00	26.42
25	ATOM 370	CA	LEU 58	28.843	6.630	54.713	1.00	26.83
	ATOM 371	CB	LEU 58	27.684	6.884	55.677	1.00	24.27
	ATOM 372	CG	LEU 58	26.440	6.043	55.386	1.00	30.26
	ATOM 373	CD1	LEU 58	25.401	6.250	56.473	1.00	28.51
	ATOM 374	CD2	LEU 58	25.874	6.430	54.016	1.00	31.10

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	ATOM 375	C	LEU 58	29.932	7.665	54.965	1.00	25.48
	ATOM 376	O	LEU 58	30.495	7.742	56.053	1.00	25.30
	ATOM 377	N	PRO 59	30.242	8.476	53.946	1.00	24.56
	ATOM 378	CD	PRO 59	29.764	8.341	52.557	1.00	24.76
5	ATOM 379	CA	PRO 59	31.262	9.528	54.063	1.00	26.48
	ATOM 380	CB	PRO 59	31.217	10.196	52.686	1.00	26.76
	ATOM 381	CG	PRO 59	30.865	9.036	51.769	1.00	26.41
	ATOM 382	C	PRO 59	30.820	10.478	55.190	1.00	26.49
	ATOM 383	O	PRO 59	29.656	10.863	55.239	1.00	28.20
10	ATOM 384	N	THR 60	31.728	10.845	56.092	1.00	27.28
	ATOM 385	CA	THR 60	31.372	11.720	57.220	1.00	27.77
	ATOM 386	CB	THR 60	31.994	11.217	58.544	1.00	24.87
	ATOM 387	OG1	THR 60	33.400	11.482	58.536	1.00	22.66
	ATOM 388	CG2	THR 60	31.767	9.713	58.726	1.00	28.80
15	ATOM 389	C	THR 60	31.800	13.196	57.085	1.00	30.72
	ATOM 390	O	THR 60	31.405	14.041	57.897	1.00	29.67
	ATOM 391	N	TYR 61	32.623	13.485	56.084	1.00	30.13
	ATOM 392	CA	TYR 61	33.144	14.824	55.844	1.00	33.87
	ATOM 393	CB	TYR 61	32.005	15.837	55.684	1.00	32.96
20	ATOM 394	CG	TYR 61	31.409	15.730	54.298	1.00	35.37
	ATOM 395	CD1	TYR 61	32.084	16.251	53.192	1.00	36.43
	ATOM 396	CE1	TYR 61	31.621	16.036	51.890	1.00	34.05
	ATOM 397	CD2	TYR 61	30.244	14.995	54.068	1.00	34.99
	ATOM 398	CE2	TYR 61	29.778	14.772	52.768	1.00	33.96
25	ATOM 399	CZ	TYR 61	30.475	15.294	51.689	1.00	33.72
	ATOM 400	OH	TYR 61	30.039	15.064	50.402	1.00	37.69
	ATOM 401	C	TYR 61	34.156	15.264	56.890	1.00	34.78
	ATOM 402	O	TYR 61	34.712	16.357	56.806	1.00	34.09
	ATOM 403	N	VAL 62	34.407	14.407	57.875	1.00	36.47

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	ATOM 404	CA	VAL 62	35.426	14.713	58.869	1.00	37.40
	ATOM 405	CB	VAL 62	35.283	13.825	60.116	1.00	37.42
	ATOM 406	CG1	VAL 62	36.410	14.107	61.089	1.00	32.97
	ATOM 407	CG2	VAL 62	33.937	14.073	60.774	1.00	36.34
5	ATOM 408	C	VAL 62	36.695	14.335	58.104	1.00	41.04
	ATOM 409	O	VAL 62	36.944	13.153	57.865	1.00	40.85
	ATOM 410	N	ARG 63	37.475	15.331	57.692	1.00	43.48
	ATOM 411	CA	ARG 63	38.682	15.070	56.909	1.00	48.27
	ATOM 412	CB	ARG 63	38.843	16.126	55.814	1.00	47.25
10	ATOM 413	CG	ARG 63	37.735	16.112	54.783	1.00	49.66
	ATOM 414	CD	ARG 63	37.648	17.447	54.061	1.00	50.62
	ATOM 415	NE	ARG 63	36.482	17.523	53.185	1.00	51.28
	ATOM 416	CZ	ARG 63	36.405	16.961	51.982	1.00	50.52
	ATOM 417	NH1	ARG 63	37.430	16.274	51.492	1.00	48.44
15	ATOM 418	NH2	ARG 63	35.295	17.089	51.268	1.00	49.50
	ATOM 419	C	ARG 63	39.952	15.006	57.728	1.00	50.30
	ATOM 420	O	ARG 63	39.998	15.478	58.860	1.00	49.69
	ATOM 421	N	SER 64	40.987	14.431	57.128	1.00	54.64
	ATOM 422	CA	SER 64	42.276	14.280	57.783	1.00	60.87
20	ATOM 423	CB	SER 64	43.315	13.760	56.794	1.00	60.13
	ATOM 424	OG	SER 64	44.492	13.381	57.481	1.00	62.83
	ATOM 425	C	SER 64	42.760	15.583	58.398	1.00	65.69
	ATOM 426	O	SER 64	42.952	16.584	57.703	1.00	65.99
	ATOM 427	N	THR 65	42.961	15.530	59.714	1.00	71.92
25	ATOM 428	CA	THR 65	43.402	16.649	60.545	1.00	77.78
	ATOM 429	CB	THR 65	44.529	16.194	61.524	1.00	78.35
	ATOM 430	OG1	THR 65	44.959	17.309	62.317	1.00	79.07
	ATOM 431	CG2	THR 65	45.714	15.611	60.757	1.00	79.19
	ATOM 432	C	THR 65	43.839	17.925	59.817	1.00	80.90

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	ATOM 433	O	THR 65	45.033	18.188	59.654	1.00	80.93
	ATOM 434	N	PRO 66	42.863	18.732	59.364	1.00	83.72
	ATOM 435	CD	PRO 66	41.410	18.469	59.372	1.00	84.56
	ATOM 436	CA	PRO 66	43.162	19.983	58.661	1.00	85.58
5	ATOM 437	CB	PRO 66	41.871	20.254	57.897	1.00	85.53
	ATOM 438	CG	PRO 66	40.827	19.776	58.864	1.00	85.36
	ATOM 439	C	PRO 66	43.468	21.057	59.710	1.00	87.07
	ATOM 440	O	PRO 66	42.581	21.812	60.119	1.00	87.87
	ATOM 441	N	GLU 67	44.726	21.109	60.144	1.00	87.71
10	ATOM 442	CA	GLU 67	45.162	22.055	61.169	1.00	87.66
	ATOM 443	CB	GLU 67	46.683	22.238	61.110	1.00	88.42
	ATOM 444	CG	GLU 67	47.283	22.824	62.384	1.00	89.15
	ATOM 445	CD	GLU 67	46.871	22.058	63.636	1.00	89.71
	ATOM 446	OE1	GLU 67	45.689	22.150	64.037	1.00	89.95
15	ATOM 447	OE2	GLU 67	47.728	21.359	64.217	1.00	89.51
	ATOM 448	C	GLU 67	44.463	23.413	61.095	1.00	86.97
	ATOM 449	O	GLU 67	44.203	23.944	60.013	1.00	86.95
	ATOM 450	N	GLY 68	44.160	23.962	62.266	1.00	85.72
	ATOM 451	CA	GLY 68	43.475	25.237	62.344	1.00	83.56
20	ATOM 452	C	GLY 68	42.274	25.073	63.251	1.00	82.01
	ATOM 453	O	GLY 68	41.136	24.970	62.784	1.00	82.39
	ATOM 454	N	SER 69	42.530	25.038	64.555	1.00	79.39
	ATOM 455	CA	SER 69	41.469	24.869	65.537	1.00	77.31
	ATOM 456	CB	SER 69	41.855	23.784	66.542	1.00	77.69
25	ATOM 457	OG	SER 69	40.877	23.677	67.561	1.00	78.20
	ATOM 458	C	SER 69	41.118	26.143	66.294	1.00	75.21
	ATOM 459	O	SER 69	41.993	26.857	66.784	1.00	74.23
	ATOM 460	N	GLU 70	39.822	26.413	66.386	1.00	73.26
	ATOM 461	CA	GLU 70	39.328	27.581	67.096	1.00	71.89

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	ATOM 462	CB	GLU 70	38.004	28.042	66.482	1.00	73.40
	ATOM 463	CG	GLU 70	37.897	29.544	66.297	1.00	77.84
	ATOM 464	CD	GLU 70	38.900	30.073	65.285	1.00	80.27
	ATOM 465	OE1	GLU 70	38.763	29.757	64.082	1.00	81.41
5	ATOM 466	OE2	GLU 70	39.830	30.801	65.692	1.00	81.33
	ATOM 467	C	GLU 70	39.107	27.144	68.543	1.00	69.48
	ATOM 468	O	GLU 70	38.409	26.163	68.789	1.00	69.73
	ATOM 469	N	VAL 71	39.701	27.853	69.499	1.00	65.92
	ATOM 470	CA	VAL 71	39.536	27.490	70.904	1.00	62.64
10	ATOM 471	CB	VAL 71	40.760	27.909	71.746	1.00	61.59
	ATOM 472	CG1	VAL 71	41.993	27.156	71.275	1.00	61.91
	ATOM 473	CG2	VAL 71	40.979	29.406	71.642	1.00	61.78
	ATOM 474	C	VAL 71	38.278	28.105	71.510	1.00	61.05
	ATOM 475	O	VAL 71	37.608	28.919	70.877	1.00	61.02
15	ATOM 476	N	GLY 72	37.952	27.700	72.734	1.00	59.60
	ATOM 477	CA	GLY 72	36.769	28.225	73.390	1.00	58.10
	ATOM 478	C	GLY 72	35.841	27.169	73.967	1.00	57.74
	ATOM 479	O	GLY 72	36.178	25.982	74.006	1.00	58.27
	ATOM 480	N	ASP 73	34.664	27.607	74.410	1.00	55.55
20	ATOM 481	CA	ASP 73	33.663	26.724	75.003	1.00	54.21
	ATOM 482	CB	ASP 73	32.973	27.426	76.181	1.00	57.20
	ATOM 483	CG	ASP 73	33.846	27.496	77.424	1.00	59.78
	ATOM 484	OD1	ASP 73	35.046	27.830	77.299	1.00	61.37
	ATOM 485	OD2	ASP 73	33.324	27.225	78.529	1.00	60.87
25	ATOM 486	C	ASP 73	32.599	26.310	73.994	1.00	52.36
	ATOM 487	O	ASP 73	31.936	27.161	73.406	1.00	52.44
	ATOM 488	N	PHE 74	32.424	25.005	73.800	1.00	49.73
	ATOM 489	CA	PHE 74	31.412	24.519	72.866	1.00	46.98
	ATOM 490	CB	PHE 74	32.019	23.571	71.837	1.00	46.41

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	ATOM 491	CG	PHE 74	33.117	24.179	71.030	1.00	47.09
	ATOM 492	CD1	PHE 74	34.335	24.492	71.618	1.00	47.62
	ATOM 493	CD2	PHE 74	32.930	24.452	69.681	1.00	47.01
	ATOM 494	CE1	PHE 74	35.359	25.071	70.874	1.00	49.47
5	ATOM 495	CE2	PHE 74	33.943	25.031	68.924	1.00	48.12
	ATOM 496	CZ	PHE 74	35.161	25.342	69.520	1.00	48.82
	ATOM 497	C	PHE 74	30.316	23.783	73.601	1.00	45.68
	ATOM 498	O	PHE 74	30.485	23.382	74.745	1.00	46.35
	ATOM 499	N	LEU 75	29.185	23.615	72.932	1.00	45.12
10	ATOM 500	CA	LEU 75	28.064	22.895	73.501	1.00	44.80
	ATOM 501	CB	LEU 75	26.769	23.686	73.333	1.00	43.29
	ATOM 502	CG	LEU 75	25.535	23.023	73.959	1.00	45.05
	ATOM 503	CD1	LEU 75	25.529	23.278	75.466	1.00	41.53
	ATOM 504	CD2	LEU 75	24.259	23.571	73.326	1.00	43.45
15	ATOM 505	C	LEU 75	27.971	21.598	72.708	1.00	46.04
	ATOM 506	O	LEU 75	28.087	21.611	71.479	1.00	46.97
	ATOM 507	N	SER 76	27.770	20.484	73.405	1.00	45.48
	ATOM 508	CA	SER 76	27.664	19.189	72.744	1.00	43.73
	ATOM 509	CB	SER 76	28.837	18.295	73.143	1.00	43.52
20	ATOM 510	OG	SER 76	30.040	18.741	72.551	1.00	44.64
	ATOM 511	C	SER 76	26.361	18.469	73.051	1.00	41.60
	ATOM 512	O	SER 76	26.026	18.242	74.209	1.00	40.88
	ATOM 513	N	LEU 77	25.617	18.130	72.007	1.00	41.06
	ATOM 514	CA	LEU 77	24.369	17.397	72.175	1.00	43.50
25	ATOM 515	CB	LEU 77	23.281	17.918	71.225	1.00	43.84
	ATOM 516	CG	LEU 77	22.750	19.346	71.401	1.00	45.70
	ATOM 517	CD1	LEU 77	21.587	19.577	70.442	1.00	45.96
	ATOM 518	CD2	LEU 77	22.284	19.550	72.835	1.00	46.75
	ATOM 519	C	LEU 77	24.662	15.933	71.851	1.00	43.78

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	ATOM 520	O	LEU 77	25.529	15.635	71.026	1.00	43.07
	ATOM 521	N	ASP 78	23.946	15.021	72.496	1.00	44.50
	ATOM 522	CA	ASP 78	24.151	13.604	72.244	1.00	44.82
	ATOM 523	CB	ASP 78	25.126	13.026	73.271	1.00	44.71
5	ATOM 524	CG	ASP 78	25.597	11.628	72.905	1.00	45.55
	ATOM 525	OD1	ASP 78	24.738	10.750	72.672	1.00	41.76
	ATOM 526	OD2	ASP 78	26.828	11.410	72.853	1.00	45.32
	ATOM 527	C	ASP 78	22.838	12.829	72.276	1.00	44.74
	ATOM 528	O	ASP 78	22.245	12.633	73.333	1.00	45.25
10	ATOM 529	N	LEU 79	22.385	12.398	71.107	1.00	45.72
	ATOM 530	CA	LEU 79	21.154	11.630	70.994	1.00	47.25
	ATOM 531	CB	LEU 79	20.137	12.351	70.116	1.00	45.37
	ATOM 532	CG	LEU 79	18.865	11.530	69.915	1.00	43.65
	ATOM 533	CD1	LEU 79	18.067	11.553	71.200	1.00	46.42
15	ATOM 534	CD2	LEU 79	18.045	12.086	68.777	1.00	43.81
	ATOM 535	C	LEU 79	21.491	10.295	70.354	1.00	49.50
	ATOM 536	O	LEU 79	22.073	10.249	69.274	1.00	49.35
	ATOM 537	N	GLY 80	21.123	9.207	71.016	1.00	52.24
	ATOM 538	CA	GLY 80	21.421	7.902	70.466	1.00	56.31
20	ATOM 539	C	GLY 80	20.965	6.833	71.420	1.00	59.13
	ATOM 540	O	GLY 80	20.278	5.896	71.027	1.00	60.86
	ATOM 541	N	GLY 81	21.360	6.966	72.679	1.00	62.30
	ATOM 542	CA	GLY 81	20.940	6.002	73.674	1.00	65.60
	ATOM 543	C	GLY 81	19.551	6.395	74.137	1.00	67.84
25	ATOM 544	O	GLY 81	18.936	7.301	73.564	1.00	69.00
	ATOM 545	N	THR 82	19.047	5.722	75.165	1.00	69.33
	ATOM 546	CA	THR 82	17.726	6.037	75.695	1.00	70.36
	ATOM 547	CB	THR 82	17.110	4.824	76.418	1.00	71.43
	ATOM 548	OG1	THR 82	18.032	4.332	77.398	1.00	71.60

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	ATOM 549	CG2	THR 82	16.784	3.716	75.420	1.00	71.87
	ATOM 550	C	THR 82	17.846	7.196	76.679	1.00	70.10
	ATOM 551	O	THR 82	16.933	7.458	77.464	1.00	71.18
	ATOM 552	N	ASN 83	18.981	7.887	76.625	1.00	69.08
5	ATOM 553	CA	ASN 83	19.232	9.017	77.508	1.00	68.14
	ATOM 554	CB	ASN 83	20.161	8.584	78.646	1.00	69.98
	ATOM 555	CG	ASN 83	19.862	9.300	79.948	1.00	70.80
	ATOM 556	OD1	ASN 83	20.627	9.213	80.909	1.00	71.46
	ATOM 557	ND2	ASN 83	18.739	10.004	79.990	1.00	72.56
10	ATOM 558	C	ASN 83	19.866	10.177	76.738	1.00	66.16
	ATOM 559	O	ASN 83	21.050	10.136	76.407	1.00	66.52
	ATOM 560	N	PHE 84	19.073	11.203	76.447	1.00	63.41
	ATOM 561	CA	PHE 84	19.567	12.375	75.728	1.00	60.93
	ATOM 562	CB	PHE 84	18.398	13.227	75.241	1.00	61.87
15	ATOM 563	CG	PHE 84	18.817	14.477	74.528	1.00	63.55
	ATOM 564	CD1	PHE 84	18.419	15.724	74.993	1.00	63.38
	ATOM 565	CD2	PHE 84	19.599	14.409	73.381	1.00	64.28
	ATOM 566	CE1	PHE 84	18.793	16.888	74.325	1.00	64.07
	ATOM 567	CE2	PHE 84	19.979	15.568	72.705	1.00	65.31
20	ATOM 568	CZ	PHE 84	19.574	16.810	73.179	1.00	64.75
	ATOM 569	C	PHE 84	20.442	13.206	76.658	1.00	59.07
	ATOM 570	O	PHE 84	20.011	13.582	77.744	1.00	59.19
	ATOM 571	N	ARG 85	21.665	13.500	76.232	1.00	57.25
	ATOM 572	CA	ARG 85	22.583	14.272	77.064	1.00	56.05
25	ATOM 573	CB	ARG 85	23.857	13.467	77.344	1.00	56.68
	ATOM 574	CG	ARG 85	23.605	12.044	77.828	1.00	58.78
	ATOM 575	CD	ARG 85	24.896	11.367	78.267	1.00	59.39
	ATOM 576	NE	ARG 85	25.908	11.348	77.213	1.00	59.87
	ATOM 577	CZ	ARG 85	27.068	11.994	77.282	1.00	60.09



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	ATOM 578	NH1	ARG	85	27.366	12.713	78.357	1.00	59.50
	ATOM 579	NH2	ARG	85	27.931	11.920	76.277	1.00	60.92
	ATOM 580	C	ARG	85	22.966	15.602	76.433	1.00	55.07
	ATOM 581	O	ARG	85	23.038	15.725	75.209	1.00	54.93
5	ATOM 582	N	VAL	86	23.211	16.593	77.288	1.00	53.13
	ATOM 583	CA	VAL	86	23.598	17.935	76.861	1.00	51.01
	ATOM 584	CB	VAL	86	22.425	18.939	77.003	1.00	51.19
	ATOM 585	CG1	VAL	86	22.851	20.313	76.509	1.00	51.39
	ATOM 586	CG2	VAL	86	21.216	18.446	76.225	1.00	50.96
10	ATOM 587	C	VAL	86	24.734	18.381	77.767	1.00	49.34
	ATOM 588	O	VAL	86	24.613	18.316	78.989	1.00	48.07
	ATOM 589	N	MET	87	25.834	18.835	77.178	1.00	49.52
	ATOM 590	CA	MET	87	26.970	19.260	77.981	1.00	50.78
	ATOM 591	CB	MET	87	27.864	18.054	78.284	1.00	52.70
15	ATOM 592	CG	MET	87	28.572	17.461	77.072	1.00	54.49
	ATOM 593	SD	MET	87	29.005	15.694	77.269	1.00	53.62
	ATOM 594	CE	MET	87	27.839	14.951	76.090	1.00	51.63
	ATOM 595	C	MET	87	27.800	20.363	77.348	1.00	50.56
	ATOM 596	O	MET	87	27.715	20.616	76.149	1.00	50.18
20	ATOM 597	N	LEU	88	28.605	21.015	78.178	1.00	50.90
	ATOM 598	CA	LEU	88	29.477	22.093	77.739	1.00	52.10
	ATOM 599	CB	LEU	88	29.278	23.325	78.631	1.00	53.23
	ATOM 600	CG	LEU	88	30.087	24.580	78.288	1.00	54.71
	ATOM 601	CD1	LEU	88	29.618	25.140	76.951	1.00	54.33
25	ATOM 602	CD2	LEU	88	29.920	25.623	79.390	1.00	54.33
	ATOM 603	C	LEU	88	30.914	21.600	77.847	1.00	52.33
	ATOM 604	O	LEU	88	31.311	21.048	78.877	1.00	53.12
	ATOM 605	N	VAL	89	31.693	21.795	76.789	1.00	52.10
	ATOM 606	CA	VAL	89	33.078	21.342	76.788	1.00	52.46

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	ATOM 607	CB	VAL 89	33.241	20.072	75.882	1.00	50.52
	ATOM 608	CG1	VAL 89	32.289	20.147	74.710	1.00	52.35
	ATOM 609	CG2	VAL 89	34.674	19.939	75.388	1.00	46.86
	ATOM 610	C	VAL 89	34.049	22.433	76.357	1.00	53.35
5	ATOM 611	O	VAL 89	33.858	23.081	75.336	1.00	54.69
	ATOM 612	N	LYS 90	35.096	22.625	77.151	1.00	55.22
	ATOM 613	CA	LYS 90	36.100	23.640	76.868	1.00	56.94
	ATOM 614	CB	LYS 90	36.656	24.205	78.181	1.00	57.66
	ATOM 615	CG	LYS 90	37.642	25.360	78.005	1.00	58.70
10	ATOM 616	CD	LYS 90	38.140	25.909	79.345	1.00	59.35
	ATOM 617	CE	LYS 90	36.995	26.399	80.226	1.00	60.64
	ATOM 618	NZ	LYS 90	36.185	27.462	79.568	1.00	61.04
	ATOM 619	C	LYS 90	37.237	23.078	76.019	1.00	57.63
	ATOM 620	O	LYS 90	37.921	22.136	76.417	1.00	57.69
15	ATOM 621	N	VAL 91	37.428	23.670	74.846	1.00	58.29
	ATOM 622	CA	VAL 91	38.473	23.254	73.919	1.00	57.11
	ATOM 623	CB	VAL 91	37.920	23.136	72.480	1.00	56.48
	ATOM 624	CG1	VAL 91	39.010	22.661	71.533	1.00	55.29
	ATOM 625	CG2	VAL 91	36.741	22.183	72.459	1.00	55.52
20	ATOM 626	C	VAL 91	39.598	24.279	73.926	1.00	57.81
	ATOM 627	O	VAL 91	39.365	25.466	73.710	1.00	59.53
	ATOM 628	N	GLY 92	40.817	23.819	74.172	1.00	58.12
	ATOM 629	CA	GLY 92	41.947	24.723	74.200	1.00	59.69
	ATOM 630	C	GLY 92	43.047	24.245	73.286	1.00	61.78
25	ATOM 631	O	GLY 92	42.821	23.381	72.448	1.00	61.06
	ATOM 632	N	GLU 93	44.240	24.803	73.449	1.00	65.18
	ATOM 633	CA	GLU 93	45.373	24.426	72.619	1.00	69.00
	ATOM 634	CB	GLU 93	45.897	25.646	71.866	1.00	71.56
	ATOM 635	CG	GLU 93	47.082	25.344	70.965	1.00	75.20

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	ATOM 636	CD	GLU 93	47.659	26.591	70.325	1.00	78.28
	ATOM 637	OE1	GLU 93	46.893	27.326	69.659	1.00	80.05
	ATOM 638	OE2	GLU 93	48.877	26.834	70.485	1.00	79.21
	ATOM 639	C	GLU 93	46.505	23.822	73.437	1.00	71.00
5	ATOM 640	O	GLU 93	47.118	24.500	74.263	1.00	70.74
	ATOM 641	N	GLY 94	46.784	22.544	73.195	1.00	72.97
	ATOM 642	CA	GLY 94	47.849	21.869	73.916	1.00	74.44
	ATOM 643	C	GLY 94	49.078	21.673	73.052	1.00	75.82
	ATOM 644	O	GLY 94	49.485	22.577	72.315	1.00	76.47
10	ATOM 645	N	GLU 95	49.682	20.496	73.145	1.00	75.73
	ATOM 646	CA	GLU 95	50.859	20.195	72.349	1.00	76.61
	ATOM 647	CB	GLU 95	52.023	19.792	73.249	1.00	76.93
	ATOM 648	CG	GLU 95	52.439	20.891	74.203	1.00	78.31
	ATOM 649	CD	GLU 95	53.614	20.497	75.065	1.00	78.40
15	ATOM 650	OE1	GLU 95	54.715	20.274	74.514	1.00	78.51
	ATOM 651	OE2	GLU 95	53.432	20.408	76.295	1.00	78.60
	ATOM 652	C	GLU 95	50.516	19.071	71.392	1.00	76.91
	ATOM 653	O	GLU 95	49.833	18.116	71.764	1.00	76.81
	ATOM 654	N	GLU 96	50.987	19.203	70.155	1.00	77.78
20	ATOM 655	CA	GLU 96	50.733	18.220	69.105	1.00	78.07
	ATOM 656	CB	GLU 96	51.408	16.881	69.440	1.00	81.32
	ATOM 657	CG	GLU 96	52.943	16.930	69.454	1.00	85.11
	ATOM 658	CD	GLU 96	53.541	17.309	68.101	1.00	87.05
	ATOM 659	OE1	GLU 96	53.346	16.551	67.124	1.00	88.73
25	ATOM 660	OE2	GLU 96	54.207	18.365	68.014	1.00	87.56
	ATOM 661	C	GLU 96	49.230	18.025	68.919	1.00	75.88
	ATOM 662	O	GLU 96	48.784	17.039	68.327	1.00	75.92
	ATOM 663	N	GLY 97	48.456	18.980	69.427	1.00	72.88
	ATOM 664	CA	GLY 97	47.013	18.910	69.309	1.00	69.37

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	ATOM 665	C	GLY 97	46.296	19.710	70.380	1.00	67.02
	ATOM 666	O	GLY 97	46.921	20.230	71.305	1.00	67.10
	ATOM 667	N	GLN 98	44.978	19.811	70.250	1.00	64.76
	ATOM 668	CA	GLN 98	44.166	20.543	71.211	1.00	62.45
5	ATOM 669	CB	GLN 98	42.872	21.045	70.562	1.00	62.69
	ATOM 670	CG	GLN 98	43.026	21.908	69.315	1.00	64.93
	ATOM 671	CD	GLN 98	43.191	21.095	68.046	1.00	65.89
	ATOM 672	OE1	GLN 98	44.299	20.684	67.696	1.00	65.96
	ATOM 673	NE2	GLN 98	42.079	20.847	67.353	1.00	65.22
10	ATOM 674	C	GLN 98	43.781	19.630	72.369	1.00	61.23
	ATOM 675	O	GLN 98	43.880	18.403	72.269	1.00	62.18
	ATOM 676	N	TRP 99	43.356	20.233	73.473	1.00	57.45
	ATOM 677	CA	TRP 99	42.893	19.459	74.611	1.00	54.44
	ATOM 678	CB	TRP 99	43.639	19.822	75.904	1.00	55.51
15	ATOM 679	CG	TRP 99	43.770	21.291	76.211	1.00	56.94
	ATOM 680	CD2	TRP 99	42.763	22.151	76.756	1.00	56.03
	ATOM 681	CE2	TRP 99	43.345	23.426	76.922	1.00	57.25
	ATOM 682	CE3	TRP 99	41.422	21.969	77.121	1.00	56.67
	ATOM 683	CD1	TRP 99	44.892	22.062	76.068	1.00	56.29
20	ATOM 684	NE1	TRP 99	44.647	23.342	76.495	1.00	56.55
	ATOM 685	CZ2	TRP 99	42.635	24.516	77.440	1.00	56.53
	ATOM 686	CZ3	TRP 99	40.712	23.053	77.637	1.00	56.67
	ATOM 687	CH2	TRP 99	41.322	24.309	77.790	1.00	56.70
	ATOM 688	C	TRP 99	41.408	19.756	74.737	1.00	52.04
25	ATOM 689	O	TRP 99	40.899	20.664	74.089	1.00	50.70
	ATOM 690	N	SER 100	40.704	18.981	75.545	1.00	49.57
	ATOM 691	CA	SER 100	39.277	19.186	75.715	1.00	48.29
	ATOM 692	CB	SER 100	38.506	18.475	74.597	1.00	49.26
	ATOM 693	OG	SER 100	39.055	17.196	74.315	1.00	47.27

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	ATOM 694	C	SER	100	38.860	18.655	77.067	1.00	47.91
	ATOM 695	O	SER	100	39.569	17.845	77.662	1.00	48.73
	ATOM 696	N	VAL	101	37.718	19.120	77.558	1.00	47.53
	ATOM 697	CA	VAL	101	37.225	18.684	78.852	1.00	47.86
5	ATOM 698	CB	VAL	101	38.102	19.233	79.995	1.00	47.92
	ATOM 699	CG1	VAL	101	38.160	20.747	79.923	1.00	49.02
	ATOM 700	CG2	VAL	101	37.545	18.783	81.342	1.00	47.98
	ATOM 701	C	VAL	101	35.784	19.102	79.101	1.00	48.77
	ATOM 702	O	VAL	101	35.391	20.228	78.798	1.00	49.05
10	ATOM 703	N	LYS	102	35.004	18.176	79.649	1.00	49.04
	ATOM 704	CA	LYS	102	33.607	18.422	79.969	1.00	50.31
	ATOM 705	CB	LYS	102	32.875	17.101	80.220	1.00	51.15
	ATOM 706	CG	LYS	102	31.385	17.263	80.452	1.00	52.57
	ATOM 707	CD	LYS	102	30.835	16.229	81.425	1.00	56.56
15	ATOM 708	CE	LYS	102	30.955	14.804	80.908	1.00	57.06
	ATOM 709	NZ	LYS	102	30.275	13.804	81.787	1.00	58.08
	ATOM 710	C	LYS	102	33.587	19.254	81.243	1.00	51.12
	ATOM 711	O	LYS	102	34.220	18.888	82.234	1.00	52.47
	ATOM 712	N	THR	103	32.859	20.366	81.217	1.00	51.40
20	ATOM 713	CA	THR	103	32.774	21.252	82.373	1.00	50.47
	ATOM 714	CB	THR	103	33.004	22.715	81.965	1.00	50.28
	ATOM 715	OG1	THR	103	31.992	23.113	81.032	1.00	51.29
	ATOM 716	CG2	THR	103	34.368	22.879	81.324	1.00	47.52
	ATOM 717	C	THR	103	31.416	21.148	83.048	1.00	50.90
25	ATOM 718	O	THR	103	31.329	21.056	84.268	1.00	50.91
	ATOM 719	N	LYS	104	30.358	21.162	82.247	1.00	52.41
	ATOM 720	CA	LYS	104	29.000	21.063	82.770	1.00	54.04
	ATOM 721	CB	LYS	104	28.310	22.436	82.714	1.00	57.21
	ATOM 722	CG	LYS	104	28.823	23.450	83.739	1.00	59.16

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	ATOM 723	CD	LYS	104	28.138	24.809	83.576	1.00	62.54
	ATOM 724	CE	LYS	104	28.398	25.734	84.766	1.00	62.99
	ATOM 725	NZ	LYS	104	27.798	25.217	86.037	1.00	64.17
	ATOM 726	C	LYS	104	28.215	20.047	81.948	1.00	53.79
5	ATOM 727	O	LYS	104	28.411	19.941	80.740	1.00	53.53
	ATOM 728	N	HIS	105	27.330	19.299	82.600	1.00	53.65
	ATOM 729	CA	HIS	105	26.539	18.295	81.903	1.00	55.05
	ATOM 730	CB	HIS	105	27.316	16.972	81.837	1.00	55.94
	ATOM 731	CG	HIS	105	27.668	16.397	83.176	1.00	55.84
10	ATOM 732	CD2	HIS	105	28.793	16.501	83.924	1.00	55.19
	ATOM 733	ND1	HIS	105	26.803	15.602	83.897	1.00	55.83
	ATOM 734	CE1	HIS	105	27.380	15.241	85.030	1.00	56.35
	ATOM 735	NE2	HIS	105	28.589	15.773	85.071	1.00	55.64
	ATOM 736	C	HIS	105	25.169	18.074	82.534	1.00	56.32
15	ATOM 737	O	HIS	105	24.903	18.535	83.640	1.00	56.55
	ATOM 738	N	GLN	106	24.302	17.365	81.817	1.00	58.21
	ATOM 739	CA	GLN	106	22.950	17.090	82.289	1.00	60.74
	ATOM 740	CB	GLN	106	22.108	18.367	82.224	1.00	61.97
	ATOM 741	CG	GLN	106	20.775	18.285	82.945	1.00	64.86
20	ATOM 742	CD	GLN	106	20.928	18.379	84.447	1.00	67.03
	ATOM 743	OE1	GLN	106	21.447	19.370	84.969	1.00	68.82
	ATOM 744	NE2	GLN	106	20.479	17.348	85.155	1.00	67.41
	ATOM 745	C	GLN	106	22.322	16.025	81.396	1.00	61.62
	ATOM 746	O	GLN	106	22.532	16.027	80.186	1.00	62.03
25	ATOM 747	N	MET	107	21.550	15.121	81.990	1.00	63.03
	ATOM 748	CA	MET	107	20.900	14.058	81.232	1.00	64.74
	ATOM 749	CB	MET	107	21.322	12.688	81.769	1.00	66.23
	ATOM 750	CG	MET	107	22.821	12.456	81.786	1.00	68.74
	ATOM 751	SD	MET	107	23.248	10.812	82.388	1.00	70.84

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	ATOM 752	CE	MET	107	23.427	9.926	80.853	1.00	71.13
	ATOM 753	C	MET	107	19.385	14.175	81.313	1.00	65.81
	ATOM 754	O	MET	107	18.837	14.489	82.369	1.00	65.52
	ATOM 755	N	TYR	108	18.712	13.915	80.196	1.00	66.87
5	ATOM 756	CA	TYR	108	17.258	13.984	80.143	1.00	68.20
	ATOM 757	CB	TYR	108	16.800	15.167	79.286	1.00	67.20
	ATOM 758	CG	TYR	108	17.436	16.484	79.660	1.00	66.35
	ATOM 759	CD1	TYR	108	18.781	16.731	79.386	1.00	65.95
	ATOM 760	CE1	TYR	108	19.380	17.929	79.746	1.00	65.76
10	ATOM 761	CD2	TYR	108	16.702	17.477	80.307	1.00	66.24
	ATOM 762	CE2	TYR	108	17.292	18.683	80.674	1.00	65.93
	ATOM 763	CZ	TYR	108	18.633	18.902	80.391	1.00	66.14
	ATOM 764	OH	TYR	108	19.235	20.083	80.763	1.00	64.27
	ATOM 765	C	TYR	108	16.706	12.700	79.549	1.00	70.20
15	ATOM 766	O	TYR	108	16.995	12.363	78.404	1.00	70.55
	ATOM 767	N	SER	109	15.912	11.982	80.331	1.00	73.54
	ATOM 768	CA	SER	109	15.322	10.739	79.863	1.00	76.84
	ATOM 769	CB	SER	109	14.524	10.082	80.992	1.00	77.63
	ATOM 770	OG	SER	109	15.353	9.837	82.120	1.00	78.13
20	ATOM 771	C	SER	109	14.419	11.020	78.664	1.00	78.98
	ATOM 772	O	SER	109	13.936	12.138	78.486	1.00	78.51
	ATOM 773	N	ILE	110	14.198	10.002	77.841	1.00	82.34
	ATOM 774	CA	ILE	110	13.369	10.143	76.651	1.00	86.07
	ATOM 775	CB	ILE	110	13.892	9.249	75.511	1.00	86.28
25	ATOM 776	CG2	ILE	110	13.092	9.505	74.242	1.00	86.56
	ATOM 777	CG1	ILE	110	15.379	9.529	75.275	1.00	86.19
	ATOM 778	CD1	ILE	110	16.025	8.612	74.258	1.00	86.76
	ATOM 779	C	ILE	110	11.916	9.772	76.927	1.00	88.58
	ATOM 780	O	ILE	110	11.596	8.606	77.152	1.00	88.69

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	ATOM 781	N	PRO	111	11.016	10.767	76.910	1.00	91.13
	ATOM 782	CD	PRO	111	11.319	12.205	76.811	1.00	91.83
	ATOM 783	CA	PRO	111	9.585	10.562	77.157	1.00	93.32
	ATOM 784	CB	PRO	111	9.015	11.975	77.062	1.00	93.16
5	ATOM 785	CG	PRO	111	10.147	12.819	77.536	1.00	92.31
	ATOM 786	C	PRO	111	8.928	9.613	76.159	1.00	95.40
	ATOM 787	O	PRO	111	9.466	9.355	75.082	1.00	95.80
	ATOM 788	N	GLU	112	7.758	9.101	76.529	1.00	97.55
	ATOM 789	CA	GLU	112	7.006	8.185	75.679	1.00	99.50
10	ATOM 790	CB	GLU	112	5.816	7.611	76.458	1.00	100.31
	ATOM 791	CG	GLU	112	4.745	6.971	75.589	1.00	101.76
	ATOM 792	CD	GLU	112	5.316	5.989	74.587	1.00	102.84
	ATOM 793	OE1	GLU	112	5.967	5.012	75.014	1.00	103.66
	ATOM 794	OE2	GLU	112	5.113	6.196	73.372	1.00	103.00
15	ATOM 795	C	GLU	112	6.508	8.884	74.418	1.00	100.37
	ATOM 796	O	GLU	112	6.914	8.545	73.304	1.00	100.17
	ATOM 797	N	ASP	113	5.625	9.859	74.606	1.00	101.44
	ATOM 798	CA	ASP	113	5.056	10.620	73.499	1.00	102.05
	ATOM 799	CB	ASP	113	4.087	11.680	74.038	1.00	102.23
20	ATOM 800	CG	ASP	113	4.682	12.494	75.177	1.00	102.33
	ATOM 801	OD1	ASP	113	4.961	11.913	76.249	1.00	102.01
	ATOM 802	OD2	ASP	113	4.870	13.716	74.999	1.00	101.99
	ATOM 803	C	ASP	113	6.131	11.282	72.638	1.00	102.09
	ATOM 804	O	ASP	113	5.843	11.789	71.553	1.00	101.96
25	ATOM 805	N	ALA	114	7.368	11.273	73.126	1.00	102.12
	ATOM 806	CA	ALA	114	8.484	11.869	72.401	1.00	102.09
	ATOM 807	CB	ALA	114	9.590	12.256	73.377	1.00	101.76
	ATOM 808	C	ALA	114	9.022	10.895	71.358	1.00	102.06
	ATOM 809	O	ALA	114	9.763	11.282	70.455	1.00	101.89



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	ATOM 810	N	MET	115	8.640	9.630	71.491	1.00102.04
	ATOM 811	CA	MET	115	9.081	8.592	70.569	1.00102.05
	ATOM 812	CB	MET	115	9.466	7.331	71.346	1.00102.77
	ATOM 813	CG	MET	115	10.637	7.509	72.307	1.00103.47
5	ATOM 814	SD	MET	115	12.256	7.549	71.502	1.00104.26
	ATOM 815	CE	MET	115	12.740	5.824	71.638	1.00103.48
	ATOM 816	C	MET	115	8.004	8.253	69.538	1.00101.77
	ATOM 817	O	MET	115	8.268	8.275	68.337	1.00102.14
	ATOM 818	N	THR	116	6.796	7.942	70.006	1.00101.14
10	ATOM 819	CA	THR	116	5.690	7.590	69.110	1.00100.36
	ATOM 820	CB	THR	116	4.517	6.927	69.880	1.00100.42
	ATOM 821	OG1	THR	116	5.004	5.805	70.625	1.00100.29
	ATOM 822	CG2	THR	116	3.441	6.441	68.911	1.00100.05
	ATOM 823	C	THR	116	5.150	8.816	68.379	1.00 99.62
15	ATOM 824	O	THR	116	4.423	8.694	67.391	1.00 99.72
	ATOM 825	N	GLY	117	5.510	9.996	68.870	1.00 98.62
	ATOM 826	CA	GLY	117	5.048	11.224	68.252	1.00 97.42
	ATOM 827	C	GLY	117	5.619	11.447	66.866	1.00 96.48
	ATOM 828	O	GLY	117	5.746	10.511	66.074	1.00 96.38
20	ATOM 829	N	THR	118	5.962	12.696	66.570	1.00 95.25
	ATOM 830	CA	THR	118	6.521	13.050	65.273	1.00 93.78
	ATOM 831	CB	THR	118	5.679	14.133	64.578	1.00 93.57
	ATOM 832	OG1	THR	118	5.735	15.343	65.342	1.00 93.50
	ATOM 833	CG2	THR	118	4.234	13.685	64.457	1.00 93.65
25	ATOM 834	C	THR	118	7.936	13.583	65.440	1.00 92.67
	ATOM 835	O	THR	118	8.335	13.976	66.537	1.00 92.39
	ATOM 836	N	ALA	119	8.687	13.593	64.343	1.00 91.30
	ATOM 837	CA	ALA	119	10.058	14.084	64.356	1.00 90.00
	ATOM 838	CB	ALA	119	10.643	14.031	62.956	1.00 89.81

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	ATOM 839	C	ALA	119	10.066	15.513	64.867	1.00	89.21
	ATOM 840	O	ALA	119	11.045	15.972	65.455	1.00	88.98
	ATOM 841	N	GLU	120	8.959	16.210	64.636	1.00	88.61
	ATOM 842	CA	GLU	120	8.819	17.593	65.063	1.00	87.61
5	ATOM 843	CB	GLU	120	7.505	18.177	64.536	1.00	87.74
	ATOM 844	CG	GLU	120	7.138	17.763	63.112	1.00	86.31
	ATOM 845	CD	GLU	120	8.269	17.956	62.120	1.00	85.84
	ATOM 846	OE1	GLU	120	8.884	19.042	62.113	1.00	84.76
	ATOM 847	OE2	GLU	120	8.535	17.020	61.336	1.00	85.71
10	ATOM 848	C	GLU	120	8.837	17.658	66.588	1.00	86.71
	ATOM 849	O	GLU	120	9.610	18.412	67.179	1.00	86.71
	ATOM 850	N	MET	121	7.980	16.859	67.216	1.00	85.74
	ATOM 851	CA	MET	121	7.895	16.817	68.671	1.00	84.85
	ATOM 852	CB	MET	121	6.798	15.842	69.111	1.00	84.04
15	ATOM 853	CG	MET	121	5.390	16.273	68.740	1.00	81.88
	ATOM 854	SD	MET	121	4.152	15.078	69.268	1.00	80.83
	ATOM 855	CE	MET	121	3.772	14.283	67.730	1.00	78.55
	ATOM 856	C	MET	121	9.226	16.397	69.286	1.00	84.73
	ATOM 857	O	MET	121	9.687	17.003	70.255	1.00	84.87
20	ATOM 858	N	LEU	122	9.839	15.360	68.717	1.00	84.21
	ATOM 859	CA	LEU	122	11.115	14.851	69.211	1.00	83.20
	ATOM 860	CB	LEU	122	11.711	13.847	68.221	1.00	83.29
	ATOM 861	CG	LEU	122	12.966	13.109	68.697	1.00	83.07
	ATOM 862	CD1	LEU	122	12.612	12.232	69.885	1.00	82.78
25	ATOM 863	CD2	LEU	122	13.533	12.261	67.572	1.00	82.52
	ATOM 864	C	LEU	122	12.110	15.980	69.448	1.00	82.61
	ATOM 865	O	LEU	122	12.546	16.204	70.575	1.00	82.47
	ATOM 866	N	PHE	123	12.467	16.694	68.385	1.00	82.28
	ATOM 867	CA	PHE	123	13.414	17.794	68.512	1.00	82.09

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	ATOM 868	CB	PHE	123	13.898	18.251	67.136	1.00	82.08
	ATOM 869	CG	PHE	123	14.948	17.357	66.547	1.00	81.61
	ATOM 870	CD1	PHE	123	14.616	16.098	66.060	1.00	81.34
	ATOM 871	CD2	PHE	123	16.281	17.756	66.523	1.00	81.33
5	ATOM 872	CE1	PHE	123	15.594	15.246	65.559	1.00	80.67
	ATOM 873	CE2	PHE	123	17.268	16.912	66.026	1.00	81.58
	ATOM 874	CZ	PHE	123	16.923	15.653	65.543	1.00	81.33
	ATOM 875	C	PHE	123	12.834	18.964	69.288	1.00	81.98
	ATOM 876	O	PHE	123	13.570	19.838	69.747	1.00	81.74
10	ATOM 877	N	ASP	124	11.512	18.980	69.429	1.00	82.09
	ATOM 878	CA	ASP	124	10.852	20.028	70.195	1.00	82.29
	ATOM 879	CB	ASP	124	9.329	19.909	70.073	1.00	81.96
	ATOM 880	CG	ASP	124	8.731	20.961	69.157	1.00	81.56
	ATOM 881	OD1	ASP	124	7.510	20.897	68.901	1.00	81.25
15	ATOM 882	OD2	ASP	124	9.477	21.855	68.701	1.00	80.94
	ATOM 883	C	ASP	124	11.279	19.808	71.641	1.00	82.22
	ATOM 884	O	ASP	124	11.819	20.707	72.287	1.00	81.61
	ATOM 885	N	TYR	125	11.047	18.595	72.133	1.00	82.59
	ATOM 886	CA	TYR	125	11.420	18.233	73.494	1.00	83.66
20	ATOM 887	CB	TYR	125	11.048	16.771	73.767	1.00	85.84
	ATOM 888	CG	TYR	125	11.533	16.240	75.100	1.00	88.74
	ATOM 889	CD1	TYR	125	12.763	15.590	75.209	1.00	89.83
	ATOM 890	CE1	TYR	125	13.222	15.110	76.437	1.00	91.28
	ATOM 891	CD2	TYR	125	10.770	16.399	76.257	1.00	90.41
25	ATOM 892	CE2	TYR	125	11.221	15.926	77.493	1.00	91.86
	ATOM 893	CZ	TYR	125	12.448	15.281	77.574	1.00	92.09
	ATOM 894	OH	TYR	125	12.896	14.807	78.789	1.00	93.08
	ATOM 895	C	TYR	125	12.917	18.451	73.704	1.00	82.86
	ATOM 896	O	TYR	125	13.352	18.829	74.792	1.00	82.74

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	ATOM 897	N	ILE	126	13.701	18.215	72.655	1.00	81.74
	ATOM 898	CA	ILE	126	15.146	18.398	72.727	1.00	80.58
	ATOM 899	CB	ILE	126	15.824	18.005	71.397	1.00	79.32
	ATOM 900	CG2	ILE	126	17.277	18.443	71.398	1.00	78.57
5	ATOM 901	CG1	ILE	126	15.719	16.494	71.194	1.00	78.47
	ATOM 902	CD1	ILE	126	16.408	15.993	69.946	1.00	78.42
	ATOM 903	C	ILE	126	15.479	19.852	73.047	1.00	80.87
	ATOM 904	O	ILE	126	16.334	20.133	73.887	1.00	79.71
	ATOM 905	N	SER	127	14.799	20.772	72.370	1.00	81.80
10	ATOM 906	CA	SER	127	15.018	22.196	72.594	1.00	82.44
	ATOM 907	CB	SER	127	14.160	23.021	71.636	1.00	82.62
	ATOM 908	OG	SER	127	14.559	22.807	70.294	1.00	83.20
	ATOM 909	C	SER	127	14.668	22.543	74.034	1.00	82.44
	ATOM 910	O	SER	127	15.318	23.382	74.660	1.00	81.86
15	ATOM 911	N	GLU	128	13.636	21.884	74.553	1.00	83.04
	ATOM 912	CA	GLU	128	13.202	22.106	75.927	1.00	83.79
	ATOM 913	CB	GLU	128	11.944	21.289	76.232	1.00	84.79
	ATOM 914	CG	GLU	128	11.408	21.490	77.645	1.00	86.70
	ATOM 915	CD	GLU	128	10.425	20.409	78.061	1.00	88.14
20	ATOM 916	OE1	GLU	128	9.408	20.222	77.357	1.00	88.36
	ATOM 917	OE2	GLU	128	10.672	19.747	79.094	1.00	88.06
	ATOM 918	C	GLU	128	14.318	21.686	76.877	1.00	83.42
	ATOM 919	O	GLU	128	14.483	22.261	77.952	1.00	84.16
	ATOM 920	N	CYS	129	15.081	20.675	76.475	1.00	82.77
25	ATOM 921	CA	CYS	129	16.177	20.179	77.295	1.00	81.21
	ATOM 922	CB	CYS	129	16.554	18.760	76.873	1.00	81.07
	ATOM 923	SG	CYS	129	15.206	17.569	77.006	1.00	80.63
	ATOM 924	C	CYS	129	17.391	21.089	77.178	1.00	80.64
	ATOM 925	O	CYS	129	18.092	21.330	78.160	1.00	79.84

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	ATOM 926	N	ILE	130	17.644	21.591	75.975	1.00	80.16
	ATOM 927	CA	ILE	130	18.782	22.475	75.775	1.00	80.33
	ATOM 928	CB	ILE	130	18.944	22.860	74.298	1.00	79.59
	ATOM 929	CG2	ILE	130	20.253	23.614	74.102	1.00	79.29
5	ATOM 930	CG1	ILE	130	18.933	21.599	73.436	1.00	79.00
	ATOM 931	CD1	ILE	130	19.069	21.860	71.958	1.00	79.73
	ATOM 932	C	ILE	130	18.559	23.735	76.595	1.00	80.49
	ATOM 933	O	ILE	130	19.475	24.241	77.239	1.00	80.22
	ATOM 934	N	SER	131	17.326	24.229	76.574	1.00	81.09
10	ATOM 935	CA	SER	131	16.970	25.428	77.320	1.00	82.28
	ATOM 936	CB	SER	131	15.525	25.826	77.006	1.00	83.15
	ATOM 937	OG	SER	131	14.641	24.736	77.195	1.00	82.88
	ATOM 938	C	SER	131	17.136	25.195	78.820	1.00	82.33
	ATOM 939	O	SER	131	17.843	25.940	79.501	1.00	82.07
15	ATOM 940	N	ASP	132	16.478	24.155	79.322	1.00	82.42
	ATOM 941	CA	ASP	132	16.540	23.792	80.735	1.00	82.24
	ATOM 942	CB	ASP	132	15.893	22.411	80.934	1.00	83.24
	ATOM 943	CG	ASP	132	15.836	21.981	82.393	1.00	83.66
	ATOM 944	OD1	ASP	132	15.165	20.963	82.678	1.00	83.28
20	ATOM 945	OD2	ASP	132	16.458	22.645	83.250	1.00	83.85
	ATOM 946	C	ASP	132	17.996	23.778	81.200	1.00	81.62
	ATOM 947	O	ASP	132	18.324	24.293	82.270	1.00	82.12
	ATOM 948	N	PHE	133	18.866	23.193	80.383	1.00	80.65
	ATOM 949	CA	PHE	133	20.286	23.118	80.698	1.00	79.47
25	ATOM 950	CB	PHE	133	21.033	22.331	79.616	1.00	77.80
	ATOM 951	CG	PHE	133	22.528	22.391	79.750	1.00	75.86
	ATOM 952	CD1	PHE	133	23.178	21.695	80.761	1.00	75.50
	ATOM 953	CD2	PHE	133	23.284	23.179	78.889	1.00	75.39
	ATOM 954	CE1	PHE	133	24.562	21.785	80.914	1.00	74.78

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	ATOM 955	CE2 PHE	133	24.667	23.275	79.035	1.00	74.59
	ATOM 956	CZ PHE	133	25.305	22.578	80.049	1.00	74.18
	ATOM 957	C PHE	133	20.876	24.519	80.786	1.00	79.33
	ATOM 958	O PHE	133	21.690	24.810	81.659	1.00	79.06
5	ATOM 959	N LEU	134	20.459	25.382	79.869	1.00	79.23
	ATOM 960	CA LEU	134	20.951	26.748	79.828	1.00	79.59
	ATOM 961	CB LEU	134	20.482	27.412	78.534	1.00	79.43
	ATOM 962	CG LEU	134	21.043	26.703	77.297	1.00	78.61
	ATOM 963	CD1 LEU	134	20.401	27.247	76.032	1.00	78.47
10	ATOM 964	CD2 LEU	134	22.554	26.878	77.264	1.00	77.75
	ATOM 965	C LEU	134	20.524	27.565	81.043	1.00	79.41
	ATOM 966	O LEU	134	21.324	28.310	81.609	1.00	78.74
	ATOM 967	N ASP	135	19.268	27.423	81.448	1.00	80.16
	ATOM 968	CA ASP	135	18.780	28.152	82.609	1.00	80.92
15	ATOM 969	CB ASP	135	17.271	27.966	82.777	1.00	80.81
	ATOM 970	CG ASP	135	16.474	28.778	81.783	1.00	81.08
	ATOM 971	OD1 ASP	135	16.801	29.970	81.599	1.00	82.67
	ATOM 972	OD2 ASP	135	15.517	28.234	81.195	1.00	81.12
	ATOM 973	C ASP	135	19.486	27.686	83.872	1.00	81.80
20	ATOM 974	O ASP	135	20.090	28.490	84.578	1.00	82.12
	ATOM 975	N LYS	136	19.418	26.384	84.143	1.00	82.43
	ATOM 976	CA LYS	136	20.041	25.811	85.333	1.00	83.25
	ATOM 977	CB LYS	136	19.750	24.307	85.418	1.00	82.64
	ATOM 978	CG LYS	136	18.288	23.970	85.677	1.00	82.57
25	ATOM 979	CD LYS	136	18.095	22.487	85.952	1.00	82.49
	ATOM 980	CE LYS	136	16.630	22.154	86.182	1.00	82.31
	ATOM 981	NZ LYS	136	16.053	22.914	87.323	1.00	82.43
	ATOM 982	C LYS	136	21.548	26.044	85.429	1.00	84.12
	ATOM 983	O LYS	136	22.185	25.610	86.390	1.00	84.51

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	ATOM 984	N	HIS	137	22.119	26.727	84.442	1.00	85.08
	ATOM 985	CA	HIS	137	23.551	27.010	84.450	1.00	86.27
	ATOM 986	CB	HIS	137	24.280	26.115	83.438	1.00	86.74
	ATOM 987	CG	HIS	137	24.169	24.649	83.730	1.00	87.04
5	ATOM 988	CD2	HIS	137	25.112	23.729	84.047	1.00	86.44
	ATOM 989	ND1	HIS	137	22.968	23.971	83.708	1.00	87.51
	ATOM 990	CE1	HIS	137	23.176	22.699	83.999	1.00	86.59
	ATOM 991	NE2	HIS	137	24.468	22.526	84.209	1.00	86.35
	ATOM 992	C	HIS	137	23.820	28.476	84.123	1.00	87.11
10	ATOM 993	O	HIS	137	24.943	28.842	83.776	1.00	86.73
	ATOM 994	N	GLN	138	22.784	29.307	84.249	1.00	88.41
	ATOM 995	CA	GLN	138	22.883	30.736	83.955	1.00	89.43
	ATOM 996	CB	GLN	138	23.469	31.512	85.140	1.00	90.47
	ATOM 997	CG	GLN	138	22.654	31.451	86.419	1.00	92.10
15	ATOM 998	CD	GLN	138	22.738	30.099	87.095	1.00	93.09
	ATOM 999	OE1	GLN	138	23.829	29.598	87.372	1.00	93.35
	ATOM 1000	NE2	GLN	138	21.584	29.501	87.371	1.00	93.71
	ATOM 1001	C	GLN	138	23.779	30.931	82.747	1.00	89.90
	ATOM 1002	O	GLN	138	24.922	31.376	82.875	1.00	89.53
20	ATOM 1003	N	MET	139	23.262	30.591	81.573	1.00	89.97
	ATOM 1004	CA	MET	139	24.046	30.725	80.359	1.00	90.27
	ATOM 1005	CB	MET	139	24.995	29.529	80.235	1.00	90.82
	ATOM 1006	CG	MET	139	26.314	29.838	79.542	1.00	91.26
	ATOM 1007	SD	MET	139	27.526	28.508	79.736	1.00	90.73
25	ATOM 1008	CE	MET	139	28.303	28.974	81.303	1.00	91.08
	ATOM 1009	C	MET	139	23.137	30.820	79.140	1.00	90.17
	ATOM 1010	O	MET	139	23.610	30.894	78.006	1.00	90.11
	ATOM 1011	N	LYS	140	21.829	30.829	79.380	1.00	89.92
	ATOM 1012	CA	LYS	140	20.851	30.921	78.300	1.00	89.78

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	ATOM	1013	CB	LYS	140	19.434	30.922	78.874	1.00	89.37
	ATOM	1014	CG	LYS	140	18.357	31.239	77.852	1.00	89.17
	ATOM	1015	CD	LYS	140	16.972	31.055	78.438	1.00	89.06
	ATOM	1016	CE	LYS	140	16.688	29.588	78.675	1.00	88.66
5	ATOM	1017	NZ	LYS	140	16.797	28.822	77.406	1.00	88.73
	ATOM	1018	C	LYS	140	21.067	32.179	77.466	1.00	89.78
	ATOM	1019	O	LYS	140	20.593	32.278	76.334	1.00	89.28
	ATOM	1020	N	HIS	141	21.794	33.133	78.037	1.00	90.38
	ATOM	1021	CA	HIS	141	22.082	34.401	77.376	1.00	90.81
10	ATOM	1022	CB	HIS	141	22.222	35.506	78.427	1.00	90.98
	ATOM	1023	CG	HIS	141	23.294	35.243	79.443	1.00	91.18
	ATOM	1024	CD2	HIS	141	24.520	35.794	79.610	1.00	91.04
	ATOM	1025	ND1	HIS	141	23.163	34.294	80.434	1.00	91.11
	ATOM	1026	CE1	HIS	141	24.262	34.273	81.168	1.00	91.45
15	ATOM	1027	NE2	HIS	141	25.102	35.174	80.688	1.00	90.96
	ATOM	1028	C	HIS	141	23.349	34.367	76.516	1.00	90.72
	ATOM	1029	O	HIS	141	24.048	35.374	76.399	1.00	91.00
	ATOM	1030	N	LYS	142	23.648	33.220	75.912	1.00	90.17
	ATOM	1031	CA	LYS	142	24.845	33.109	75.082	1.00	89.12
20	ATOM	1032	CB	LYS	142	26.000	32.529	75.908	1.00	89.54
	ATOM	1033	CG	LYS	142	26.424	33.406	77.079	1.00	90.51
	ATOM	1034	CD	LYS	142	27.490	32.730	77.926	1.00	91.91
	ATOM	1035	CE	LYS	142	27.867	33.579	79.131	1.00	92.42
	ATOM	1036	NZ	LYS	142	28.820	32.863	80.026	1.00	92.34
25	ATOM	1037	C	LYS	142	24.643	32.276	73.815	1.00	87.58
	ATOM	1038	O	LYS	142	23.763	31.418	73.749	1.00	87.74
	ATOM	1039	N	LYS	143	25.465	32.554	72.808	1.00	85.65
	ATOM	1040	CA	LYS	143	25.414	31.849	71.532	1.00	83.45
	ATOM	1041	CB	LYS	143	25.052	32.819	70.402	1.00	83.10



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	ATOM	1042	CG	LYS	143	25.199	32.262	68.988	1.00	82.55
	ATOM	1043	CD	LYS	143	24.890	33.339	67.951	1.00	82.36
	ATOM	1044	CE	LYS	143	25.289	32.922	66.540	1.00	82.46
	ATOM	1045	NZ	LYS	143	24.519	31.749	66.045	1.00	82.29
5	ATOM	1046	C	LYS	143	26.790	31.252	71.283	1.00	82.32
	ATOM	1047	O	LYS	143	27.751	31.974	71.002	1.00	82.33
	ATOM	1048	N	LEU	144	26.884	29.932	71.409	1.00	79.90
	ATOM	1049	CA	LEU	144	28.146	29.233	71.198	1.00	77.12
	ATOM	1050	CB	LEU	144	28.653	28.634	72.517	1.00	78.89
10	ATOM	1051	CG	LEU	144	29.417	29.543	73.491	1.00	80.11
	ATOM	1052	CD1	LEU	144	28.560	30.727	73.924	1.00	81.77
	ATOM	1053	CD2	LEU	144	29.836	28.721	74.698	1.00	80.96
	ATOM	1054	C	LEU	144	27.993	28.132	70.156	1.00	73.23
	ATOM	1055	O	LEU	144	26.876	27.742	69.810	1.00	72.89
15	ATOM	1056	N	PRO	145	29.119	27.628	69.628	1.00	70.01
	ATOM	1057	CD	PRO	145	30.498	28.104	69.833	1.00	68.83
	ATOM	1058	CA	PRO	145	29.081	26.565	68.621	1.00	67.77
	ATOM	1059	CB	PRO	145	30.555	26.356	68.285	1.00	68.79
	ATOM	1060	CG	PRO	145	31.159	27.706	68.542	1.00	69.21
20	ATOM	1061	C	PRO	145	28.434	25.299	69.181	1.00	65.49
	ATOM	1062	O	PRO	145	28.615	24.963	70.351	1.00	64.23
	ATOM	1063	N	LEU	146	27.677	24.603	68.340	1.00	63.31
	ATOM	1064	CA	LEU	146	27.007	23.383	68.757	1.00	61.72
	ATOM	1065	CB	LEU	146	25.492	23.532	68.602	1.00	62.15
25	ATOM	1066	CG	LEU	146	24.678	22.285	68.945	1.00	62.90
	ATOM	1067	CD1	LEU	146	25.011	21.842	70.353	1.00	64.57
	ATOM	1068	CD2	LEU	146	23.194	22.577	68.817	1.00	65.06
	ATOM	1069	C	LEU	146	27.473	22.152	67.985	1.00	59.94
	ATOM	1070	O	LEU	146	27.342	22.086	66.763	1.00	59.04

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	ATOM	1071	N	GLY	147	28.028	21.189	68.721	1.00	58.65
	ATOM	1072	CA	GLY	147	28.492	19.939	68.136	1.00	54.15
	ATOM	1073	C	GLY	147	27.444	18.891	68.465	1.00	49.71
	ATOM	1074	O	GLY	147	27.175	18.628	69.635	1.00	50.70
5	ATOM	1075	N	PHE	148	26.854	18.287	67.440	1.00	46.12
	ATOM	1076	CA	PHE	148	25.795	17.297	67.635	1.00	42.39
	ATOM	1077	CB	PHE	148	24.610	17.675	66.740	1.00	39.68
	ATOM	1078	CG	PHE	148	23.366	16.864	66.977	1.00	38.24
	ATOM	1079	CD1	PHE	148	22.326	16.901	66.056	1.00	36.04
10	ATOM	1080	CD2	PHE	148	23.212	16.102	68.132	1.00	36.13
	ATOM	1081	CE1	PHE	148	21.148	16.194	66.279	1.00	38.53
	ATOM	1082	CE2	PHE	148	22.042	15.395	68.365	1.00	35.28
	ATOM	1083	CZ	PHE	148	21.005	15.440	67.437	1.00	37.48
	ATOM	1084	C	PHE	148	26.197	15.840	67.354	1.00	41.67
15	ATOM	1085	O	PHE	148	26.463	15.475	66.205	1.00	42.24
	ATOM	1086	N	THR	149	26.247	15.013	68.398	1.00	40.23
	ATOM	1087	CA	THR	149	26.562	13.593	68.222	1.00	36.30
	ATOM	1088	CB	THR	149	27.281	13.001	69.442	1.00	36.36
	ATOM	1089	OG1	THR	149	28.580	13.597	69.560	1.00	37.54
20	ATOM	1090	CG2	THR	149	27.444	11.492	69.286	1.00	37.01
	ATOM	1091	C	THR	149	25.212	12.909	68.039	1.00	34.65
	ATOM	1092	O	THR	149	24.412	12.836	68.967	1.00	31.13
	ATOM	1093	N	PHE	150	24.972	12.422	66.825	1.00	33.67
	ATOM	1094	CA	PHE	150	23.714	11.782	66.456	1.00	34.60
25	ATOM	1095	CB	PHE	150	23.061	12.614	65.336	1.00	32.78
	ATOM	1096	CG	PHE	150	21.739	12.086	64.854	1.00	30.57
	ATOM	1097	CD1	PHE	150	21.625	11.513	63.595	1.00	30.43
	ATOM	1098	CD2	PHE	150	20.598	12.213	65.637	1.00	31.90
	ATOM	1099	CE1	PHE	150	20.382	11.076	63.115	1.00	34.54

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	ATOM	1100	CE2	PHE	150	19.356	11.783	65.176	1.00	30.63
	ATOM	1101	CZ	PHE	150	19.241	11.213	63.913	1.00	32.01
	ATOM	1102	C	PHE	150	24.011	10.358	65.991	1.00	35.95
	ATOM	1103	O	PHE	150	24.369	10.128	64.836	1.00	38.42
5	ATOM	1104	N	SER	151	23.843	9.412	66.908	1.00	36.96
	ATOM	1105	CA	SER	151	24.129	7.995	66.680	1.00	34.37
	ATOM	1106	CB	SER	151	24.186	7.271	68.025	1.00	35.80
	ATOM	1107	OG	SER	151	25.111	7.897	68.892	1.00	39.97
	ATOM	1108	C	SER	151	23.189	7.228	65.770	1.00	32.05
10	ATOM	1109	O	SER	151	22.537	6.292	66.215	1.00	32.11
	ATOM	1110	N	PHE	152	23.110	7.611	64.505	1.00	31.41
	ATOM	1111	CA	PHE	152	22.253	6.902	63.563	1.00	31.81
	ATOM	1112	CB	PHE	152	20.824	7.464	63.570	1.00	34.43
	ATOM	1113	CG	PHE	152	20.149	7.372	64.904	1.00	34.95
15	ATOM	1114	CD1	PHE	152	20.278	8.401	65.838	1.00	32.95
	ATOM	1115	CD2	PHE	152	19.439	6.228	65.256	1.00	35.34
	ATOM	1116	CE1	PHE	152	19.713	8.291	67.108	1.00	35.00
	ATOM	1117	CE2	PHE	152	18.868	6.102	66.526	1.00	35.79
	ATOM	1118	CZ	PHE	152	19.005	7.135	67.454	1.00	38.15
20	ATOM	1119	C	PHE	152	22.845	7.010	62.171	1.00	31.95
	ATOM	1120	O	PHE	152	23.727	7.831	61.921	1.00	31.72
	ATOM	1121	N	PRO	153	22.386	6.164	61.247	1.00	32.44
	ATOM	1122	CD	PRO	153	21.374	5.098	61.343	1.00	30.73
	ATOM	1123	CA	PRO	153	22.942	6.248	59.896	1.00	34.59
25	ATOM	1124	CB	PRO	153	22.397	4.991	59.225	1.00	31.34
	ATOM	1125	CG	PRO	153	21.072	4.812	59.884	1.00	31.98
	ATOM	1126	C	PRO	153	22.507	7.535	59.201	1.00	37.30
	ATOM	1127	O	PRO	153	21.310	7.813	59.067	1.00	39.02
	ATOM	1128	N	VAL	154	23.483	8.325	58.770	1.00	39.02

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	ATOM	1129	CA	VAL	154	23.187	9.581	58.092	1.00	40.43
	ATOM	1130	CB	VAL	154	23.446	10.792	59.007	1.00	39.28
	ATOM	1131	CG1	VAL	154	23.191	12.081	58.238	1.00	41.18
	ATOM	1132	CG2	VAL	154	22.557	10.727	60.221	1.00	38.37
5	ATOM	1133	C	VAL	154	24.023	9.785	56.837	1.00	41.48
	ATOM	1134	O	VAL	154	25.241	9.602	56.861	1.00	41.28
	ATOM	1135	N	ARG	155	23.365	10.162	55.743	1.00	43.31
	ATOM	1136	CA	ARG	155	24.072	10.441	54.495	1.00	46.32
	ATOM	1137	CB	ARG	155	23.233	10.058	53.280	1.00	47.31
10	ATOM	1138	CG	ARG	155	23.809	10.586	51.968	1.00	52.20
	ATOM	1139	CD	ARG	155	23.563	9.614	50.844	1.00	55.56
	ATOM	1140	NE	ARG	155	24.419	8.437	50.968	1.00	59.93
	ATOM	1141	CZ	ARG	155	24.068	7.217	50.573	1.00	61.41
	ATOM	1142	NH1	ARG	155	22.874	7.011	50.032	1.00	63.00
15	ATOM	1143	NH2	ARG	155	24.910	6.203	50.717	1.00	63.35
	ATOM	1144	C	ARG	155	24.367	11.934	54.456	1.00	46.23
	ATOM	1145	O	ARG	155	23.486	12.737	54.166	1.00	47.64
	ATOM	1146	N	HIS	156	25.613	12.291	54.754	1.00	47.03
	ATOM	1147	CA	HIS	156	26.046	13.682	54.791	1.00	48.05
20	ATOM	1148	CB	HIS	156	27.318	13.834	55.632	1.00	49.62
	ATOM	1149	CG	HIS	156	27.157	13.444	57.066	1.00	52.65
	ATOM	1150	CD2	HIS	156	26.274	12.619	57.676	1.00	53.99
	ATOM	1151	ND1	HIS	156	27.990	13.916	58.057	1.00	53.35
	ATOM	1152	CE1	HIS	156	27.625	13.401	59.218	1.00	54.78
25	ATOM	1153	NE2	HIS	156	26.586	12.610	59.014	1.00	54.28
	ATOM	1154	C	HIS	156	26.334	14.317	53.440	1.00	48.30
	ATOM	1155	O	HIS	156	26.872	13.677	52.535	1.00	47.38
	ATOM	1156	N	GLU	157	25.969	15.589	53.319	1.00	47.98
	ATOM	1157	CA	GLU	157	26.256	16.343	52.114	1.00	48.38

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	ATOM	1158	CB	GLU	157	25.113	17.296	51.749	1.00	51.05
	ATOM	1159	CG	GLU	157	25.462	18.198	50.558	1.00	57.22
	ATOM	1160	CD	GLU	157	24.422	19.276	50.275	1.00	58.92
	ATOM	1161	OE1	GLU	157	23.299	18.931	49.845	1.00	60.91
5	ATOM	1162	OE2	GLU	157	24.734	20.471	50.485	1.00	60.69
	ATOM	1163	C	GLU	157	27.475	17.138	52.547	1.00	45.12
	ATOM	1164	O	GLU	157	28.349	17.457	51.749	1.00	43.91
	ATOM	1165	N	ASP	158	27.529	17.427	53.843	1.00	43.85
	ATOM	1166	CA	ASP	158	28.633	18.174	54.416	1.00	43.81
10	ATOM	1167	CB	ASP	158	28.479	19.654	54.085	1.00	46.74
	ATOM	1168	CG	ASP	158	29.743	20.445	54.349	1.00	49.54
	ATOM	1169	OD1	ASP	158	29.760	21.651	54.016	1.00	53.34
	ATOM	1170	OD2	ASP	158	30.716	19.869	54.884	1.00	49.62
	ATOM	1171	C	ASP	158	28.671	17.972	55.928	1.00	43.93
15	ATOM	1172	O	ASP	158	27.724	17.447	56.518	1.00	43.97
	ATOM	1173	N	ILE	159	29.767	18.399	56.547	1.00	43.75
	ATOM	1174	CA	ILE	159	29.963	18.250	57.983	1.00	44.27
	ATOM	1175	CB	ILE	159	31.248	18.971	58.452	1.00	45.07
	ATOM	1176	CG2	ILE	159	31.069	20.480	58.354	1.00	47.24
20	ATOM	1177	CG1	ILE	159	31.544	18.617	59.907	1.00	45.29
	ATOM	1178	CD1	ILE	159	31.733	17.140	60.152	1.00	48.99
	ATOM	1179	C	ILE	159	28.795	18.744	58.829	1.00	44.47
	ATOM	1180	O	ILE	159	28.583	18.254	59.941	1.00	44.15
	ATOM	1181	N	ASP	160	28.037	19.709	58.317	1.00	44.10
25	ATOM	1182	CA	ASP	160	26.904	20.239	59.072	1.00	42.92
	ATOM	1183	CB	ASP	160	27.103	21.734	59.360	1.00	44.13
	ATOM	1184	CG	ASP	160	27.448	22.533	58.118	1.00	45.52
	ATOM	1185	OD1	ASP	160	28.258	23.479	58.239	1.00	47.57
	ATOM	1186	OD2	ASP	160	26.912	22.228	57.031	1.00	45.51

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	ATOM	1187	C	ASP	160	25.559	20.005	58.410	1.00	42.92
	ATOM	1188	O	ASP	160	24.579	20.691	58.706	1.00	44.48
	ATOM	1189	N	LYS	161	25.509	19.026	57.518	1.00	41.57
	ATOM	1190	CA	LYS	161	24.267	18.692	56.838	1.00	41.51
5	ATOM	1191	CB	LYS	161	24.067	19.597	55.618	1.00	41.19
	ATOM	1192	CG	LYS	161	22.783	19.306	54.863	1.00	41.39
	ATOM	1193	CD	LYS	161	22.687	20.094	53.557	1.00	43.25
	ATOM	1194	CE	LYS	161	21.366	19.809	52.860	1.00	40.06
	ATOM	1195	NZ	LYS	161	21.335	20.312	51.468	1.00	41.02
10	ATOM	1196	C	LYS	161	24.258	17.224	56.397	1.00	41.66
	ATOM	1197	O	LYS	161	25.239	16.725	55.838	1.00	39.36
	ATOM	1198	N	GLY	162	23.143	16.546	56.654	1.00	40.90
	ATOM	1199	CA	GLY	162	23.005	15.152	56.276	1.00	42.70
	ATOM	1200	C	GLY	162	21.618	14.645	56.615	1.00	43.15
15	ATOM	1201	O	GLY	162	21.019	15.085	57.594	1.00	43.59
	ATOM	1202	N	ILE	163	21.096	13.722	55.816	1.00	43.93
	ATOM	1203	CA	ILE	163	19.763	13.190	56.068	1.00	45.03
	ATOM	1204	CB	ILE	163	18.958	13.031	54.755	1.00	46.16
	ATOM	1205	CG2	ILE	163	18.943	14.352	53.985	1.00	45.82
20	ATOM	1206	CG1	ILE	163	19.585	11.938	53.889	1.00	46.11
	ATOM	1207	CD1	ILE	163	18.812	11.638	52.613	1.00	48.51
	ATOM	1208	C	ILE	163	19.812	11.833	56.764	1.00	46.49
	ATOM	1209	O	ILE	163	20.771	11.074	56.609	1.00	45.36
	ATOM	1210	N	LEU	164	18.767	11.545	57.533	1.00	47.21
25	ATOM	1211	CA	LEU	164	18.649	10.286	58.253	1.00	47.53
	ATOM	1212	CB	LEU	164	17.623	10.414	59.379	1.00	47.11
	ATOM	1213	CG	LEU	164	17.135	9.126	60.049	1.00	47.15
	ATOM	1214	CD1	LEU	164	18.265	8.469	60.832	1.00	45.45
	ATOM	1215	CD2	LEU	164	15.981	9.465	60.977	1.00	47.00

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	ATOM	1216	C	LEU	164	18.189	9.220	57.277	1.00	48.06
	ATOM	1217	O	LEU	164	17.137	9.352	56.657	1.00	48.49
	ATOM	1218	N	LEU	165	18.977	8.161	57.137	1.00	48.32
	ATOM	1219	CA	LEU	165	18.614	7.093	56.224	1.00	47.47
5	ATOM	1220	CB	LEU	165	19.827	6.208	55.954	1.00	45.44
	ATOM	1221	CG	LEU	165	20.867	6.978	55.140	1.00	47.60
	ATOM	1222	CD1	LEU	165	22.128	6.155	54.956	1.00	47.47
	ATOM	1223	CD2	LEU	165	20.261	7.342	53.786	1.00	48.48
	ATOM	1224	C	LEU	165	17.460	6.300	56.814	1.00	46.86
10	ATOM	1225	O	LEU	165	16.497	5.985	56.120	1.00	46.90
	ATOM	1226	N	ASN	166	17.562	5.992	58.101	1.00	46.60
	ATOM	1227	CA	ASN	166	16.521	5.266	58.817	1.00	47.23
	ATOM	1228	CB	ASN	166	16.282	3.883	58.200	1.00	49.17
	ATOM	1229	CG	ASN	166	17.542	3.053	58.118	1.00	50.36
15	ATOM	1230	OD1	ASN	166	18.205	2.997	57.076	1.00	50.62
	ATOM	1231	ND2	ASN	166	17.888	2.406	59.223	1.00	50.50
	ATOM	1232	C	ASN	166	16.913	5.123	60.279	1.00	47.60
	ATOM	1233	O	ASN	166	18.096	5.177	60.623	1.00	48.53
	ATOM	1234	N	TRP	167	15.916	4.966	61.142	1.00	46.96
20	ATOM	1235	CA	TRP	167	16.166	4.815	62.571	1.00	45.46
	ATOM	1236	CB	TRP	167	14.890	5.085	63.376	1.00	47.63
	ATOM	1237	CG	TRP	167	14.433	6.519	63.454	1.00	49.15
	ATOM	1238	CD2	TRP	167	15.093	7.602	64.126	1.00	49.07
	ATOM	1239	CE2	TRP	167	14.237	8.725	64.050	1.00	48.21
25	ATOM	1240	CE3	TRP	167	16.321	7.732	64.787	1.00	49.17
	ATOM	1241	CD1	TRP	167	13.242	7.022	63.003	1.00	49.03
	ATOM	1242	NE1	TRP	167	13.117	8.343	63.361	1.00	48.46
	ATOM	1243	CZ2	TRP	167	14.569	9.962	64.614	1.00	47.68
	ATOM	1244	CZ3	TRP	167	16.652	8.966	65.348	1.00	49.58

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	ATOM	1245	CH2	TRP	167	15.777	10.064	65.256	1.00	48.80
	ATOM	1246	C	TRP	167	16.647	3.394	62.890	1.00	43.28
	ATOM	1247	O	TRP	167	16.425	2.461	62.119	1.00	42.86
	ATOM	1248	N	THR	168	17.297	3.245	64.038	1.00	41.63
5	ATOM	1249	CA	THR	168	17.796	1.953	64.501	1.00	40.13
	ATOM	1250	CB	THR	168	19.275	1.723	64.086	1.00	37.87
	ATOM	1251	OG1	THR	168	20.082	2.795	64.587	1.00	33.52
	ATOM	1252	CG2	THR	168	19.417	1.647	62.566	1.00	34.11
	ATOM	1253	C	THR	168	17.719	1.943	66.029	1.00	41.33
10	ATOM	1254	O	THR	168	17.382	2.953	66.649	1.00	41.41
	ATOM	1255	N	LYS	169	18.025	0.799	66.631	1.00	42.06
	ATOM	1256	CA	LYS	169	18.013	0.672	68.083	1.00	42.59
	ATOM	1257	CB	LYS	169	19.077	1.594	68.683	1.00	39.56
	ATOM	1258	CG	LYS	169	20.497	1.209	68.287	1.00	36.24
15	ATOM	1259	CD	LYS	169	21.528	2.170	68.840	1.00	33.26
	ATOM	1260	CE	LYS	169	21.481	3.514	68.133	1.00	30.26
	ATOM	1261	NZ	LYS	169	22.589	4.373	68.610	1.00	32.75
	ATOM	1262	C	LYS	169	16.661	0.933	68.751	1.00	45.26
	ATOM	1263	O	LYS	169	16.598	1.191	69.955	1.00	45.85
20	ATOM	1264	N	GLY	170	15.583	0.881	67.975	1.00	47.46
	ATOM	1265	CA	GLY	170	14.267	1.083	68.555	1.00	52.44
	ATOM	1266	C	GLY	170	13.552	2.394	68.295	1.00	55.24
	ATOM	1267	O	GLY	170	12.324	2.422	68.275	1.00	56.11
	ATOM	1268	N	PHE	171	14.293	3.482	68.118	1.00	58.10
25	ATOM	1269	CA	PHE	171	13.668	4.777	67.861	1.00	61.86
	ATOM	1270	CB	PHE	171	14.734	5.846	67.613	1.00	62.35
	ATOM	1271	CG	PHE	171	15.449	6.285	68.856	1.00	64.08
	ATOM	1272	CD1	PHE	171	16.060	5.354	69.691	1.00	66.00
	ATOM	1273	CD2	PHE	171	15.511	7.630	69.196	1.00	64.53



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	ATOM	1274	CE1	PHE	171	16.721	5.760	70.851	1.00	66.96
	ATOM	1275	CE2	PHE	171	16.170	8.046	70.352	1.00	65.93
	ATOM	1276	CZ	PHE	171	16.776	7.109	71.180	1.00	66.07
	ATOM	1277	C	PHE	171	12.727	4.697	66.663	1.00	63.91
5	ATOM	1278	O	PHE	171	12.994	3.975	65.702	1.00	63.50
	ATOM	1279	N	LYS	172	11.620	5.430	66.727	1.00	65.77
	ATOM	1280	CA	LYS	172	10.657	5.424	65.633	1.00	68.37
	ATOM	1281	CB	LYS	172	9.738	4.197	65.727	1.00	70.16
	ATOM	1282	CG	LYS	172	8.814	4.035	64.517	1.00	72.04
10	ATOM	1283	CD	LYS	172	7.867	2.842	64.647	1.00	73.43
	ATOM	1284	CE	LYS	172	6.977	2.718	63.406	1.00	74.42
	ATOM	1285	NZ	LYS	172	5.933	1.655	63.525	1.00	73.62
	ATOM	1286	C	LYS	172	9.808	6.688	65.606	1.00	69.18
	ATOM	1287	O	LYS	172	8.599	6.642	65.838	1.00	70.01
15	ATOM	1288	N	ALA	173	10.445	7.820	65.332	1.00	68.98
	ATOM	1289	CA	ALA	173	9.734	9.086	65.251	1.00	69.07
	ATOM	1290	CB	ALA	173	10.598	10.210	65.818	1.00	68.41
	ATOM	1291	C	ALA	173	9.424	9.339	63.776	1.00	69.07
	ATOM	1292	O	ALA	173	10.336	9.471	62.962	1.00	69.61
20	ATOM	1293	N	SER	174	8.139	9.394	63.432	1.00	69.06
	ATOM	1294	CA	SER	174	7.735	9.620	62.047	1.00	68.32
	ATOM	1295	CB	SER	174	6.217	9.491	61.901	1.00	69.02
	ATOM	1296	OG	SER	174	5.546	10.503	62.632	1.00	68.18
	ATOM	1297	C	SER	174	8.173	10.996	61.568	1.00	67.71
25	ATOM	1298	O	SER	174	8.410	11.897	62.370	1.00	68.23
	ATOM	1299	N	GLY	175	8.288	11.148	60.254	1.00	67.37
	ATOM	1300	CA	GLY	175	8.688	12.424	59.690	1.00	67.08
	ATOM	1301	C	GLY	175	10.143	12.787	59.915	1.00	66.86
	ATOM	1302	O	GLY	175	10.507	13.962	59.855	1.00	67.38

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	ATOM	1303	N	ALA	176	10.979	11.786	60.172	1.00	66.42
	ATOM	1304	CA	ALA	176	12.400	12.018	60.401	1.00	64.67
	ATOM	1305	CB	ALA	176	12.828	11.360	61.699	1.00	64.11
	ATOM	1306	C	ALA	176	13.229	11.475	59.242	1.00	64.02
5	ATOM	1307	O	ALA	176	14.053	12.183	58.667	1.00	65.00
	ATOM	1308	N	GLU	177	12.993	10.214	58.903	1.00	63.24
	ATOM	1309	CA	GLU	177	13.710	9.544	57.825	1.00	63.08
	ATOM	1310	CB	GLU	177	13.147	8.127	57.639	1.00	62.97
	ATOM	1311	CG	GLU	177	13.315	7.224	58.865	1.00	64.81
10	ATOM	1312	CD	GLU	177	12.712	5.837	58.682	1.00	64.99
	ATOM	1313	OE1	GLU	177	12.948	4.972	59.552	1.00	65.80
	ATOM	1314	OE2	GLU	177	12.003	5.612	57.677	1.00	64.52
	ATOM	1315	C	GLU	177	13.669	10.293	56.491	1.00	62.92
	ATOM	1316	O	GLU	177	12.602	10.489	55.908	1.00	63.26
15	ATOM	1317	N	GLY	178	14.838	10.708	56.013	1.00	62.46
	ATOM	1318	CA	GLY	178	14.911	11.406	54.741	1.00	61.36
	ATOM	1319	C	GLY	178	15.095	12.911	54.805	1.00	60.52
	ATOM	1320	O	GLY	178	15.337	13.539	53.777	1.00	61.73
	ATOM	1321	N	ASN	179	14.990	13.498	55.993	1.00	59.84
20	ATOM	1322	CA	ASN	179	15.139	14.942	56.134	1.00	59.11
	ATOM	1323	CB	ASN	179	13.985	15.512	56.959	1.00	59.72
	ATOM	1324	CG	ASN	179	12.630	15.217	56.342	1.00	61.46
	ATOM	1325	OD1	ASN	179	12.423	15.416	55.143	1.00	61.86
	ATOM	1326	ND2	ASN	179	11.696	14.743	57.161	1.00	61.02
25	ATOM	1327	C	ASN	179	16.463	15.349	56.765	1.00	58.81
	ATOM	1328	O	ASN	179	17.108	14.553	57.441	1.00	59.10
	ATOM	1329	N	ASN	180	16.860	16.599	56.537	1.00	58.30
	ATOM	1330	CA	ASN	180	18.107	17.130	57.079	1.00	57.96
	ATOM	1331	CB	ASN	180	18.362	18.539	56.539	1.00	58.57

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	ATOM	1332	CG	ASN	180	19.693	19.112	57.001	1.00	60.99
	ATOM	1333	OD1	ASN	180	20.278	18.647	57.983	1.00	60.88
	ATOM	1334	ND2	ASN	180	20.171	20.139	56.302	1.00	60.74
	ATOM	1335	C	ASN	180	18.036	17.183	58.600	1.00	57.30
5	ATOM	1336	O	ASN	180	17.388	18.064	59.162	1.00	57.94
	ATOM	1337	N	VAL	181	18.709	16.245	59.261	1.00	55.49
	ATOM	1338	CA	VAL	181	18.716	16.189	60.720	1.00	54.19
	ATOM	1339	CB	VAL	181	19.698	15.109	61.229	1.00	53.15
	ATOM	1340	CG1	VAL	181	19.756	15.121	62.748	1.00	50.90
10	ATOM	1341	CG2	VAL	181	19.258	13.742	60.731	1.00	51.33
	ATOM	1342	C	VAL	181	19.089	17.534	61.333	1.00	54.31
	ATOM	1343	O	VAL	181	18.473	17.979	62.299	1.00	53.21
	ATOM	1344	N	VAL	182	20.110	18.174	60.777	1.00	56.27
	ATOM	1345	CA	VAL	182	20.533	19.472	61.271	1.00	58.32
15	ATOM	1346	CB	VAL	182	21.706	20.033	60.447	1.00	58.42
	ATOM	1347	CG1	VAL	182	22.135	21.373	61.007	1.00	58.05
	ATOM	1348	CG2	VAL	182	22.867	19.054	60.460	1.00	59.02
	ATOM	1349	C	VAL	182	19.339	20.410	61.125	1.00	60.16
	ATOM	1350	O	VAL	182	19.052	21.220	62.008	1.00	59.87
20	ATOM	1351	N	GLY	183	18.640	20.275	60.003	1.00	61.05
	ATOM	1352	CA	GLY	183	17.480	21.103	59.741	1.00	63.47
	ATOM	1353	C	GLY	183	16.412	20.967	60.805	1.00	64.68
	ATOM	1354	O	GLY	183	15.873	21.966	61.280	1.00	64.59
	ATOM	1355	N	LEU	184	16.103	19.733	61.187	1.00	65.39
25	ATOM	1356	CA	LEU	184	15.091	19.502	62.203	1.00	66.47
	ATOM	1357	CB	LEU	184	14.855	18.005	62.387	1.00	66.17
	ATOM	1358	CG	LEU	184	14.407	17.254	61.132	1.00	67.51
	ATOM	1359	CD1	LEU	184	14.116	15.805	61.486	1.00	66.63
	ATOM	1360	CD2	LEU	184	13.168	17.913	60.546	1.00	68.22

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	ATOM	1361	C	LEU	184	15.502	20.130	63.528	1.00	67.67
	ATOM	1362	O	LEU	184	14.651	20.570	64.301	1.00	68.91
	ATOM	1363	N	LEU	185	16.804	20.176	63.790	1.00	68.11
	ATOM	1364	CA	LEU	185	17.297	20.759	65.031	1.00	68.91
5	ATOM	1365	CB	LEU	185	18.797	20.501	65.194	1.00	67.32
	ATOM	1366	CG	LEU	185	19.409	21.060	66.482	1.00	66.21
	ATOM	1367	CD1	LEU	185	18.776	20.375	67.676	1.00	65.16
	ATOM	1368	CD2	LEU	185	20.913	20.851	66.486	1.00	66.43
	ATOM	1369	C	LEU	185	17.034	22.262	65.058	1.00	70.10
10	ATOM	1370	O	LEU	185	16.422	22.776	65.991	1.00	70.26
	ATOM	1371	N	ARG	186	17.505	22.962	64.033	1.00	71.83
	ATOM	1372	CA	ARG	186	17.314	24.403	63.948	1.00	73.78
	ATOM	1373	CB	ARG	186	18.015	24.941	62.700	1.00	73.97
	ATOM	1374	CG	ARG	186	19.533	24.881	62.804	1.00	74.09
15	ATOM	1375	CD	ARG	186	20.206	24.984	61.448	1.00	74.37
	ATOM	1376	NE	ARG	186	21.662	24.945	61.571	1.00	75.77
	ATOM	1377	CZ	ARG	186	22.503	24.860	60.543	1.00	75.94
	ATOM	1378	NH1	ARG	186	22.036	24.800	59.303	1.00	75.97
	ATOM	1379	NH2	ARG	186	23.815	24.841	60.755	1.00	75.99
20	ATOM	1380	C	ARG	186	15.825	24.737	63.927	1.00	74.93
	ATOM	1381	O	ARG	186	15.365	25.609	64.665	1.00	74.59
	ATOM	1382	N	ASP	187	15.074	24.023	63.095	1.00	76.23
	ATOM	1383	CA	ASP	187	13.632	24.225	62.981	1.00	77.59
	ATOM	1384	CB	ASP	187	13.018	23.128	62.102	1.00	75.83
25	ATOM	1385	CG	ASP	187	13.203	23.391	60.614	1.00	74.87
	ATOM	1386	OD1	ASP	187	14.193	24.051	60.234	1.00	73.64
	ATOM	1387	OD2	ASP	187	12.359	22.924	59.820	1.00	74.33
	ATOM	1388	C	ASP	187	12.945	24.236	64.349	1.00	79.78
	ATOM	1389	O	ASP	187	11.963	24.952	64.551	1.00	80.50

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	ATOM	1390	N	ALA	188	13.461	23.445	65.286	1.00	81.21
	ATOM	1391	CA	ALA	188	12.883	23.379	66.625	1.00	82.86
	ATOM	1392	CB	ALA	188	13.118	22.000	67.230	1.00	83.00
	ATOM	1393	C	ALA	188	13.477	24.456	67.525	1.00	84.14
5	ATOM	1394	O	ALA	188	12.783	25.019	68.376	1.00	84.10
	ATOM	1395	N	ILE	189	14.763	24.736	67.338	1.00	85.33
	ATOM	1396	CA	ILE	189	15.445	25.753	68.127	1.00	86.87
	ATOM	1397	CB	ILE	189	16.947	25.819	67.776	1.00	86.40
	ATOM	1398	CG2	ILE	189	17.585	27.049	68.409	1.00	85.37
10	ATOM	1399	CG1	ILE	189	17.641	24.541	68.253	1.00	86.52
	ATOM	1400	CD1	ILE	189	19.136	24.516	68.004	1.00	86.36
	ATOM	1401	C	ILE	189	14.812	27.114	67.871	1.00	88.85
	ATOM	1402	O	ILE	189	14.802	27.978	68.748	1.00	89.64
	ATOM	1403	N	LYS	190	14.278	27.295	66.666	1.00	90.36
15	ATOM	1404	CA	LYS	190	13.638	28.551	66.291	1.00	91.75
	ATOM	1405	CB	LYS	190	13.678	28.729	64.770	1.00	92.26
	ATOM	1406	CG	LYS	190	15.032	29.205	64.234	1.00	93.56
	ATOM	1407	CD	LYS	190	16.174	28.282	64.652	1.00	94.17
	ATOM	1408	CE	LYS	190	17.507	28.722	64.064	1.00	94.42
20	ATOM	1409	NZ	LYS	190	18.605	27.773	64.409	1.00	93.91
	ATOM	1410	C	LYS	190	12.202	28.645	66.803	1.00	92.34
	ATOM	1411	O	LYS	190	11.612	29.723	66.817	1.00	92.82
	ATOM	1412	N	ARG	191	11.639	27.516	67.221	1.00	92.78
	ATOM	1413	CA	ARG	191	10.286	27.502	67.763	1.00	93.41
25	ATOM	1414	CB	ARG	191	9.674	26.108	67.658	1.00	93.77
	ATOM	1415	CG	ARG	191	9.711	25.497	66.275	1.00	93.66
	ATOM	1416	CD	ARG	191	9.530	23.993	66.378	1.00	93.81
	ATOM	1417	NE	ARG	191	9.816	23.310	65.123	1.00	93.99
	ATOM	1418	CZ	ARG	191	10.012	22.000	65.017	1.00	94.26

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	ATOM	1419	NH1	ARG	191	9.954	21.231	66.095	1.00	94.65
	ATOM	1420	NH2	ARG	191	10.269	21.459	63.835	1.00	94.96
	ATOM	1421	C	ARG	191	10.432	27.866	69.233	1.00	94.00
	ATOM	1422	O	ARG	191	9.526	27.654	70.036	1.00	94.16
5	ATOM	1423	N	ARG	192	11.596	28.408	69.574	1.00	94.91
	ATOM	1424	CA	ARG	192	11.897	28.795	70.943	1.00	96.15
	ATOM	1425	CB	ARG	192	13.049	27.944	71.482	1.00	96.57
	ATOM	1426	CG	ARG	192	12.733	26.469	71.581	1.00	97.44
	ATOM	1427	CD	ARG	192	11.737	26.209	72.689	1.00	98.38
10	ATOM	1428	NE	ARG	192	11.339	24.808	72.745	1.00	98.97
	ATOM	1429	CZ	ARG	192	10.624	24.278	73.730	1.00	99.63
	ATOM	1430	NH1	ARG	192	10.230	25.035	74.746	1.00	99.17
	ATOM	1431	NH2	ARG	192	10.300	22.992	73.700	1.00	99.97
	ATOM	1432	C	ARG	192	12.273	30.265	71.062	1.00	96.50
15	ATOM	1433	O	ARG	192	11.603	31.035	71.752	1.00	96.60
	ATOM	1434	N	GLY	193	13.352	30.652	70.386	1.00	96.89
	ATOM	1435	CA	GLY	193	13.812	32.026	70.465	1.00	97.08
	ATOM	1436	C	GLY	193	14.385	32.217	71.855	1.00	97.08
	ATOM	1437	O	GLY	193	15.060	33.204	72.147	1.00	96.46
20	ATOM	1438	N	ASP	194	14.104	31.235	72.707	1.00	97.36
	ATOM	1439	CA	ASP	194	14.552	31.205	74.092	1.00	97.35
	ATOM	1440	CB	ASP	194	13.938	29.984	74.789	1.00	98.43
	ATOM	1441	CG	ASP	194	13.764	30.181	76.284	1.00	99.62
	ATOM	1442	OD1	ASP	194	13.117	31.173	76.683	1.00	100.29
25	ATOM	1443	OD2	ASP	194	14.262	29.338	77.059	1.00	99.87
	ATOM	1444	C	ASP	194	16.078	31.122	74.122	1.00	96.90
	ATOM	1445	O	ASP	194	16.715	31.471	75.118	1.00	97.50
	ATOM	1446	N	PHE	195	16.657	30.655	73.018	1.00	95.62
	ATOM	1447	CA	PHE	195	18.105	30.524	72.896	1.00	94.15

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	ATOM	1448	CB	PHE	195	18.598	29.309	73.697	1.00	94.86
	ATOM	1449	CG	PHE	195	18.043	27.988	73.224	1.00	95.10
	ATOM	1450	CD1	PHE	195	18.560	27.360	72.095	1.00	95.09
	ATOM	1451	CD2	PHE	195	17.005	27.369	73.916	1.00	95.17
5	ATOM	1452	CE1	PHE	195	18.053	26.136	71.663	1.00	95.14
	ATOM	1453	CE2	PHE	195	16.491	26.145	73.492	1.00	95.12
	ATOM	1454	CZ	PHE	195	17.016	25.528	72.364	1.00	94.97
	ATOM	1455	C	PHE	195	18.508	30.393	71.430	1.00	92.64
	ATOM	1456	O	PHE	195	17.667	30.131	70.569	1.00	92.22
10	ATOM	1457	N	GLU	196	19.793	30.583	71.148	1.00	90.93
	ATOM	1458	CA	GLU	196	20.292	30.486	69.779	1.00	89.04
	ATOM	1459	CB	GLU	196	20.249	31.861	69.102	1.00	89.55
	ATOM	1460	CG	GLU	196	18.846	32.395	68.832	1.00	90.25
	ATOM	1461	CD	GLU	196	18.859	33.771	68.187	1.00	90.61
15	ATOM	1462	OE1	GLU	196	19.342	34.728	68.830	1.00	90.30
	ATOM	1463	OE2	GLU	196	18.390	33.895	67.035	1.00	90.79
	ATOM	1464	C	GLU	196	21.711	29.923	69.694	1.00	87.11
	ATOM	1465	O	GLU	196	22.681	30.589	70.066	1.00	86.83
	ATOM	1466	N	MET	197	21.824	28.692	69.201	1.00	84.23
20	ATOM	1467	CA	MET	197	23.121	28.043	69.045	1.00	80.79
	ATOM	1468	CB	MET	197	23.067	26.586	69.524	1.00	81.16
	ATOM	1469	CG	MET	197	22.633	26.389	70.967	1.00	80.14
	ATOM	1470	SD	MET	197	23.597	27.356	72.135	1.00	81.93
	ATOM	1471	CE	MET	197	25.195	26.640	71.968	1.00	81.72
25	ATOM	1472	C	MET	197	23.502	28.070	67.568	1.00	77.74
	ATOM	1473	O	MET	197	22.695	28.436	66.716	1.00	76.30
	ATOM	1474	N	ASP	198	24.733	27.672	67.269	1.00	75.73
	ATOM	1475	CA	ASP	198	25.214	27.652	65.894	1.00	72.50
	ATOM	1476	CB	ASP	198	26.297	28.723	65.720	1.00	73.47

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	ATOM	1477	CG	ASP	198	26.573	29.046	64.265	1.00	75.34
	ATOM	1478	OD1	ASP	198	27.407	29.941	64.005	1.00	75.72
	ATOM	1479	OD2	ASP	198	25.954	28.407	63.384	1.00	76.53
	ATOM	1480	C	ASP	198	25.769	26.265	65.544	1.00	69.75
5	ATOM	1481	O	ASP	198	26.962	26.005	65.703	1.00	69.48
	ATOM	1482	N	VAL	199	24.892	25.383	65.068	1.00	66.43
	ATOM	1483	CA	VAL	199	25.266	24.018	64.697	1.00	62.47
	ATOM	1484	CB	VAL	199	24.055	23.266	64.113	1.00	62.19
	ATOM	1485	CG1	VAL	199	24.426	21.823	63.827	1.00	61.88
10	ATOM	1486	CG2	VAL	199	22.886	23.340	65.083	1.00	61.21
	ATOM	1487	C	VAL	199	26.409	23.986	63.682	1.00	60.44
	ATOM	1488	O	VAL	199	26.192	24.135	62.479	1.00	59.37
	ATOM	1489	N	VAL	200	27.624	23.774	64.180	1.00	58.00
	ATOM	1490	CA	VAL	200	28.820	23.741	63.341	1.00	56.24
15	ATOM	1491	CB	VAL	200	30.048	24.278	64.128	1.00	57.42
	ATOM	1492	CG1	VAL	200	31.326	24.071	63.331	1.00	57.94
	ATOM	1493	CG2	VAL	200	29.859	25.761	64.433	1.00	59.29
	ATOM	1494	C	VAL	200	29.159	22.357	62.785	1.00	54.53
	ATOM	1495	O	VAL	200	29.759	22.242	61.715	1.00	54.29
20	ATOM	1496	N	ALA	201	28.779	21.306	63.503	1.00	52.88
	ATOM	1497	CA	ALA	201	29.085	19.953	63.048	1.00	49.83
	ATOM	1498	CB	ALA	201	30.541	19.627	63.349	1.00	47.49
	ATOM	1499	C	ALA	201	28.196	18.887	63.654	1.00	46.62
	ATOM	1500	O	ALA	201	27.803	18.973	64.810	1.00	47.96
25	ATOM	1501	N	MET	202	27.873	17.883	62.851	1.00	44.82
	ATOM	1502	CA	MET	202	27.065	16.762	63.309	1.00	42.12
	ATOM	1503	CB	MET	202	25.731	16.695	62.567	1.00	39.23
	ATOM	1504	CG	MET	202	24.886	15.520	63.014	1.00	38.13
	ATOM	1505	SD	MET	202	23.425	15.193	62.026	1.00	40.98



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	ATOM	1506	CE	MET	202	24.134	15.162	60.401	1.00	37.63
	ATOM	1507	C	MET	202	27.865	15.489	63.027	1.00	40.68
	ATOM	1508	O	MET	202	28.274	15.251	61.888	1.00	38.74
	ATOM	1509	N	VAL	203	28.092	14.679	64.060	1.00	39.90
5	ATOM	1510	CA	VAL	203	28.851	13.438	63.901	1.00	37.47
	ATOM	1511	CB	VAL	203	30.264	13.549	64.517	1.00	36.73
	ATOM	1512	CG1	VAL	203	31.078	14.615	63.796	1.00	34.96
	ATOM	1513	CG2	VAL	203	30.155	13.852	65.996	1.00	37.90
	ATOM	1514	C	VAL	203	28.190	12.199	64.505	1.00	37.09
10	ATOM	1515	O	VAL	203	27.250	12.284	65.309	1.00	36.61
	ATOM	1516	N	ASN	204	28.707	11.039	64.101	1.00	36.09
	ATOM	1517	CA	ASN	204	28.228	9.749	64.584	1.00	31.60
	ATOM	1518	CB	ASN	204	28.461	8.695	63.497	1.00	32.07
	ATOM	1519	CG	ASN	204	27.949	7.322	63.888	1.00	31.63
15	ATOM	1520	OD1	ASN	204	28.729	6.443	64.250	1.00	30.91
	ATOM	1521	ND2	ASN	204	26.634	7.135	63.824	1.00	28.99
	ATOM	1522	C	ASN	204	29.027	9.454	65.853	1.00	28.81
	ATOM	1523	O	ASN	204	30.122	9.990	66.019	1.00	30.24
	ATOM	1524	N	ASP	205	28.498	8.639	66.765	1.00	27.90
20	ATOM	1525	CA	ASP	205	29.240	8.361	67.995	1.00	26.70
	ATOM	1526	CB	ASP	205	28.369	7.627	69.028	1.00	27.65
	ATOM	1527	CG	ASP	205	27.642	6.438	68.455	1.00	30.26
	ATOM	1528	OD1	ASP	205	27.079	5.655	69.256	1.00	28.60
	ATOM	1529	OD2	ASP	205	27.623	6.289	67.213	1.00	31.99
25	ATOM	1530	C	ASP	205	30.573	7.630	67.791	1.00	26.87
	ATOM	1531	O	ASP	205	31.498	7.810	68.581	1.00	27.79
	ATOM	1532	N	THR	206	30.686	6.816	66.740	1.00	24.79
	ATOM	1533	CA	THR	206	31.951	6.146	66.476	1.00	24.03
	ATOM	1534	CB	THR	206	31.886	5.236	65.206	1.00	25.43

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	ATOM	1535	OG1 THR	206	31.401	5.999	64.089	1.00	26.30
	ATOM	1536	CG2 THR	206	30.976	4.032	65.444	1.00	16.83
	ATOM	1537	C THR	206	32.970	7.258	66.220	1.00	24.75
	ATOM	1538	O THR	206	34.025	7.326	66.858	1.00	25.65
5	ATOM	1539	N VAL	207	32.632	8.136	65.285	1.00	22.49
	ATOM	1540	CA VAL	207	33.487	9.257	64.917	1.00	23.51
	ATOM	1541	CB VAL	207	32.775	10.133	63.855	1.00	25.35
	ATOM	1542	CG1 VAL	207	33.617	11.362	63.521	1.00	24.61
	ATOM	1543	CG2 VAL	207	32.509	9.299	62.609	1.00	21.66
10	ATOM	1544	C VAL	207	33.897	10.119	66.126	1.00	23.48
	ATOM	1545	O VAL	207	35.061	10.470	66.279	1.00	26.51
	ATOM	1546	N ALA	208	32.948	10.452	66.989	1.00	24.53
	ATOM	1547	CA ALA	208	33.262	11.251	68.169	1.00	26.32
	ATOM	1548	CB ALA	208	31.980	11.533	68.958	1.00	27.56
15	ATOM	1549	C ALA	208	34.287	10.530	69.055	1.00	28.84
	ATOM	1550	O ALA	208	35.247	11.138	69.549	1.00	27.69
	ATOM	1551	N THR	209	34.084	9.228	69.258	1.00	28.76
	ATOM	1552	CA THR	209	35.006	8.447	70.075	1.00	28.08
	ATOM	1553	CB THR	209	34.474	7.001	70.271	1.00	31.76
20	ATOM	1554	OG1 THR	209	33.373	7.027	71.181	1.00	33.12
	ATOM	1555	CG2 THR	209	35.550	6.080	70.818	1.00	30.03
	ATOM	1556	C THR	209	36.382	8.414	69.418	1.00	26.73
	ATOM	1557	O THR	209	37.399	8.611	70.078	1.00	28.00
	ATOM	1558	N MET	210	36.421	8.191	68.110	1.00	28.44
25	ATOM	1559	CA MET	210	37.703	8.143	67.419	1.00	28.08
	ATOM	1560	CB MET	210	37.516	7.851	65.932	1.00	26.94
	ATOM	1561	CG MET	210	38.842	7.766	65.168	1.00	28.59
	ATOM	1562	SD MET	210	38.643	7.734	63.374	1.00	32.14
	ATOM	1563	CE MET	210	38.216	9.518	63.083	1.00	33.30

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	ATOM	1564	C	MET	210	38.467	9.452	67.578	1.00	29.43
	ATOM	1565	O	MET	210	39.636	9.459	67.972	1.00	30.57
	ATOM	1566	N	ILE	211	37.799	10.561	67.281	1.00	31.16
	ATOM	1567	CA	ILE	211	38.433	11.873	67.376	1.00	30.57
5	ATOM	1568	CB	ILE	211	37.418	13.012	67.019	1.00	29.75
	ATOM	1569	CG2	ILE	211	38.086	14.390	67.177	1.00	28.08
	ATOM	1570	CG1	ILE	211	36.928	12.837	65.578	1.00	22.83
	ATOM	1571	CD1	ILE	211	38.021	12.979	64.553	1.00	26.28
	ATOM	1572	C	ILE	211	39.014	12.128	68.762	1.00	30.30
10	ATOM	1573	O	ILE	211	40.185	12.489	68.897	1.00	31.89
	ATOM	1574	N	SER	212	38.203	11.914	69.792	1.00	32.78
	ATOM	1575	CA	SER	212	38.639	12.146	71.164	1.00	35.84
	ATOM	1576	CB	SER	212	37.499	11.852	72.140	1.00	35.91
	ATOM	1577	OG	SER	212	37.317	10.455	72.307	1.00	41.55
15	ATOM	1578	C	SER	212	39.864	11.334	71.566	1.00	37.74
	ATOM	1579	O	SER	212	40.684	11.803	72.354	1.00	41.44
	ATOM	1580	N	CYS	213	39.990	10.121	71.040	1.00	38.07
	ATOM	1581	CA	CYS	213	41.132	9.273	71.374	1.00	39.83
	ATOM	1582	CB	CYS	213	40.802	7.799	71.108	1.00	38.31
20	ATOM	1583	SG	CYS	213	39.513	7.129	72.185	1.00	38.48
	ATOM	1584	C	CYS	213	42.372	9.666	70.582	1.00	41.86
	ATOM	1585	O	CYS	213	43.503	9.426	71.012	1.00	38.47
	ATOM	1586	N	TYR	214	42.149	10.261	69.413	1.00	45.32
	ATOM	1587	CA	TYR	214	43.243	10.701	68.554	1.00	45.02
25	ATOM	1588	CB	TYR	214	42.705	11.506	67.370	1.00	45.88
	ATOM	1589	CG	TYR	214	43.798	12.171	66.573	1.00	45.72
	ATOM	1590	CD1	TYR	214	44.509	11.465	65.608	1.00	46.39
	ATOM	1591	CE1	TYR	214	45.556	12.061	64.913	1.00	47.16
	ATOM	1592	CD2	TYR	214	44.160	13.498	66.823	1.00	44.53

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	ATOM	1593	CE2	TYR	214	45.203	14.099	66.134	1.00	45.20
	ATOM	1594	CZ	TYR	214	45.896	13.375	65.183	1.00	46.22
	ATOM	1595	OH	TYR	214	46.942	13.955	64.510	1.00	50.31
	ATOM	1596	C	TYR	214	44.226	11.573	69.322	1.00	44.69
5	ATOM	1597	O	TYR	214	45.420	11.296	69.363	1.00	44.40
	ATOM	1598	N	TYR	215	43.713	12.635	69.924	1.00	45.92
	ATOM	1599	CA	TYR	215	44.556	13.552	70.667	1.00	48.38
	ATOM	1600	CB	TYR	215	43.713	14.716	71.175	1.00	51.93
	ATOM	1601	CG	TYR	215	43.192	15.545	70.021	1.00	57.70
10	ATOM	1602	CD1	TYR	215	41.918	15.330	69.484	1.00	58.41
	ATOM	1603	CE1	TYR	215	41.478	16.047	68.363	1.00	61.27
	ATOM	1604	CD2	TYR	215	44.011	16.498	69.413	1.00	59.13
	ATOM	1605	CE2	TYR	215	43.586	17.214	68.300	1.00	61.22
	ATOM	1606	CZ	TYR	215	42.325	16.991	67.780	1.00	62.20
15	ATOM	1607	OH	TYR	215	41.928	17.728	66.688	1.00	61.67
	ATOM	1608	C	TYR	215	45.304	12.871	71.792	1.00	48.87
	ATOM	1609	O	TYR	215	46.282	13.407	72.318	1.00	49.38
	ATOM	1610	N	GLU	216	44.852	11.672	72.142	1.00	47.69
	ATOM	1611	CA	GLU	216	45.496	10.889	73.181	1.00	47.03
20	ATOM	1612	CB	GLU	216	44.474	9.979	73.863	1.00	49.83
	ATOM	1613	CG	GLU	216	44.837	9.550	75.270	1.00	55.37
	ATOM	1614	CD	GLU	216	44.998	10.735	76.208	1.00	59.31
	ATOM	1615	OE1	GLU	216	44.285	11.747	76.012	1.00	59.95
	ATOM	1616	OE2	GLU	216	45.824	10.649	77.146	1.00	60.13
25	ATOM	1617	C	GLU	216	46.552	10.044	72.477	1.00	45.45
	ATOM	1618	O	GLU	216	47.673	9.905	72.958	1.00	45.05
	ATOM	1619	N	ASP	217	46.183	9.495	71.321	1.00	43.73
	ATOM	1620	CA	ASP	217	47.074	8.643	70.530	1.00	41.33
	ATOM	1621	CB	ASP	217	46.776	7.171	70.845	1.00	40.13

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	ATOM	1622	CG	ASP	217	47.780	6.208	70.226	1.00	39.76
	ATOM	1623	OD1	ASP	217	48.461	6.571	69.249	1.00	40.95
	ATOM	1624	OD2	ASP	217	47.876	5.062	70.712	1.00	42.61
	ATOM	1625	C	ASP	217	46.852	8.921	69.033	1.00	40.53
5	ATOM	1626	O	ASP	217	45.862	8.474	68.443	1.00	37.20
	ATOM	1627	N	HIS	218	47.779	9.657	68.427	1.00	41.94
	ATOM	1628	CA	HIS	218	47.689	10.008	67.007	1.00	44.23
	ATOM	1629	CB	HIS	218	48.912	10.828	66.603	1.00	47.00
	ATOM	1630	CG	HIS	218	48.860	12.244	67.079	1.00	51.95
10	ATOM	1631	CD2	HIS	218	49.230	13.402	66.483	1.00	54.47
	ATOM	1632	ND1	HIS	218	48.371	12.592	68.320	1.00	54.33
	ATOM	1633	CE1	HIS	218	48.439	13.903	68.467	1.00	55.83
	ATOM	1634	NE2	HIS	218	48.957	14.419	67.367	1.00	55.95
	ATOM	1635	C	HIS	218	47.528	8.810	66.074	1.00	42.66
15	ATOM	1636	O	HIS	218	47.157	8.963	64.909	1.00	42.00
	ATOM	1637	N	GLN	219	47.793	7.620	66.597	1.00	41.40
	ATOM	1638	CA	GLN	219	47.667	6.394	65.820	1.00	41.15
	ATOM	1639	CB	GLN	219	48.592	5.321	66.397	1.00	45.16
	ATOM	1640	CG	GLN	219	50.070	5.611	66.214	1.00	49.72
20	ATOM	1641	CD	GLN	219	50.566	5.230	64.832	1.00	55.92
	ATOM	1642	OE1	GLN	219	49.997	5.646	63.813	1.00	57.28
	ATOM	1643	NE2	GLN	219	51.636	4.429	64.787	1.00	57.32
	ATOM	1644	C	GLN	219	46.228	5.869	65.792	1.00	37.41
	ATOM	1645	O	GLN	219	45.927	4.904	65.091	1.00	37.06
25	ATOM	1646	N	CYS	220	45.342	6.488	66.562	1.00	34.18
	ATOM	1647	CA	CYS	220	43.955	6.038	66.578	1.00	32.52
	ATOM	1648	CB	CYS	220	43.199	6.597	67.783	1.00	28.93
	ATOM	1649	SG	CYS	220	41.420	6.288	67.739	1.00	31.90
	ATOM	1650	C	CYS	220	43.272	6.474	65.303	1.00	32.01

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	ATOM	1651	O	CYS	220	43.010	7.664	65.096	1.00	32.91
	ATOM	1652	N	GLU	221	42.993	5.505	64.442	1.00	29.12
	ATOM	1653	CA	GLU	221	42.343	5.785	63.176	1.00	28.98
	ATOM	1654	CB	GLU	221	43.273	5.437	62.009	1.00	30.00
5	ATOM	1655	CG	GLU	221	44.481	6.366	61.853	1.00	35.29
	ATOM	1656	CD	GLU	221	45.190	6.166	60.515	1.00	36.83
	ATOM	1657	OE1	GLU	221	44.490	6.007	59.498	1.00	38.09
	ATOM	1658	OE2	GLU	221	46.436	6.176	60.465	1.00	40.80
	ATOM	1659	C	GLU	221	41.057	4.991	63.059	1.00	25.46
10	ATOM	1660	O	GLU	221	40.513	4.835	61.970	1.00	22.65
	ATOM	1661	N	VAL	222	40.569	4.491	64.185	1.00	25.43
	ATOM	1662	CA	VAL	222	39.337	3.703	64.179	1.00	25.45
	ATOM	1663	CB	VAL	222	39.625	2.172	64.189	1.00	24.36
	ATOM	1664	CG1	VAL	222	38.318	1.391	64.122	1.00	21.56
15	ATOM	1665	CG2	VAL	222	40.533	1.795	63.029	1.00	21.70
	ATOM	1666	C	VAL	222	38.527	4.016	65.414	1.00	25.44
	ATOM	1667	O	VAL	222	39.076	4.192	66.492	1.00	25.99
	ATOM	1668	N	GLY	223	37.217	4.090	65.240	1.00	25.97
	ATOM	1669	CA	GLY	223	36.328	4.347	66.349	1.00	25.83
20	ATOM	1670	C	GLY	223	35.337	3.201	66.340	1.00	25.37
	ATOM	1671	O	GLY	223	34.852	2.812	65.273	1.00	25.38
	ATOM	1672	N	MET	224	35.044	2.647	67.511	1.00	24.88
	ATOM	1673	CA	MET	224	34.114	1.527	67.587	1.00	25.47
	ATOM	1674	CB	MET	224	34.881	0.187	67.638	1.00	22.66
25	ATOM	1675	CG	MET	224	33.956	-1.041	67.634	1.00	25.14
	ATOM	1676	SD	MET	224	34.806	-2.680	67.748	1.00	22.18
	ATOM	1677	CE	MET	224	35.380	-2.594	69.396	1.00	16.01
	ATOM	1678	C	MET	224	33.177	1.618	68.780	1.00	22.20
	ATOM	1679	O	MET	224	33.577	1.978	69.881	1.00	22.65

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	ATOM	1680	N	ILE	225	31.915	1.295	68.543	1.00	21.12
	ATOM	1681	CA	ILE	225	30.936	1.314	69.604	1.00	21.34
	ATOM	1682	CB	ILE	225	29.757	2.295	69.293	1.00	25.85
	ATOM	1683	CG2	ILE	225	28.739	2.268	70.446	1.00	25.47
5	ATOM	1684	CG1	ILE	225	30.273	3.734	69.107	1.00	25.08
	ATOM	1685	CD1	ILE	225	30.838	4.355	70.382	1.00	22.09
	ATOM	1686	C	ILE	225	30.321	-0.080	69.789	1.00	22.30
	ATOM	1687	O	ILE	225	29.885	-0.712	68.826	1.00	24.03
	ATOM	1688	N	VAL	226	30.313	-0.563	71.025	1.00	22.67
10	ATOM	1689	CA	VAL	226	29.645	-1.817	71.341	1.00	21.60
	ATOM	1690	CB	VAL	226	30.618	-2.993	71.634	1.00	21.77
	ATOM	1691	CG1	VAL	226	29.821	-4.291	71.718	1.00	21.54
	ATOM	1692	CG2	VAL	226	31.663	-3.113	70.541	1.00	17.23
	ATOM	1693	C	VAL	226	28.838	-1.493	72.604	1.00	21.49
15	ATOM	1694	O	VAL	226	29.316	-1.633	73.723	1.00	18.90
	ATOM	1695	N	GLY	227	27.615	-1.016	72.402	1.00	25.39
	ATOM	1696	CA	GLY	227	26.744	-0.675	73.518	1.00	26.76
	ATOM	1697	C	GLY	227	25.353	-1.140	73.150	1.00	28.03
	ATOM	1698	O	GLY	227	25.155	-2.315	72.846	1.00	29.80
20	ATOM	1699	N	THR	228	24.384	-0.235	73.161	1.00	27.62
	ATOM	1700	CA	THR	228	23.031	-0.607	72.788	1.00	27.59
	ATOM	1701	CB	THR	228	22.083	0.601	72.911	1.00	29.15
	ATOM	1702	OG1	THR	228	21.937	0.932	74.294	1.00	32.52
	ATOM	1703	CG2	THR	228	20.719	0.291	72.339	1.00	28.08
25	ATOM	1704	C	THR	228	23.094	-1.080	71.345	1.00	26.98
	ATOM	1705	O	THR	228	22.460	-2.065	70.960	1.00	27.95
	ATOM	1706	N	GLY	229	23.890	-0.374	70.554	1.00	26.02
	ATOM	1707	CA	GLY	229	24.050	-0.718	69.154	1.00	25.33
	ATOM	1708	C	GLY	229	25.503	-1.055	68.911	1.00	24.09

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	ATOM	1709	O	GLY	229	26.312	-1.004	69.838	1.00	23.25
	ATOM	1710	N	CYS	230	25.850	-1.395	67.677	1.00	24.12
	ATOM	1711	CA	CYS	230	27.235	-1.750	67.376	1.00	23.83
	ATOM	1712	CB	CYS	230	27.395	-3.280	67.425	1.00	20.39
5	ATOM	1713	SG	CYS	230	29.076	-3.879	67.182	1.00	25.34
	ATOM	1714	C	CYS	230	27.627	-1.204	66.010	1.00	20.45
	ATOM	1715	O	CYS	230	26.919	-1.406	65.035	1.00	20.28
	ATOM	1716	N	ASN	231	28.763	-0.526	65.935	1.00	23.86
	ATOM	1717	CA	ASN	231	29.196	0.076	64.669	1.00	24.35
10	ATOM	1718	CB	ASN	231	28.267	1.261	64.355	1.00	25.51
	ATOM	1719	CG	ASN	231	28.598	1.962	63.042	1.00	27.76
	ATOM	1720	OD1	ASN	231	28.930	1.331	62.039	1.00	24.60
	ATOM	1721	ND2	ASN	231	28.472	3.288	63.043	1.00	30.91
	ATOM	1722	C	ASN	231	30.640	0.553	64.784	1.00	23.81
15	ATOM	1723	O	ASN	231	31.184	0.624	65.885	1.00	23.94
	ATOM	1724	N	ALA	232	31.249	0.885	63.651	1.00	22.70
	ATOM	1725	CA	ALA	232	32.626	1.359	63.636	1.00	25.15
	ATOM	1726	CB	ALA	232	33.580	0.169	63.463	1.00	24.36
	ATOM	1727	C	ALA	232	32.867	2.372	62.511	1.00	26.31
20	ATOM	1728	O	ALA	232	32.127	2.416	61.530	1.00	28.47
	ATOM	1729	N	CYS	233	33.911	3.176	62.664	1.00	24.88
	ATOM	1730	CA	CYS	233	34.291	4.160	61.653	1.00	26.51
	ATOM	1731	CB	CYS	233	33.899	5.583	62.076	1.00	24.89
	ATOM	1732	SG	CYS	233	34.875	6.224	63.436	1.00	25.76
25	ATOM	1733	C	CYS	233	35.805	4.055	61.555	1.00	25.08
	ATOM	1734	O	CYS	233	36.450	3.564	62.480	1.00	25.19
	ATOM	1735	N	TYR	234	36.373	4.505	60.442	1.00	25.32
	ATOM	1736	CA	TYR	234	37.820	4.427	60.245	1.00	23.93
	ATOM	1737	CB	TYR	234	38.200	3.020	59.760	1.00	20.70



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	ATOM	1738	CG	TYR	234	37.782	2.771	58.328	1.00	16.78
	ATOM	1739	CD1	TYR	234	38.712	2.786	57.302	1.00	18.75
	ATOM	1740	CE1	TYR	234	38.326	2.668	55.975	1.00	18.89
	ATOM	1741	CD2	TYR	234	36.443	2.622	57.990	1.00	19.60
5	ATOM	1742	CE2	TYR	234	36.043	2.506	56.666	1.00	18.40
	ATOM	1743	CZ	TYR	234	36.990	2.535	55.665	1.00	21.55
	ATOM	1744	OH	TYR	234	36.603	2.479	54.346	1.00	23.25
	ATOM	1745	C	TYR	234	38.254	5.452	59.194	1.00	26.41
	ATOM	1746	O	TYR	234	37.436	5.929	58.404	1.00	27.14
10	ATOM	1747	N	MET	235	39.543	5.769	59.179	1.00	27.10
	ATOM	1748	CA	MET	235	40.094	6.722	58.224	1.00	28.74
	ATOM	1749	CB	MET	235	41.383	7.331	58.789	1.00	29.38
	ATOM	1750	CG	MET	235	41.169	8.180	60.035	1.00	31.43
	ATOM	1751	SD	MET	235	39.947	9.503	59.750	1.00	32.30
15	ATOM	1752	CE	MET	235	40.866	10.535	58.591	1.00	34.11
	ATOM	1753	C	MET	235	40.374	6.066	56.869	1.00	29.42
	ATOM	1754	O	MET	235	41.170	5.134	56.767	1.00	30.49
	ATOM	1755	N	GLU	236	39.714	6.565	55.829	1.00	31.08
	ATOM	1756	CA	GLU	236	39.867	6.040	54.476	1.00	31.04
20	ATOM	1757	CB	GLU	236	38.491	5.743	53.879	1.00	31.57
	ATOM	1758	CG	GLU	236	38.536	5.161	52.474	1.00	32.18
	ATOM	1759	CD	GLU	236	39.330	3.875	52.427	1.00	32.52
	ATOM	1760	OE1	GLU	236	40.565	3.952	52.273	1.00	34.34
	ATOM	1761	OE2	GLU	236	38.723	2.789	52.571	1.00	30.79
25	ATOM	1762	C	GLU	236	40.598	7.030	53.574	1.00	33.43
	ATOM	1763	O	GLU	236	40.583	8.238	53.818	1.00	29.93
	ATOM	1764	N	GLU	237	41.240	6.506	52.532	1.00	35.85
	ATOM	1765	CA	GLU	237	41.969	7.333	51.575	1.00	37.83
	ATOM	1766	CB	GLU	237	42.934	6.462	50.764	1.00	40.16

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	ATOM	1767	CG	GLU	237	43.684	5.426	51.602	1.00	43.86
	ATOM	1768	CD	GLU	237	44.466	6.049	52.743	1.00	47.85
	ATOM	1769	OE1	GLU	237	44.806	5.322	53.704	1.00	51.02
	ATOM	1770	OE2	GLU	237	44.747	7.264	52.681	1.00	48.78
5	ATOM	1771	C	GLU	237	40.920	7.969	50.657	1.00	37.87
	ATOM	1772	O	GLU	237	40.058	7.268	50.122	1.00	38.29
	ATOM	1773	N	MET	238	40.987	9.287	50.477	1.00	37.42
	ATOM	1774	CA	MET	238	40.009	9.987	49.644	1.00	37.50
	ATOM	1775	CB	MET	238	40.375	11.467	49.501	1.00	38.62
10	ATOM	1776	CG	MET	238	39.772	12.355	50.587	1.00	40.32
	ATOM	1777	SD	MET	238	37.956	12.144	50.764	1.00	42.83
	ATOM	1778	CE	MET	238	37.308	13.116	49.410	1.00	44.06
	ATOM	1779	C	MET	238	39.796	9.374	48.270	1.00	36.21
	ATOM	1780	O	MET	238	38.685	9.413	47.740	1.00	33.93
15	ATOM	1781	N	GLN	239	40.848	8.803	47.690	1.00	35.50
	ATOM	1782	CA	GLN	239	40.714	8.184	46.378	1.00	36.82
	ATOM	1783	CB	GLN	239	42.078	7.732	45.846	1.00	39.35
	ATOM	1784	CG	GLN	239	42.839	6.804	46.774	1.00	44.12
	ATOM	1785	CD	GLN	239	43.900	7.534	47.584	1.00	49.18
20	ATOM	1786	OE1	GLN	239	43.635	8.580	48.192	1.00	49.88
	ATOM	1787	NE2	GLN	239	45.111	6.981	47.600	1.00	49.95
	ATOM	1788	C	GLN	239	39.762	6.986	46.395	1.00	35.72
	ATOM	1789	O	GLN	239	39.276	6.568	45.348	1.00	37.20
	ATOM	1790	N	ASN	240	39.503	6.419	47.570	1.00	34.56
25	ATOM	1791	CA	ASN	240	38.604	5.272	47.648	1.00	33.20
	ATOM	1792	CB	ASN	240	39.118	4.239	48.658	1.00	33.68
	ATOM	1793	CG	ASN	240	40.548	3.802	48.369	1.00	34.24
	ATOM	1794	OD1	ASN	240	40.963	3.710	47.210	1.00	33.87
	ATOM	1795	ND2	ASN	240	41.306	3.523	49.424	1.00	34.32

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	ATOM	1796	C	ASN	240	37.190	5.690	48.011	1.00	33.25
	ATOM	1797	O	ASN	240	36.259	4.886	47.936	1.00	33.86
	ATOM	1798	N	VAL	241	37.024	6.946	48.414	1.00	32.52
	ATOM	1799	CA	VAL	241	35.702	7.441	48.753	1.00	31.62
5	ATOM	1800	CB	VAL	241	35.755	8.559	49.811	1.00	29.14
	ATOM	1801	CG1	VAL	241	34.339	8.948	50.204	1.00	31.00
	ATOM	1802	CG2	VAL	241	36.530	8.107	51.021	1.00	26.87
	ATOM	1803	C	VAL	241	35.102	8.010	47.474	1.00	33.73
	ATOM	1804	O	VAL	241	35.048	9.224	47.286	1.00	35.18
10	ATOM	1805	N	GLU	242	34.643	7.132	46.595	1.00	33.33
	ATOM	1806	CA	GLU	242	34.075	7.572	45.324	1.00	33.69
	ATOM	1807	CB	GLU	242	33.788	6.364	44.431	1.00	31.05
	ATOM	1808	CG	GLU	242	34.983	5.457	44.222	1.00	33.00
	ATOM	1809	CD	GLU	242	34.767	4.451	43.115	1.00	33.45
15	ATOM	1810	OE1	GLU	242	33.595	4.162	42.776	1.00	33.74
	ATOM	1811	OE2	GLU	242	35.778	3.940	42.592	1.00	35.96
	ATOM	1812	C	GLU	242	32.812	8.437	45.427	1.00	34.45
	ATOM	1813	O	GLU	242	32.406	9.061	44.442	1.00	32.92
	ATOM	1814	N	LEU	243	32.192	8.471	46.602	1.00	33.82
20	ATOM	1815	CA	LEU	243	30.982	9.262	46.799	1.00	36.13
	ATOM	1816	CB	LEU	243	30.080	8.598	47.844	1.00	33.99
	ATOM	1817	CG	LEU	243	29.168	7.490	47.297	1.00	37.04
	ATOM	1818	CD1	LEU	243	27.999	8.096	46.545	1.00	36.01
	ATOM	1819	CD2	LEU	243	29.969	6.560	46.384	1.00	36.49
25	ATOM	1820	C	LEU	243	31.290	10.700	47.199	1.00	35.69
	ATOM	1821	O	LEU	243	30.406	11.458	47.585	1.00	37.51
	ATOM	1822	N	VAL	244	32.560	11.062	47.117	1.00	37.53
	ATOM	1823	CA	VAL	244	32.992	12.411	47.426	1.00	37.50
	ATOM	1824	CB	VAL	244	33.537	12.547	48.861	1.00	36.75

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	ATOM	1825	CG1	VAL	244	33.967	13.990	49.109	1.00	36.55
	ATOM	1826	CG2	VAL	244	32.465	12.160	49.870	1.00	37.02
	ATOM	1827	C	VAL	244	34.099	12.727	46.446	1.00	39.75
	ATOM	1828	O	VAL	244	35.090	12.003	46.361	1.00	39.55
5	ATOM	1829	N	GLU	245	33.909	13.802	45.688	1.00	42.16
	ATOM	1830	CA	GLU	245	34.880	14.232	44.695	1.00	42.30
	ATOM	1831	CB	GLU	245	34.372	15.487	43.989	1.00	45.34
	ATOM	1832	CG	GLU	245	34.886	15.636	42.576	1.00	48.54
	ATOM	1833	CD	GLU	245	34.377	16.893	41.901	1.00	50.12
10	ATOM	1834	OE1	GLU	245	33.192	17.249	42.107	1.00	49.37
	ATOM	1835	OE2	GLU	245	35.164	17.511	41.152	1.00	52.40
	ATOM	1836	C	GLU	245	36.203	14.532	45.378	1.00	41.00
	ATOM	1837	O	GLU	245	36.230	15.132	46.446	1.00	42.20
	ATOM	1838	N	GLY	246	37.297	14.107	44.761	1.00	41.28
15	ATOM	1839	CA	GLY	246	38.606	14.349	45.336	1.00	42.88
	ATOM	1840	C	GLY	246	39.362	13.066	45.618	1.00	45.38
	ATOM	1841	O	GLY	246	38.774	12.056	45.997	1.00	45.50
	ATOM	1842	N	ASP	247	40.675	13.105	45.443	1.00	47.31
	ATOM	1843	CA	ASP	247	41.509	11.940	45.687	1.00	49.13
20	ATOM	1844	CB	ASP	247	42.139	11.454	44.384	1.00	51.65
	ATOM	1845	CG	ASP	247	41.131	10.836	43.449	1.00	56.09
	ATOM	1846	OD1	ASP	247	41.534	10.410	42.345	1.00	58.83
	ATOM	1847	OD2	ASP	247	39.936	10.770	43.819	1.00	59.44
	ATOM	1848	C	ASP	247	42.611	12.274	46.667	1.00	49.51
25	ATOM	1849	O	ASP	247	43.406	11.415	47.039	1.00	49.57
	ATOM	1850	N	GLU	248	42.661	13.531	47.086	1.00	50.49
	ATOM	1851	CA	GLU	248	43.696	13.957	48.011	1.00	50.97
	ATOM	1852	CB	GLU	248	44.198	15.351	47.634	1.00	54.71
	ATOM	1853	CG	GLU	248	45.670	15.391	47.259	1.00	62.15

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	ATOM	1854	CD	GLU	248	46.067	14.259	46.317	1.00	66.63
	ATOM	1855	OE1	GLU	248	46.196	13.105	46.788	1.00	68.58
	ATOM	1856	OE2	GLU	248	46.241	14.520	45.105	1.00	68.21
	ATOM	1857	C	GLU	248	43.222	13.955	49.446	1.00	47.90
5	ATOM	1858	O	GLU	248	42.063	14.250	49.726	1.00	46.55
	ATOM	1859	N	GLY	249	44.133	13.614	50.351	1.00	45.49
	ATOM	1860	CA	GLY	249	43.799	13.590	51.759	1.00	44.30
	ATOM	1861	C	GLY	249	43.138	12.301	52.205	1.00	42.85
	ATOM	1862	O	GLY	249	43.257	11.259	51.552	1.00	42.97
10	ATOM	1863	N	ARG	250	42.444	12.380	53.335	1.00	41.43
	ATOM	1864	CA	ARG	250	41.747	11.232	53.897	1.00	39.63
	ATOM	1865	CB	ARG	250	42.625	10.532	54.931	1.00	40.69
	ATOM	1866	CG	ARG	250	44.092	10.454	54.559	1.00	43.91
	ATOM	1867	CD	ARG	250	44.903	9.902	55.714	1.00	45.22
15	ATOM	1868	NE	ARG	250	44.630	8.487	55.940	1.00	45.43
	ATOM	1869	CZ	ARG	250	45.040	7.813	57.007	1.00	44.67
	ATOM	1870	NH1	ARG	250	45.738	8.426	57.954	1.00	46.95
	ATOM	1871	NH2	ARG	250	44.761	6.524	57.121	1.00	46.99
	ATOM	1872	C	ARG	250	40.486	11.726	54.580	1.00	37.70
20	ATOM	1873	O	ARG	250	40.430	12.865	55.042	1.00	37.51
	ATOM	1874	N	MET	251	39.473	10.867	54.630	1.00	35.10
	ATOM	1875	CA	MET	251	38.216	11.197	55.277	1.00	32.34
	ATOM	1876	CB	MET	251	37.137	11.517	54.242	1.00	33.00
	ATOM	1877	CG	MET	251	35.803	11.907	54.868	1.00	31.56
25	ATOM	1878	SD	MET	251	34.474	12.160	53.677	1.00	37.84
	ATOM	1879	CE	MET	251	35.067	13.715	52.885	1.00	32.92
	ATOM	1880	C	MET	251	37.764	10.007	56.121	1.00	32.47
	ATOM	1881	O	MET	251	38.024	8.852	55.777	1.00	31.05
	ATOM	1882	N	CYS	252	37.088	10.292	57.229	1.00	30.16

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	ATOM	1883	CA	CYS	252	36.595	9.236	58.092	1.00	30.32
	ATOM	1884	CB	CYS	252	36.364	9.762	59.517	1.00	30.54
	ATOM	1885	SG	CYS	252	35.601	8.557	60.676	1.00	28.61
	ATOM	1886	C	CYS	252	35.292	8.717	57.511	1.00	29.86
5	ATOM	1887	O	CYS	252	34.422	9.495	57.114	1.00	29.84
	ATOM	1888	N	VAL	253	35.170	7.397	57.438	1.00	28.79
	ATOM	1889	CA	VAL	253	33.960	6.776	56.921	1.00	27.69
	ATOM	1890	CB	VAL	253	34.291	5.761	55.816	1.00	28.07
	ATOM	1891	CG1	VAL	253	33.033	5.005	55.405	1.00	26.98
10	ATOM	1892	CG2	VAL	253	34.898	6.484	54.624	1.00	24.14
	ATOM	1893	C	VAL	253	33.200	6.069	58.038	1.00	28.79
	ATOM	1894	O	VAL	253	33.801	5.448	58.922	1.00	31.23
	ATOM	1895	N	ASN	254	31.879	6.188	58.000	1.00	28.38
	ATOM	1896	CA	ASN	254	31.003	5.557	58.976	1.00	27.73
15	ATOM	1897	CB	ASN	254	29.834	6.473	59.328	1.00	27.41
	ATOM	1898	CG	ASN	254	28.803	5.779	60.181	1.00	31.67
	ATOM	1899	OD1	ASN	254	29.048	4.675	60.677	1.00	32.14
	ATOM	1900	ND2	ASN	254	27.643	6.415	60.367	1.00	29.17
	ATOM	1901	C	ASN	254	30.480	4.295	58.299	1.00	27.41
20	ATOM	1902	O	ASN	254	29.575	4.372	57.467	1.00	25.53
	ATOM	1903	N	THR	255	31.049	3.142	58.654	1.00	24.66
	ATOM	1904	CA	THR	255	30.662	1.883	58.016	1.00	24.86
	ATOM	1905	CB	THR	255	31.501	0.665	58.527	1.00	23.42
	ATOM	1906	OG1	THR	255	31.071	0.310	59.849	1.00	23.50
25	ATOM	1907	CG2	THR	255	32.973	0.982	58.558	1.00	23.88
	ATOM	1908	C	THR	255	29.207	1.488	58.195	1.00	23.00
	ATOM	1909	O	THR	255	28.589	0.984	57.259	1.00	24.38
	ATOM	1910	N	GLU	256	28.673	1.710	59.394	1.00	23.70
	ATOM	1911	CA	GLU	256	27.306	1.305	59.721	1.00	26.37

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	ATOM	1912	CB	GLU	256	26.271	2.017	58.838	1.00	26.22
	ATOM	1913	CG	GLU	256	25.974	3.471	59.204	1.00	29.32
	ATOM	1914	CD	GLU	256	25.284	3.644	60.558	1.00	31.10
	ATOM	1915	OE1	GLU	256	24.489	2.764	60.953	1.00	31.47
5	ATOM	1916	OE2	GLU	256	25.523	4.682	61.218	1.00	30.04
	ATOM	1917	C	GLU	256	27.269	-0.203	59.458	1.00	27.40
	ATOM	1918	O	GLU	256	26.369	-0.713	58.782	1.00	26.71
	ATOM	1919	N	TRP	257	28.269	-0.912	59.982	1.00	25.98
	ATOM	1920	CA	TRP	257	28.335	-2.356	59.774	1.00	24.56
10	ATOM	1921	CB	TRP	257	29.714	-2.928	60.180	1.00	21.05
	ATOM	1922	CG	TRP	257	30.100	-2.891	61.653	1.00	17.51
	ATOM	1923	CD2	TRP	257	31.429	-3.026	62.182	1.00	16.19
	ATOM	1924	CE2	TRP	257	31.320	-3.077	63.588	1.00	14.42
	ATOM	1925	CE3	TRP	257	32.705	-3.112	61.597	1.00	16.23
15	ATOM	1926	CD1	TRP	257	29.264	-2.862	62.733	1.00	18.14
	ATOM	1927	NE1	TRP	257	29.990	-2.977	63.902	1.00	19.95
	ATOM	1928	CZ2	TRP	257	32.435	-3.214	64.421	1.00	17.46
	ATOM	1929	CZ3	TRP	257	33.815	-3.246	62.424	1.00	13.91
	ATOM	1930	CH2	TRP	257	33.672	-3.294	63.822	1.00	14.28
20	ATOM	1931	C	TRP	257	27.218	-3.091	60.500	1.00	24.58
	ATOM	1932	O	TRP	257	27.067	-4.305	60.352	1.00	24.81
	ATOM	1933	N	GLY	258	26.427	-2.354	61.273	1.00	23.21
	ATOM	1934	CA	GLY	258	25.328	-2.981	61.982	1.00	23.11
	ATOM	1935	C	GLY	258	24.385	-3.640	60.991	1.00	25.72
25	ATOM	1936	O	GLY	258	23.758	-4.660	61.285	1.00	28.37
	ATOM	1937	N	ALA	259	24.288	-3.067	59.796	1.00	24.64
	ATOM	1938	CA	ALA	259	23.406	-3.630	58.789	1.00	25.53
	ATOM	1939	CB	ALA	259	22.866	-2.519	57.874	1.00	25.11
	ATOM	1940	C	ALA	259	24.084	-4.724	57.961	1.00	25.44

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	ATOM	1941	O	ALA	259	23.515	-5.205	56.985	1.00	24.68
	ATOM	1942	N	PHE	260	25.306	-5.101	58.329	1.00	26.96
	ATOM	1943	CA	PHE	260	25.995	-6.175	57.614	1.00	28.11
	ATOM	1944	CB	PHE	260	27.359	-6.440	58.254	1.00	30.88
5	ATOM	1945	CG	PHE	260	28.127	-7.569	57.625	1.00	33.87
	ATOM	1946	CD1	PHE	260	28.496	-7.525	56.286	1.00	33.60
	ATOM	1947	CD2	PHE	260	28.499	-8.675	58.380	1.00	37.30
	ATOM	1948	CE1	PHE	260	29.220	-8.564	55.716	1.00	33.58
	ATOM	1949	CE2	PHE	260	29.229	-9.720	57.808	1.00	35.65
10	ATOM	1950	CZ	PHE	260	29.586	-9.660	56.478	1.00	34.41
	ATOM	1951	C	PHE	260	25.080	-7.388	57.783	1.00	28.87
	ATOM	1952	O	PHE	260	24.487	-7.576	58.849	1.00	27.08
	ATOM	1953	N	GLY	261	24.941	-8.193	56.737	1.00	28.88
	ATOM	1954	CA	GLY	261	24.074	-9.357	56.826	1.00	30.83
15	ATOM	1955	C	GLY	261	22.664	-9.092	56.317	1.00	32.15
	ATOM	1956	O	GLY	261	21.905	-10.021	56.043	1.00	34.22
	ATOM	1957	N	ASP	262	22.307	-7.822	56.175	1.00	33.45
	ATOM	1958	CA	ASP	262	20.975	-7.456	55.701	1.00	35.91
	ATOM	1959	CB	ASP	262	20.761	-5.948	55.868	1.00	35.78
20	ATOM	1960	CG	ASP	262	20.674	-5.541	57.323	1.00	35.93
	ATOM	1961	OD1	ASP	262	20.903	-6.415	58.182	1.00	37.70
	ATOM	1962	OD2	ASP	262	20.382	-4.364	57.615	1.00	35.14
	ATOM	1963	C	ASP	262	20.676	-7.884	54.262	1.00	36.35
	ATOM	1964	O	ASP	262	19.546	-7.758	53.799	1.00	37.40
25	ATOM	1965	N	SER	263	21.685	-8.380	53.554	1.00	37.07
	ATOM	1966	CA	SER	263	21.488	-8.863	52.189	1.00	37.53
	ATOM	1967	CB	SER	263	22.420	-8.155	51.200	1.00	37.00
	ATOM	1968	OG	SER	263	22.028	-6.815	50.991	1.00	38.85
	ATOM	1969	C	SER	263	21.770	-10.359	52.161	1.00	37.06



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	ATOM	1970	O	SER	263	22.062	-10.923	51.107	1.00	36.90
	ATOM	1971	N	GLY	264	21.697	-10.988	53.331	1.00	36.97
	ATOM	1972	CA	GLY	264	21.934	-12.418	53.428	1.00	37.50
	ATOM	1973	C	GLY	264	23.370	-12.857	53.663	1.00	38.59
5	ATOM	1974	O	GLY	264	23.666	-14.050	53.573	1.00	40.28
	ATOM	1975	N	GLU	265	24.263	-11.915	53.961	1.00	37.52
	ATOM	1976	CA	GLU	265	25.671	-12.237	54.199	1.00	36.34
	ATOM	1977	CB	GLU	265	26.488	-10.965	54.438	1.00	35.82
	ATOM	1978	CG	GLU	265	26.535	-9.976	53.289	1.00	38.57
10	ATOM	1979	CD	GLU	265	25.270	-9.148	53.158	1.00	39.55
	ATOM	1980	OE1	GLU	265	24.600	-8.901	54.173	1.00	38.51
	ATOM	1981	OE2	GLU	265	24.953	-8.722	52.031	1.00	43.82
	ATOM	1982	C	GLU	265	25.906	-13.171	55.391	1.00	36.38
	ATOM	1983	O	GLU	265	26.899	-13.906	55.425	1.00	35.35
15	ATOM	1984	N	LEU	266	24.996	-13.140	56.362	1.00	34.63
	ATOM	1985	CA	LEU	266	25.130	-13.955	57.567	1.00	35.02
	ATOM	1986	CB	LEU	266	25.008	-13.054	58.803	1.00	31.68
	ATOM	1987	CG	LEU	266	26.017	-11.914	58.973	1.00	33.35
	ATOM	1988	CD1	LEU	266	25.555	-10.975	60.077	1.00	32.52
20	ATOM	1989	CD2	LEU	266	27.383	-12.480	59.294	1.00	32.43
	ATOM	1990	C	LEU	266	24.108	-15.092	57.674	1.00	35.37
	ATOM	1991	O	LEU	266	24.047	-15.779	58.696	1.00	35.21
	ATOM	1992	N	ASP	267	23.321	-15.300	56.627	1.00	36.35
	ATOM	1993	CA	ASP	267	22.286	-16.332	56.643	1.00	39.50
25	ATOM	1994	CB	ASP	267	21.664	-16.480	55.248	1.00	42.21
	ATOM	1995	CG	ASP	267	20.666	-15.369	54.921	1.00	45.43
	ATOM	1996	OD1	ASP	267	20.205	-15.320	53.759	1.00	48.41
	ATOM	1997	OD2	ASP	267	20.332	-14.554	55.813	1.00	45.57
	ATOM	1998	C	ASP	267	22.676	-17.715	57.171	1.00	38.87

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	ATOM	1999	O	ASP	267	21.888	-18.353	57.867	1.00	39.64
	ATOM	2000	N	GLU	268	23.879	-18.179	56.860	1.00	38.72
	ATOM	2001	CA	GLU	268	24.301	-19.502	57.313	1.00	39.91
	ATOM	2002	CB	GLU	268	25.510	-19.971	56.495	1.00	40.60
5	ATOM	2003	CG	GLU	268	26.847	-19.444	56.976	1.00	43.85
	ATOM	2004	CD	GLU	268	27.969	-19.710	55.981	1.00	47.64
	ATOM	2005	OE1	GLU	268	28.013	-19.017	54.941	1.00	49.73
	ATOM	2006	OE2	GLU	268	28.802	-20.612	56.232	1.00	48.40
	ATOM	2007	C	GLU	268	24.633	-19.577	58.807	1.00	40.59
10	ATOM	2008	O	GLU	268	24.790	-20.667	59.360	1.00	41.43
	ATOM	2009	N	PHE	269	24.734	-18.427	59.462	1.00	39.17
	ATOM	2010	CA	PHE	269	25.070	-18.402	60.882	1.00	37.75
	ATOM	2011	CB	PHE	269	26.182	-17.385	61.127	1.00	34.69
	ATOM	2012	CG	PHE	269	27.435	-17.675	60.369	1.00	35.74
15	ATOM	2013	CD1	PHE	269	28.144	-18.853	60.599	1.00	35.94
	ATOM	2014	CD2	PHE	269	27.910	-16.781	59.416	1.00	34.75
	ATOM	2015	CE1	PHE	269	29.306	-19.136	59.891	1.00	34.71
	ATOM	2016	CE2	PHE	269	29.068	-17.050	58.701	1.00	34.58
	ATOM	2017	CZ	PHE	269	29.770	-18.233	58.939	1.00	35.80
20	ATOM	2018	C	PHE	269	23.898	-18.085	61.793	1.00	36.73
	ATOM	2019	O	PHE	269	23.932	-18.384	62.984	1.00	36.59
	ATOM	2020	N	LEU	270	22.861	-17.480	61.231	1.00	37.18
	ATOM	2021	CA	LEU	270	21.696	-17.107	62.012	1.00	37.71
	ATOM	2022	CB	LEU	270	20.712	-16.332	61.135	1.00	36.52
25	ATOM	2023	CG	LEU	270	21.264	-15.036	60.521	1.00	37.18
	ATOM	2024	CD1	LEU	270	20.299	-14.516	59.466	1.00	38.72
	ATOM	2025	CD2	LEU	270	21.488	-13.990	61.604	1.00	34.72
	ATOM	2026	C	LEU	270	21.010	-18.312	62.644	1.00	38.27
	ATOM	2027	O	LEU	270	20.794	-19.333	61.995	1.00	39.49

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	ATOM	2028	N	LEU	271	20.685	-18.176	63.924	1.00	37.92
	ATOM	2029	CA	LEU	271	20.010	-19.212	64.693	1.00	38.22
	ATOM	2030	CB	LEU	271	20.657	-19.339	66.078	1.00	37.71
	ATOM	2031	CG	LEU	271	21.897	-20.220	66.261	1.00	38.14
5	ATOM	2032	CD1	LEU	271	22.827	-20.111	65.075	1.00	39.09
	ATOM	2033	CD2	LEU	271	22.596	-19.830	67.549	1.00	35.73
	ATOM	2034	C	LEU	271	18.536	-18.845	64.855	1.00	39.78
	ATOM	2035	O	LEU	271	18.125	-17.721	64.538	1.00	38.05
	ATOM	2036	N	GLU	272	17.751	-19.794	65.358	1.00	39.69
10	ATOM	2037	CA	GLU	272	16.322	-19.590	65.575	1.00	41.03
	ATOM	2038	CB	GLU	272	15.697	-20.842	66.219	1.00	43.64
	ATOM	2039	CG	GLU	272	16.221	-21.179	67.627	1.00	47.44
	ATOM	2040	CD	GLU	272	15.685	-22.509	68.182	1.00	49.81
	ATOM	2041	OE1	GLU	272	16.081	-23.580	67.666	1.00	51.29
15	ATOM	2042	OE2	GLU	272	14.869	-22.484	69.134	1.00	47.60
	ATOM	2043	C	GLU	272	16.084	-18.377	66.466	1.00	39.89
	ATOM	2044	O	GLU	272	15.151	-17.602	66.250	1.00	40.35
	ATOM	2045	N	TYR	273	16.944	-18.208	67.465	1.00	38.65
	ATOM	2046	CA	TYR	273	16.813	-17.095	68.393	1.00	35.97
20	ATOM	2047	CB	TYR	273	17.829	-17.238	69.530	1.00	35.50
	ATOM	2048	CG	TYR	273	18.008	-18.658	70.009	1.00	34.45
	ATOM	2049	CD1	TYR	273	19.109	-19.416	69.611	1.00	32.53
	ATOM	2050	CE1	TYR	273	19.252	-20.740	70.017	1.00	35.58
	ATOM	2051	CD2	TYR	273	17.053	-19.258	70.830	1.00	34.35
25	ATOM	2052	CE2	TYR	273	17.185	-20.580	71.241	1.00	34.82
	ATOM	2053	CZ	TYR	273	18.281	-21.314	70.830	1.00	35.96
	ATOM	2054	OH	TYR	273	18.381	-22.626	71.208	1.00	38.31
	ATOM	2055	C	TYR	273	17.021	-15.763	67.680	1.00	35.11
	ATOM	2056	O	TYR	273	16.404	-14.752	68.031	1.00	34.85

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	ATOM	2057	N	ASP	274	17.888	-15.763	66.676	1.00	36.47
	ATOM	2058	CA	ASP	274	18.164	-14.541	65.933	1.00	36.65
	ATOM	2059	CB	ASP	274	19.405	-14.718	65.059	1.00	32.36
	ATOM	2060	CG	ASP	274	20.627	-15.072	65.869	1.00	32.89
5	ATOM	2061	OD1	ASP	274	20.949	-14.315	66.810	1.00	30.53
	ATOM	2062	OD2	ASP	274	21.265	-16.104	65.569	1.00	32.08
	ATOM	2063	C	ASP	274	16.968	-14.165	65.081	1.00	37.27
	ATOM	2064	O	ASP	274	16.571	-13.001	65.040	1.00	37.20
	ATOM	2065	N	ARG	275	16.380	-15.148	64.410	1.00	39.32
10	ATOM	2066	CA	ARG	275	15.222	-14.866	63.574	1.00	41.70
	ATOM	2067	CB	ARG	275	14.803	-16.121	62.809	1.00	44.47
	ATOM	2068	CG	ARG	275	15.908	-16.666	61.914	1.00	49.05
	ATOM	2069	CD	ARG	275	15.516	-18.002	61.303	1.00	53.46
	ATOM	2070	NE	ARG	275	16.668	-18.740	60.779	1.00	57.36
15	ATOM	2071	CZ	ARG	275	17.352	-18.408	59.685	1.00	58.81
	ATOM	2072	NH1	ARG	275	18.383	-19.148	59.296	1.00	60.43
	ATOM	2073	NH2	ARG	275	17.005	-17.341	58.976	1.00	61.75
	ATOM	2074	C	ARG	275	14.079	-14.353	64.446	1.00	41.43
	ATOM	2075	O	ARG	275	13.350	-13.444	64.059	1.00	40.04
20	ATOM	2076	N	LEU	276	13.939	-14.927	65.637	1.00	40.97
	ATOM	2077	CA	LEU	276	12.888	-14.507	66.556	1.00	42.14
	ATOM	2078	CB	LEU	276	12.831	-15.450	67.761	1.00	44.12
	ATOM	2079	CG	LEU	276	12.315	-16.862	67.468	1.00	47.86
	ATOM	2080	CD1	LEU	276	12.662	-17.800	68.618	1.00	48.62
25	ATOM	2081	CD2	LEU	276	10.808	-16.808	67.236	1.00	47.43
	ATOM	2082	C	LEU	276	13.094	-13.072	67.034	1.00	40.87
	ATOM	2083	O	LEU	276	12.152	-12.281	67.072	1.00	41.20
	ATOM	2084	N	VAL	277	14.322	-12.740	67.412	1.00	39.68
	ATOM	2085	CA	VAL	277	14.617	-11.390	67.876	1.00	40.86

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	ATOM	2086	CB	VAL	277	16.084	-11.263	68.331	1.00	41.86
	ATOM	2087	CG1	VAL	277	16.447	-9.802	68.497	1.00	43.25
	ATOM	2088	CG2	VAL	277	16.290	-12.012	69.647	1.00	41.47
	ATOM	2089	C	VAL	277	14.363	-10.381	66.761	1.00	40.10
5	ATOM	2090	O	VAL	277	13.813	-9.305	66.993	1.00	41.12
	ATOM	2091	N	ASP	278	14.767	-10.738	65.550	1.00	39.42
	ATOM	2092	CA	ASP	278	14.592	-9.867	64.398	1.00	40.24
	ATOM	2093	CB	ASP	278	15.356	-10.434	63.195	1.00	38.24
	ATOM	2094	CG	ASP	278	15.179	-9.598	61.943	1.00	40.23
10	ATOM	2095	OD1	ASP	278	15.260	-8.351	62.043	1.00	39.72
	ATOM	2096	OD2	ASP	278	14.969	-10.187	60.860	1.00	38.10
	ATOM	2097	C	ASP	278	13.120	-9.669	64.043	1.00	41.19
	ATOM	2098	O	ASP	278	12.693	-8.545	63.791	1.00	40.82
	ATOM	2099	N	GLU	279	12.347	-10.754	64.035	1.00	43.34
15	ATOM	2100	CA	GLU	279	10.922	-10.688	63.696	1.00	46.81
	ATOM	2101	CB	GLU	279	10.321	-12.097	63.627	1.00	50.53
	ATOM	2102	CG	GLU	279	10.870	-12.965	62.496	1.00	56.10
	ATOM	2103	CD	GLU	279	10.320	-14.382	62.523	1.00	59.07
	ATOM	2104	OE1	GLU	279	10.336	-15.006	63.607	1.00	60.28
20	ATOM	2105	OE2	GLU	279	9.880	-14.876	61.461	1.00	60.79
	ATOM	2106	C	GLU	279	10.086	-9.840	64.652	1.00	47.25
	ATOM	2107	O	GLU	279	9.048	-9.303	64.260	1.00	46.34
	ATOM	2108	N	SER	280	10.535	-9.722	65.899	1.00	46.87
	ATOM	2109	CA	SER	280	9.809	-8.948	66.900	1.00	47.53
25	ATOM	2110	CB	SER	280	9.769	-9.708	68.228	1.00	49.98
	ATOM	2111	OG	SER	280	9.043	-10.919	68.093	1.00	52.36
	ATOM	2112	C	SER	280	10.415	-7.575	67.129	1.00	47.33
	ATOM	2113	O	SER	280	9.909	-6.788	67.936	1.00	45.86
	ATOM	2114	N	SER	281	11.499	-7.289	66.416	1.00	46.95

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	ATOM	2115	CA	SER	281	12.172	-6.004	66.552	1.00	46.75
	ATOM	2116	CB	SER	281	13.581	-6.081	65.971	1.00	47.24
	ATOM	2117	OG	SER	281	13.524	-6.172	64.559	1.00	47.80
	ATOM	2118	C	SER	281	11.391	-4.915	65.824	1.00	45.65
5	ATOM	2119	O	SER	281	10.514	-5.199	65.013	1.00	45.10
	ATOM	2120	N	ALA	282	11.723	-3.667	66.123	1.00	45.75
	ATOM	2121	CA	ALA	282	11.066	-2.530	65.500	1.00	45.70
	ATOM	2122	CB	ALA	282	11.257	-1.289	66.354	1.00	45.60
	ATOM	2123	C	ALA	282	11.617	-2.286	64.100	1.00	46.48
10	ATOM	2124	O	ALA	282	11.252	-1.303	63.449	1.00	48.61
	ATOM	2125	N	ASN	283	12.493	-3.172	63.633	1.00	43.90
	ATOM	2126	CA	ASN	283	13.076	-3.015	62.306	1.00	41.45
	ATOM	2127	CB	ASN	283	14.300	-2.092	62.384	1.00	40.08
	ATOM	2128	CG	ASN	283	15.398	-2.631	63.289	1.00	39.25
15	ATOM	2129	OD1	ASN	283	15.136	-3.308	64.289	1.00	37.65
	ATOM	2130	ND2	ASN	283	16.641	-2.310	62.950	1.00	37.96
	ATOM	2131	C	ASN	283	13.433	-4.350	61.655	1.00	41.06
	ATOM	2132	O	ASN	283	14.585	-4.606	61.318	1.00	40.48
	ATOM	2133	N	PRO	284	12.423	-5.211	61.455	1.00	40.23
20	ATOM	2134	CD	PRO	284	11.013	-4.898	61.751	1.00	40.75
	ATOM	2135	CA	PRO	284	12.534	-6.540	60.851	1.00	40.08
	ATOM	2136	CB	PRO	284	11.080	-6.914	60.581	1.00	40.52
	ATOM	2137	CG	PRO	284	10.364	-6.260	61.712	1.00	41.21
	ATOM	2138	C	PRO	284	13.366	-6.565	59.579	1.00	39.55
25	ATOM	2139	O	PRO	284	13.054	-5.868	58.617	1.00	40.95
	ATOM	2140	N	GLY	285	14.416	-7.382	59.576	1.00	38.56
	ATOM	2141	CA	GLY	285	15.266	-7.491	58.407	1.00	35.73
	ATOM	2142	C	GLY	285	16.428	-6.516	58.371	1.00	35.10
	ATOM	2143	O	GLY	285	17.288	-6.624	57.500	1.00	36.22

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	ATOM	2144	N	GLN	286	16.468	-5.573	59.308	1.00	34.06
	ATOM	2145	CA	GLN	286	17.547	-4.584	59.348	1.00	34.96
	ATOM	2146	CB	GLN	286	16.974	-3.166	59.321	1.00	39.16
	ATOM	2147	CG	GLN	286	16.189	-2.825	58.067	1.00	45.72
5	ATOM	2148	CD	GLN	286	15.698	-1.384	58.074	1.00	51.15
	ATOM	2149	OE1	GLN	286	14.816	-1.018	58.860	1.00	52.21
	ATOM	2150	NE2	GLN	286	16.276	-0.555	57.203	1.00	50.85
	ATOM	2151	C	GLN	286	18.439	-4.719	60.573	1.00	33.59
	ATOM	2152	O	GLN	286	17.993	-5.157	61.637	1.00	33.18
10	ATOM	2153	N	GLN	287	19.701	-4.334	60.408	1.00	32.85
	ATOM	2154	CA	GLN	287	20.691	-4.375	61.484	1.00	32.45
	ATOM	2155	CB	GLN	287	20.248	-3.456	62.636	1.00	33.34
	ATOM	2156	CG	GLN	287	19.955	-1.999	62.251	1.00	31.48
	ATOM	2157	CD	GLN	287	21.188	-1.259	61.743	1.00	31.78
15	ATOM	2158	OE1	GLN	287	21.330	-1.010	60.544	1.00	33.25
	ATOM	2159	NE2	GLN	287	22.090	-0.921	62.652	1.00	27.51
	ATOM	2160	C	GLN	287	20.924	-5.788	62.032	1.00	30.79
	ATOM	2161	O	GLN	287	21.120	-5.957	63.229	1.00	29.31
	ATOM	2162	N	LEU	288	20.921	-6.791	61.158	1.00	29.33
20	ATOM	2163	CA	LEU	288	21.101	-8.181	61.585	1.00	27.53
	ATOM	2164	CB	LEU	288	20.940	-9.129	60.393	1.00	28.13
	ATOM	2165	CG	LEU	288	19.599	-9.090	59.647	1.00	29.14
	ATOM	2166	CD1	LEU	288	19.390	-10.418	58.922	1.00	27.60
	ATOM	2167	CD2	LEU	288	18.453	-8.844	60.621	1.00	27.42
25	ATOM	2168	C	LEU	288	22.418	-8.476	62.297	1.00	27.92
	ATOM	2169	O	LEU	288	22.438	-9.184	63.303	1.00	28.24
	ATOM	2170	N	TYR	289	23.520	-7.946	61.776	1.00	27.17
	ATOM	2171	CA	TYR	289	24.819	-8.153	62.399	1.00	24.83
	ATOM	2172	CB	TYR	289	25.899	-7.458	61.583	1.00	24.32

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	ATOM	2173	CG	TYR	289	27.303	-7.575	62.137	1.00	21.26
	ATOM	2174	CD1	TYR	289	27.951	-8.814	62.208	1.00	20.00
	ATOM	2175	CE1	TYR	289	29.281	-8.909	62.616	1.00	18.43
	ATOM	2176	CD2	TYR	289	28.013	-6.441	62.503	1.00	18.12
5	ATOM	2177	CE2	TYR	289	29.338	-6.520	62.918	1.00	20.65
	ATOM	2178	CZ	TYR	289	29.976	-7.762	62.966	1.00	21.27
	ATOM	2179	OH	TYR	289	31.314	-7.833	63.326	1.00	19.02
	ATOM	2180	C	TYR	289	24.771	-7.566	63.799	1.00	26.94
	ATOM	2181	O	TYR	289	25.221	-8.175	64.776	1.00	27.95
10	ATOM	2182	N	GLU	290	24.198	-6.374	63.892	1.00	27.68
	ATOM	2183	CA	GLU	290	24.078	-5.686	65.165	1.00	26.41
	ATOM	2184	CB	GLU	290	23.484	-4.309	64.927	1.00	26.55
	ATOM	2185	CG	GLU	290	23.059	-3.595	66.180	1.00	27.05
	ATOM	2186	CD	GLU	290	22.815	-2.142	65.913	1.00	25.47
15	ATOM	2187	OE1	GLU	290	23.716	-1.336	66.204	1.00	27.17
	ATOM	2188	OE2	GLU	290	21.731	-1.815	65.398	1.00	29.09
	ATOM	2189	C	GLU	290	23.218	-6.463	66.159	1.00	26.59
	ATOM	2190	O	GLU	290	23.458	-6.430	67.371	1.00	25.62
	ATOM	2191	N	LYS	291	22.216	-7.166	65.646	1.00	26.31
20	ATOM	2192	CA	LYS	291	21.343	-7.942	66.509	1.00	27.77
	ATOM	2193	CB	LYS	291	20.110	-8.394	65.722	1.00	28.30
	ATOM	2194	CG	LYS	291	19.096	-7.263	65.585	1.00	33.35
	ATOM	2195	CD	LYS	291	18.005	-7.529	64.555	1.00	33.56
	ATOM	2196	CE	LYS	291	17.038	-6.330	64.522	1.00	36.46
25	ATOM	2197	NZ	LYS	291	16.150	-6.319	63.327	1.00	36.55
	ATOM	2198	C	LYS	291	22.073	-9.123	67.138	1.00	26.53
	ATOM	2199	O	LYS	291	21.584	-9.736	68.084	1.00	27.81
	ATOM	2200	N	LEU	292	23.261	-9.426	66.628	1.00	26.02
	ATOM	2201	CA	LEU	292	24.043	-10.523	67.168	1.00	25.35



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	ATOM	2202	CB	LEU	292	24.922	-11.140	66.079	1.00	25.16
	ATOM	2203	CG	LEU	292	24.229	-11.746	64.856	1.00	26.25
	ATOM	2204	CD1	LEU	292	25.274	-12.190	63.827	1.00	23.09
	ATOM	2205	CD2	LEU	292	23.359	-12.912	65.297	1.00	24.40
5	ATOM	2206	C	LEU	292	24.942	-10.030	68.283	1.00	25.18
	ATOM	2207	O	LEU	292	25.392	-10.808	69.120	1.00	23.84
	ATOM	2208	N	ILE	293	25.179	-8.723	68.308	1.00	24.94
	ATOM	2209	CA	ILE	293	26.107	-8.140	69.267	1.00	23.59
	ATOM	2210	CB	ILE	293	27.259	-7.468	68.476	1.00	24.66
10	ATOM	2211	CG2	ILE	293	28.233	-6.762	69.409	1.00	21.05
	ATOM	2212	CG1	ILE	293	27.952	-8.527	67.618	1.00	24.42
	ATOM	2213	CD1	ILE	293	28.715	-7.965	66.441	1.00	25.64
	ATOM	2214	C	ILE	293	25.560	-7.148	70.278	1.00	25.10
	ATOM	2215	O	ILE	293	25.797	-7.289	71.474	1.00	23.79
15	ATOM	2216	N	GLY	294	24.845	-6.136	69.781	1.00	28.83
	ATOM	2217	CA	GLY	294	24.302	-5.071	70.615	1.00	26.73
	ATOM	2218	C	GLY	294	23.551	-5.379	71.898	1.00	29.79
	ATOM	2219	O	GLY	294	22.757	-6.318	71.964	1.00	27.85
	ATOM	2220	N	GLY	295	23.794	-4.553	72.918	1.00	30.56
20	ATOM	2221	CA	GLY	295	23.136	-4.722	74.204	1.00	33.01
	ATOM	2222	C	GLY	295	21.628	-4.539	74.144	1.00	34.05
	ATOM	2223	O	GLY	295	20.927	-4.810	75.107	1.00	34.93
	ATOM	2224	N	LYS	296	21.124	-4.058	73.016	1.00	35.19
	ATOM	2225	CA	LYS	296	19.690	-3.868	72.851	1.00	36.24
25	ATOM	2226	CB	LYS	296	19.419	-2.988	71.626	1.00	38.05
	ATOM	2227	CG	LYS	296	17.961	-2.910	71.181	1.00	40.26
	ATOM	2228	CD	LYS	296	17.122	-2.093	72.141	1.00	43.32
	ATOM	2229	CE	LYS	296	15.730	-1.862	71.579	1.00	44.42
	ATOM	2230	NZ	LYS	296	14.842	-1.175	72.562	1.00	44.77

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	ATOM	2231	C	LYS	296	19.045	-5.235	72.654	1.00	36.63
	ATOM	2232	O	LYS	296	17.867	-5.420	72.963	1.00	38.56
	ATOM	2233	N	TYR	297	19.836	-6.193	72.168	1.00	34.63
	ATOM	2234	CA	TYR	297	19.346	-7.539	71.890	1.00	33.22
5	ATOM	2235	CB	TYR	297	19.487	-7.810	70.389	1.00	34.65
	ATOM	2236	CG	TYR	297	19.073	-6.631	69.535	1.00	36.28
	ATOM	2237	CD1	TYR	297	20.010	-5.677	69.125	1.00	34.21
	ATOM	2238	CE1	TYR	297	19.622	-4.548	68.404	1.00	36.22
	ATOM	2239	CD2	TYR	297	17.732	-6.431	69.195	1.00	34.24
10	ATOM	2240	CE2	TYR	297	17.330	-5.305	68.476	1.00	35.71
	ATOM	2241	CZ	TYR	297	18.280	-4.368	68.082	1.00	37.38
	ATOM	2242	OH	TYR	297	17.887	-3.258	67.375	1.00	35.33
	ATOM	2243	C	TYR	297	19.968	-8.713	72.670	1.00	33.21
	ATOM	2244	O	TYR	297	19.392	-9.800	72.716	1.00	33.78
15	ATOM	2245	N	MET	298	21.126	-8.504	73.283	1.00	31.19
	ATOM	2246	CA	MET	298	21.803	-9.576	74.005	1.00	30.16
	ATOM	2247	CB	MET	298	23.075	-9.038	74.644	1.00	30.05
	ATOM	2248	CG	MET	298	23.957	-10.104	75.231	1.00	26.86
	ATOM	2249	SD	MET	298	25.486	-9.405	75.850	1.00	32.83
20	ATOM	2250	CE	MET	298	26.409	-9.201	74.338	1.00	29.59
	ATOM	2251	C	MET	298	20.963	-10.296	75.066	1.00	31.27
	ATOM	2252	O	MET	298	20.882	-11.529	75.077	1.00	29.78
	ATOM	2253	N	GLY	299	20.353	-9.530	75.963	1.00	30.40
	ATOM	2254	CA	GLY	299	19.534	-10.132	76.998	1.00	31.32
25	ATOM	2255	C	GLY	299	18.354	-10.869	76.393	1.00	33.32
	ATOM	2256	O	GLY	299	17.988	-11.962	76.831	1.00	33.97
	ATOM	2257	N	GLU	300	17.752	-10.265	75.377	1.00	31.78
	ATOM	2258	CA	GLU	300	16.617	-10.874	74.707	1.00	31.93
	ATOM	2259	CB	GLU	300	16.080	-9.937	73.621	1.00	29.00

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	ATOM	2260	CG	GLU	300	14.877	-10.486	72.881	1.00	32.60
	ATOM	2261	CD	GLU	300	13.655	-10.655	73.769	1.00	31.13
	ATOM	2262	OE1	GLU	300	12.629	-11.144	73.265	1.00	34.55
	ATOM	2263	OE2	GLU	300	13.714	-10.299	74.963	1.00	33.16
5	ATOM	2264	C	GLU	300	17.013	-12.215	74.092	1.00	30.90
	ATOM	2265	O	GLU	300	16.225	-13.156	74.090	1.00	32.89
	ATOM	2266	N	LEU	301	18.234	-12.301	73.570	1.00	31.16
	ATOM	2267	CA	LEU	301	18.714	-13.546	72.973	1.00	28.93
	ATOM	2268	CB	LEU	301	20.085	-13.339	72.325	1.00	24.69
10	ATOM	2269	CG	LEU	301	20.152	-12.667	70.952	1.00	24.17
	ATOM	2270	CD1	LEU	301	21.607	-12.326	70.628	1.00	23.70
	ATOM	2271	CD2	LEU	301	19.560	-13.598	69.886	1.00	23.13
	ATOM	2272	C	LEU	301	18.814	-14.616	74.056	1.00	29.42
	ATOM	2273	O	LEU	301	18.408	-15.761	73.853	1.00	32.03
15	ATOM	2274	N	VAL	302	19.365	-14.239	75.204	1.00	28.73
	ATOM	2275	CA	VAL	302	19.505	-15.164	76.317	1.00	29.42
	ATOM	2276	CB	VAL	302	20.265	-14.510	77.497	1.00	26.51
	ATOM	2277	CG1	VAL	302	20.172	-15.395	78.740	1.00	25.63
	ATOM	2278	CG2	VAL	302	21.731	-14.301	77.117	1.00	25.98
20	ATOM	2279	C	VAL	302	18.127	-15.624	76.795	1.00	31.88
	ATOM	2280	O	VAL	302	17.934	-16.795	77.112	1.00	32.71
	ATOM	2281	N	ARG	303	17.171	-14.703	76.835	1.00	32.91
	ATOM	2282	CA	ARG	303	15.818	-15.039	77.270	1.00	36.08
	ATOM	2283	CB	ARG	303	14.910	-13.802	77.250	1.00	35.86
25	ATOM	2284	CG	ARG	303	13.524	-14.055	77.847	1.00	36.97
	ATOM	2285	CD	ARG	303	12.660	-12.802	77.833	1.00	39.15
	ATOM	2286	NE	ARG	303	12.105	-12.529	76.511	1.00	41.95
	ATOM	2287	CZ	ARG	303	11.090	-13.197	75.968	1.00	43.84
	ATOM	2288	NH1	ARG	303	10.502	-14.182	76.631	1.00	42.47

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	ATOM	2289	NH2	ARG	303	10.666	-12.885	74.750	1.00	43.86
	ATOM	2290	C	ARG	303	15.215	-16.110	76.373	1.00	36.97
	ATOM	2291	O	ARG	303	14.554	-17.032	76.851	1.00	37.22
	ATOM	2292	N	LEU	304	15.432	-15.970	75.068	1.00	37.86
5	ATOM	2293	CA	LEU	304	14.914	-16.924	74.103	1.00	37.63
	ATOM	2294	CB	LEU	304	15.113	-16.387	72.687	1.00	38.69
	ATOM	2295	CG	LEU	304	13.944	-15.590	72.104	1.00	40.35
	ATOM	2296	CD1	LEU	304	13.486	-14.516	73.062	1.00	40.85
	ATOM	2297	CD2	LEU	304	14.378	-14.986	70.785	1.00	42.07
10	ATOM	2298	C	LEU	304	15.602	-18.272	74.262	1.00	37.69
	ATOM	2299	O	LEU	304	14.978	-19.324	74.120	1.00	38.84
	ATOM	2300	N	VAL	305	16.893	-18.238	74.558	1.00	36.28
	ATOM	2301	CA	VAL	305	17.647	-19.466	74.753	1.00	34.31
	ATOM	2302	CB	VAL	305	19.148	-19.184	74.908	1.00	32.24
15	ATOM	2303	CG1	VAL	305	19.868	-20.438	75.390	1.00	28.85
	ATOM	2304	CG2	VAL	305	19.717	-18.713	73.578	1.00	29.80
	ATOM	2305	C	VAL	305	17.153	-20.158	76.012	1.00	35.48
	ATOM	2306	O	VAL	305	17.079	-21.389	76.070	1.00	34.47
	ATOM	2307	N	LEU	306	16.820	-19.362	77.023	1.00	34.14
20	ATOM	2308	CA	LEU	306	16.328	-19.921	78.273	1.00	35.52
	ATOM	2309	CB	LEU	306	16.257	-18.841	79.353	1.00	32.11
	ATOM	2310	CG	LEU	306	17.601	-18.289	79.829	1.00	32.53
	ATOM	2311	CD1	LEU	306	17.359	-17.326	80.964	1.00	33.54
	ATOM	2312	CD2	LEU	306	18.515	-19.420	80.287	1.00	30.60
25	ATOM	2313	C	LEU	306	14.948	-20.532	78.049	1.00	37.53
	ATOM	2314	O	LEU	306	14.637	-21.608	78.566	1.00	33.87
	ATOM	2315	N	LEU	307	14.129	-19.850	77.257	1.00	39.39
	ATOM	2316	CA	LEU	307	12.787	-20.336	76.971	1.00	41.43
	ATOM	2317	CB	LEU	307	12.011	-19.296	76.165	1.00	40.84

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	ATOM	2318	CG	LEU	307	10.932	-18.527	76.935	1.00	43.43
	ATOM	2319	CD1	LEU	307	11.389	-18.243	78.356	1.00	43.36
	ATOM	2320	CD2	LEU	307	10.610	-17.233	76.197	1.00	41.75
	ATOM	2321	C	LEU	307	12.802	-21.674	76.239	1.00	42.39
5	ATOM	2322	O	LEU	307	11.974	-22.537	76.514	1.00	42.90
	ATOM	2323	N	ARG	308	13.729	-21.860	75.306	1.00	42.02
	ATOM	2324	CA	ARG	308	13.771	-23.132	74.605	1.00	42.88
	ATOM	2325	CB	ARG	308	14.765	-23.125	73.445	1.00	43.55
	ATOM	2326	CG	ARG	308	14.891	-24.514	72.837	1.00	47.00
10	ATOM	2327	CD	ARG	308	15.908	-24.626	71.729	1.00	49.25
	ATOM	2328	NE	ARG	308	16.079	-26.026	71.349	1.00	52.10
	ATOM	2329	CZ	ARG	308	16.915	-26.456	70.410	1.00	52.45
	ATOM	2330	NH1	ARG	308	17.663	-25.591	69.739	1.00	54.77
	ATOM	2331	NH2	ARG	308	17.016	-27.756	70.154	1.00	51.73
15	ATOM	2332	C	ARG	308	14.181	-24.222	75.582	1.00	43.27
	ATOM	2333	O	ARG	308	13.654	-25.333	75.540	1.00	42.09
	ATOM	2334	N	LEU	309	15.135	-23.895	76.452	1.00	42.54
	ATOM	2335	CA	LEU	309	15.627	-24.837	77.447	1.00	42.29
	ATOM	2336	CB	LEU	309	16.771	-24.207	78.248	1.00	40.55
20	ATOM	2337	CG	LEU	309	18.193	-24.656	77.886	1.00	39.65
	ATOM	2338	CD1	LEU	309	18.313	-24.973	76.416	1.00	38.56
	ATOM	2339	CD2	LEU	309	19.171	-23.569	78.284	1.00	37.67
	ATOM	2340	C	LEU	309	14.515	-25.302	78.379	1.00	42.66
	ATOM	2341	O	LEU	309	14.509	-26.450	78.818	1.00	41.33
25	ATOM	2342	N	VAL	310	13.570	-24.416	78.676	1.00	44.27
	ATOM	2343	CA	VAL	310	12.464	-24.789	79.543	1.00	46.40
	ATOM	2344	CB	VAL	310	11.711	-23.546	80.111	1.00	46.06
	ATOM	2345	CG1	VAL	310	12.682	-22.613	80.807	1.00	45.43
	ATOM	2346	CG2	VAL	310	10.976	-22.825	79.014	1.00	48.29

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	ATOM	2347	C	VAL	310	11.479	-25.666	78.769	1.00	48.00
	ATOM	2348	O	VAL	310	10.952	-26.638	79.311	1.00	47.71
	ATOM	2349	N	ASP	311	11.242	-25.333	77.501	1.00	49.58
	ATOM	2350	CA	ASP	311	10.313	-26.104	76.683	1.00	52.37
5	ATOM	2351	CB	ASP	311	9.978	-25.365	75.382	1.00	54.70
	ATOM	2352	CG	ASP	311	9.318	-24.014	75.626	1.00	58.89
	ATOM	2353	OD1	ASP	311	8.742	-23.808	76.719	1.00	60.74
	ATOM	2354	OD2	ASP	311	9.364	-23.158	74.713	1.00	60.54
	ATOM	2355	C	ASP	311	10.872	-27.485	76.365	1.00	52.35
10	ATOM	2356	O	ASP	311	10.131	-28.388	75.982	1.00	55.07
	ATOM	2357	N	GLU	312	12.180	-27.642	76.515	1.00	51.23
	ATOM	2358	CA	GLU	312	12.828	-28.926	76.279	1.00	51.12
	ATOM	2359	CB	GLU	312	14.277	-28.729	75.834	1.00	52.62
	ATOM	2360	CG	GLU	312	14.445	-28.141	74.448	1.00	57.13
15	ATOM	2361	CD	GLU	312	14.187	-29.153	73.358	1.00	58.40
	ATOM	2362	OE1	GLU	312	14.831	-30.222	73.385	1.00	59.31
	ATOM	2363	OE2	GLU	312	13.346	-28.879	72.476	1.00	60.41
	ATOM	2364	C	GLU	312	12.810	-29.660	77.611	1.00	50.76
	ATOM	2365	O	GLU	312	13.292	-30.787	77.720	1.00	50.64
20	ATOM	2366	N	ASN	313	12.265	-28.989	78.624	1.00	50.08
	ATOM	2367	CA	ASN	313	12.154	-29.533	79.974	1.00	51.37
	ATOM	2368	CB	ASN	313	11.428	-30.886	79.932	1.00	53.51
	ATOM	2369	CG	ASN	313	10.846	-31.275	81.271	1.00	55.73
	ATOM	2370	OD1	ASN	313	10.011	-30.560	81.824	1.00	58.95
25	ATOM	2371	ND2	ASN	313	11.281	-32.415	81.803	1.00	59.16
	ATOM	2372	C	ASN	313	13.524	-29.693	80.635	1.00	50.00
	ATOM	2373	O	ASN	313	13.733	-30.595	81.447	1.00	50.40
	ATOM	2374	N	LEU	314	14.449	-28.799	80.296	1.00	48.35
	ATOM	2375	CA	LEU	314	15.805	-28.843	80.835	1.00	45.12

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	ATOM	2376	CB	LEU	314	16.819	-28.785	79.688	1.00	44.25
	ATOM	2377	CG	LEU	314	16.759	-29.872	78.611	1.00	45.98
	ATOM	2378	CD1	LEU	314	17.619	-29.465	77.416	1.00	43.63
	ATOM	2379	CD2	LEU	314	17.232	-31.201	79.196	1.00	45.09
5	ATOM	2380	C	LEU	314	16.119	-27.724	81.829	1.00	43.38
	ATOM	2381	O	LEU	314	17.180	-27.732	82.449	1.00	41.90
	ATOM	2382	N	LEU	315	15.211	-26.765	81.982	1.00	41.74
	ATOM	2383	CA	LEU	315	15.446	-25.645	82.899	1.00	42.39
	ATOM	2384	CB	LEU	315	15.907	-24.407	82.116	1.00	40.17
10	ATOM	2385	CG	LEU	315	17.243	-23.721	82.428	1.00	39.81
	ATOM	2386	CD1	LEU	315	17.262	-22.383	81.689	1.00	41.89
	ATOM	2387	CD2	LEU	315	17.421	-23.482	83.920	1.00	37.58
	ATOM	2388	C	LEU	315	14.198	-25.278	83.694	1.00	42.28
	ATOM	2389	O	LEU	315	13.103	-25.214	83.144	1.00	40.83
15	ATOM	2390	N	PHE	316	14.377	-25.021	84.986	1.00	43.70
	ATOM	2391	CA	PHE	316	13.271	-24.648	85.863	1.00	46.70
	ATOM	2392	CB	PHE	316	12.717	-23.278	85.459	1.00	47.06
	ATOM	2393	CG	PHE	316	13.776	-22.247	85.187	1.00	47.07
	ATOM	2394	CD1	PHE	316	14.824	-22.051	86.082	1.00	47.24
20	ATOM	2395	CD2	PHE	316	13.722	-21.467	84.037	1.00	47.25
	ATOM	2396	CE1	PHE	316	15.803	-21.094	85.835	1.00	46.12
	ATOM	2397	CE2	PHE	316	14.695	-20.507	83.782	1.00	47.70
	ATOM	2398	CZ	PHE	316	15.738	-20.321	84.683	1.00	47.68
	ATOM	2399	C	PHE	316	12.131	-25.672	85.857	1.00	48.45
25	ATOM	2400	O	PHE	316	10.960	-25.306	85.967	1.00	48.86
	ATOM	2401	N	HIS	317	12.473	-26.950	85.725	1.00	50.80
	ATOM	2402	CA	HIS	317	11.469	-28.009	85.712	1.00	53.83
	ATOM	2403	CB	HIS	317	10.655	-27.986	87.010	1.00	57.67
	ATOM	2404	CG	HIS	317	11.496	-27.985	88.246	1.00	61.10

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	ATOM	2405	CD2	HIS	317	11.558	-27.116	89.282	1.00	63.07
	ATOM	2406	ND1	HIS	317	12.430	-28.965	88.509	1.00	62.35
	ATOM	2407	CE1	HIS	317	13.032	-28.699	89.655	1.00	64.77
	ATOM	2408	NE2	HIS	317	12.521	-27.582	90.144	1.00	65.99
5	ATOM	2409	C	HIS	317	10.521	-27.859	84.534	1.00	53.57
	ATOM	2410	O	HIS	317	9.429	-28.425	84.537	1.00	53.60
	ATOM	2411	N	GLY	318	10.939	-27.090	83.534	1.00	52.50
	ATOM	2412	CA	GLY	318	10.113	-26.881	82.358	1.00	51.83
	ATOM	2413	C	GLY	318	8.940	-25.958	82.615	1.00	51.72
10	ATOM	2414	O	GLY	318	7.939	-25.999	81.904	1.00	50.88
	ATOM	2415	N	GLU	319	9.073	-25.110	83.627	1.00	53.43
	ATOM	2416	CA	GLU	319	8.014	-24.182	83.996	1.00	55.73
	ATOM	2417	CB	GLU	319	7.510	-24.544	85.392	1.00	58.85
	ATOM	2418	CG	GLU	319	6.145	-23.998	85.761	1.00	63.60
15	ATOM	2419	CD	GLU	319	5.590	-24.664	87.016	1.00	66.32
	ATOM	2420	OE1	GLU	319	6.206	-24.527	88.100	1.00	65.47
	ATOM	2421	OE2	GLU	319	4.540	-25.335	86.913	1.00	67.45
	ATOM	2422	C	GLU	319	8.538	-22.748	83.966	1.00	55.18
	ATOM	2423	O	GLU	319	9.278	-22.324	84.851	1.00	55.23
20	ATOM	2424	N	ALA	320	8.145	-22.006	82.938	1.00	55.14
	ATOM	2425	CA	ALA	320	8.585	-20.630	82.780	1.00	55.95
	ATOM	2426	CB	ALA	320	8.609	-20.265	81.304	1.00	55.13
	ATOM	2427	C	ALA	320	7.708	-19.649	83.544	1.00	56.88
	ATOM	2428	O	ALA	320	6.487	-19.789	83.584	1.00	58.58
25	ATOM	2429	N	SER	321	8.344	-18.648	84.141	1.00	57.00
	ATOM	2430	CA	SER	321	7.644	-17.625	84.902	1.00	56.57
	ATOM	2431	CB	SER	321	8.649	-16.808	85.705	1.00	56.74
	ATOM	2432	OG	SER	321	8.013	-15.725	86.349	1.00	57.41
	ATOM	2433	C	SER	321	6.853	-16.689	83.995	1.00	58.61



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	ATOM	2434	O	SER	321	7.054	-16.665	82.783	1.00	58.41
	ATOM	2435	N	GLU	322	5.955	-15.914	84.595	1.00	60.41
	ATOM	2436	CA	GLU	322	5.133	-14.960	83.858	1.00	62.09
	ATOM	2437	CB	GLU	322	4.171	-14.254	84.819	1.00	65.34
5	ATOM	2438	CG	GLU	322	3.185	-13.299	84.165	1.00	69.70
	ATOM	2439	CD	GLU	322	2.075	-14.020	83.418	1.00	73.68
	ATOM	2440	OE1	GLU	322	1.379	-14.851	84.046	1.00	74.78
	ATOM	2441	OE2	GLU	322	1.896	-13.751	82.208	1.00	75.02
	ATOM	2442	C	GLU	322	6.047	-13.929	83.204	1.00	61.24
10	ATOM	2443	O	GLU	322	5.913	-13.612	82.022	1.00	60.81
	ATOM	2444	N	GLN	323	6.987	-13.420	83.991	1.00	60.42
	ATOM	2445	CA	GLN	323	7.935	-12.422	83.521	1.00	58.63
	ATOM	2446	CB	GLN	323	8.729	-11.863	84.700	1.00	59.77
	ATOM	2447	CG	GLN	323	7.902	-11.039	85.658	1.00	61.20
15	ATOM	2448	CD	GLN	323	8.690	-10.608	86.873	1.00	63.03
	ATOM	2449	OE1	GLN	323	9.672	-9.866	86.767	1.00	63.70
	ATOM	2450	NE2	GLN	323	8.266	-11.074	88.044	1.00	64.05
	ATOM	2451	C	GLN	323	8.904	-12.955	82.478	1.00	56.96
	ATOM	2452	O	GLN	323	9.244	-12.255	81.526	1.00	56.89
20	ATOM	2453	N	LEU	324	9.351	-14.190	82.652	1.00	53.93
	ATOM	2454	CA	LEU	324	10.298	-14.763	81.713	1.00	52.62
	ATOM	2455	CB	LEU	324	10.745	-16.151	82.180	1.00	51.22
	ATOM	2456	CG	LEU	324	11.830	-16.826	81.334	1.00	50.58
	ATOM	2457	CD1	LEU	324	13.076	-15.952	81.299	1.00	49.50
25	ATOM	2458	CD2	LEU	324	12.160	-18.192	81.909	1.00	49.35
	ATOM	2459	C	LEU	324	9.730	-14.855	80.306	1.00	52.38
	ATOM	2460	O	LEU	324	10.485	-14.870	79.337	1.00	51.83
	ATOM	2461	N	ARG	325	8.405	-14.902	80.193	1.00	52.63
	ATOM	2462	CA	ARG	325	7.759	-15.015	78.887	1.00	53.00

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	ATOM	2463	CB	ARG	325	6.477	-15.848	79.000	1.00	54.77
	ATOM	2464	CG	ARG	325	6.585	-17.005	79.985	1.00	58.57
	ATOM	2465	CD	ARG	325	6.013	-18.330	79.458	1.00	60.34
	ATOM	2466	NE	ARG	325	6.881	-18.961	78.464	1.00	62.28
5	ATOM	2467	CZ	ARG	325	6.953	-20.273	78.249	1.00	62.81
	ATOM	2468	NH1	ARG	325	6.208	-21.109	78.963	1.00	62.98
	ATOM	2469	NH2	ARG	325	7.769	-20.752	77.317	1.00	62.50
	ATOM	2470	C	ARG	325	7.430	-13.663	78.266	1.00	52.20
	ATOM	2471	O	ARG	325	6.835	-13.595	77.194	1.00	51.65
10	ATOM	2472	N	THR	326	7.820	-12.589	78.940	1.00	51.52
	ATOM	2473	CA	THR	326	7.562	-11.248	78.438	1.00	53.54
	ATOM	2474	CB	THR	326	7.031	-10.343	79.570	1.00	54.40
	ATOM	2475	OG1	THR	326	8.068	-10.120	80.534	1.00	56.68
	ATOM	2476	CG2	THR	326	5.858	-11.012	80.274	1.00	53.00
15	ATOM	2477	C	THR	326	8.853	-10.655	77.850	1.00	54.00
	ATOM	2478	O	THR	326	9.891	-10.626	78.515	1.00	53.48
	ATOM	2479	N	ARG	327	8.782	-10.191	76.604	1.00	54.30
	ATOM	2480	CA	ARG	327	9.948	-9.628	75.923	1.00	55.25
	ATOM	2481	CB	ARG	327	9.568	-9.074	74.550	1.00	58.73
20	ATOM	2482	CG	ARG	327	9.050	-10.101	73.572	1.00	62.94
	ATOM	2483	CD	ARG	327	9.189	-9.599	72.143	1.00	66.63
	ATOM	2484	NE	ARG	327	8.462	-10.454	71.213	1.00	70.25
	ATOM	2485	CZ	ARG	327	7.136	-10.522	71.154	1.00	72.29
	ATOM	2486	NH1	ARG	327	6.399	-9.778	71.969	1.00	72.86
25	ATOM	2487	NH2	ARG	327	6.546	-11.338	70.288	1.00	73.24
	ATOM	2488	C	ARG	327	10.660	-8.529	76.688	1.00	53.79
	ATOM	2489	O	ARG	327	10.027	-7.690	77.326	1.00	55.10
	ATOM	2490	N	GLY	328	11.986	-8.535	76.604	1.00	50.97
	ATOM	2491	CA	GLY	328	12.773	-7.520	77.276	1.00	50.03

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	ATOM	2492	C	GLY	328	12.922	-7.715	78.770	1.00	49.36
	ATOM	2493	O	GLY	328	13.622	-6.942	79.426	1.00	49.68
	ATOM	2494	N	ALA	329	12.274	-8.740	79.315	1.00	47.47
	ATOM	2495	CA	ALA	329	12.354	-9.007	80.749	1.00	46.93
5	ATOM	2496	CB	ALA	329	11.468	-10.184	81.115	1.00	48.23
	ATOM	2497	C	ALA	329	13.786	-9.287	81.173	1.00	45.48
	ATOM	2498	O	ALA	329	14.247	-8.794	82.203	1.00	44.91
	ATOM	2499	N	PHE	330	14.490	-10.088	80.383	1.00	43.75
	ATOM	2500	CA	PHE	330	15.870	-10.392	80.710	1.00	42.95
10	ATOM	2501	CB	PHE	330	16.271	-11.760	80.156	1.00	39.40
	ATOM	2502	CG	PHE	330	17.478	-12.350	80.829	1.00	36.90
	ATOM	2503	CD1	PHE	330	18.761	-11.985	80.436	1.00	35.73
	ATOM	2504	CD2	PHE	330	17.330	-13.241	81.893	1.00	35.23
	ATOM	2505	CE1	PHE	330	19.878	-12.496	81.093	1.00	33.48
15	ATOM	2506	CE2	PHE	330	18.443	-13.759	82.558	1.00	31.61
	ATOM	2507	CZ	PHE	330	19.716	-13.387	82.160	1.00	33.39
	ATOM	2508	C	PHE	330	16.752	-9.292	80.130	1.00	43.51
	ATOM	2509	O	PHE	330	17.202	-9.373	78.986	1.00	44.11
	ATOM	2510	N	GLU	331	16.962	-8.254	80.935	1.00	43.95
20	ATOM	2511	CA	GLU	331	17.777	-7.099	80.569	1.00	43.11
	ATOM	2512	CB	GLU	331	17.767	-6.068	81.697	1.00	46.19
	ATOM	2513	CG	GLU	331	16.393	-5.551	82.092	1.00	50.13
	ATOM	2514	CD	GLU	331	16.458	-4.651	83.316	1.00	53.54
	ATOM	2515	OE1	GLU	331	17.324	-3.745	83.343	1.00	55.03
25	ATOM	2516	OE2	GLU	331	15.646	-4.846	84.247	1.00	53.56
	ATOM	2517	C	GLU	331	19.216	-7.511	80.310	1.00	42.02
	ATOM	2518	O	GLU	331	19.742	-8.411	80.968	1.00	42.05
	ATOM	2519	N	THR	332	19.855	-6.830	79.365	1.00	39.23
	ATOM	2520	CA	THR	332	21.235	-7.122	79.017	1.00	36.08

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	ATOM	2521	CB	THR	332	21.713	-6.200	77.869	1.00	36.47
	ATOM	2522	OG1	THR	332	21.297	-6.762	76.618	1.00	33.61
	ATOM	2523	CG2	THR	332	23.235	-6.030	77.884	1.00	31.36
	ATOM	2524	C	THR	332	22.159	-6.987	80.219	1.00	35.73
5	ATOM	2525	O	THR	332	23.209	-7.634	80.280	1.00	35.30
	ATOM	2526	N	ARG	333	21.782	-6.151	81.180	1.00	34.21
	ATOM	2527	CA	ARG	333	22.632	-6.003	82.353	1.00	34.18
	ATOM	2528	CB	ARG	333	22.211	-4.786	83.193	1.00	36.60
	ATOM	2529	CG	ARG	333	20.830	-4.854	83.835	1.00	39.58
10	ATOM	2530	CD	ARG	333	20.488	-3.518	84.520	1.00	42.78
	ATOM	2531	NE	ARG	333	19.264	-3.590	85.316	1.00	45.29
	ATOM	2532	CZ	ARG	333	19.205	-4.039	86.567	1.00	47.32
	ATOM	2533	NH1	ARG	333	20.305	-4.455	87.182	1.00	49.55
	ATOM	2534	NH2	ARG	333	18.042	-4.080	87.205	1.00	48.70
15	ATOM	2535	C	ARG	333	22.609	-7.298	83.181	1.00	31.65
	ATOM	2536	O	ARG	333	23.584	-7.625	83.863	1.00	31.61
	ATOM	2537	N	PHE	334	21.513	-8.049	83.105	1.00	31.01
	ATOM	2538	CA	PHE	334	21.431	-9.317	83.835	1.00	30.67
	ATOM	2539	CB	PHE	334	20.048	-9.967	83.678	1.00	30.39
20	ATOM	2540	CG	PHE	334	18.923	-9.210	84.330	1.00	30.58
	ATOM	2541	CD1	PHE	334	19.170	-8.214	85.269	1.00	29.37
	ATOM	2542	CD2	PHE	334	17.600	-9.522	84.019	1.00	31.94
	ATOM	2543	CE1	PHE	334	18.113	-7.539	85.891	1.00	31.67
	ATOM	2544	CE2	PHE	334	16.535	-8.851	84.636	1.00	32.25
25	ATOM	2545	CZ	PHE	334	16.796	-7.857	85.575	1.00	28.89
	ATOM	2546	C	PHE	334	22.496	-10.287	83.295	1.00	30.73
	ATOM	2547	O	PHE	334	23.136	-11.016	84.064	1.00	30.77
	ATOM	2548	N	VAL	335	22.685	-10.290	81.973	1.00	29.44
	ATOM	2549	CA	VAL	335	23.672	-11.165	81.350	1.00	30.61

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	ATOM	2550	CB	VAL	335	23.777	-10.921	79.831	1.00	30.75
	ATOM	2551	CG1	VAL	335	24.774	-11.898	79.216	1.00	32.48
	ATOM	2552	CG2	VAL	335	22.424	-11.078	79.181	1.00	29.80
	ATOM	2553	C	VAL	335	25.041	-10.904	81.964	1.00	31.64
5	ATOM	2554	O	VAL	335	25.759	-11.830	82.356	1.00	31.87
	ATOM	2555	N	SER	336	25.382	-9.623	82.048	1.00	33.23
	ATOM	2556	CA	SER	336	26.655	-9.173	82.593	1.00	32.42
	ATOM	2557	CB	SER	336	26.778	-7.660	82.384	1.00	33.94
	ATOM	2558	OG	SER	336	28.080	-7.204	82.682	1.00	38.27
10	ATOM	2559	C	SER	336	26.793	-9.524	84.078	1.00	32.82
	ATOM	2560	O	SER	336	27.863	-9.917	84.529	1.00	33.76
	ATOM	2561	N	GLN	337	25.711	-9.389	84.839	1.00	32.64
	ATOM	2562	CA	GLN	337	25.753	-9.715	86.260	1.00	34.83
	ATOM	2563	CB	GLN	337	24.480	-9.233	86.958	1.00	37.43
15	ATOM	2564	CG	GLN	337	24.339	-7.721	86.972	1.00	42.29
	ATOM	2565	CD	GLN	337	22.984	-7.260	87.471	1.00	44.59
	ATOM	2566	OE1	GLN	337	22.710	-6.062	87.525	1.00	46.49
	ATOM	2567	NE2	GLN	337	22.128	-8.209	87.835	1.00	43.79
	ATOM	2568	C	GLN	337	25.899	-11.217	86.447	1.00	33.66
20	ATOM	2569	O	GLN	337	26.663	-11.674	87.297	1.00	35.28
	ATOM	2570	N	VAL	338	25.159	-11.983	85.655	1.00	31.29
	ATOM	2571	CA	VAL	338	25.236	-13.432	85.743	1.00	29.21
	ATOM	2572	CB	VAL	338	24.326	-14.102	84.690	1.00	28.27
	ATOM	2573	CG1	VAL	338	24.687	-15.571	84.525	1.00	27.17
25	ATOM	2574	CG2	VAL	338	22.877	-13.984	85.129	1.00	26.99
	ATOM	2575	C	VAL	338	26.678	-13.877	85.547	1.00	27.35
	ATOM	2576	O	VAL	338	27.176	-14.722	86.284	1.00	26.69
	ATOM	2577	N	GLU	339	27.361	-13.283	84.576	1.00	27.29
	ATOM	2578	CA	GLU	339	28.747	-13.657	84.314	1.00	27.15

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	ATOM	2579	CB	GLU	339	29.136	-13.303	82.871	1.00	27.02
	ATOM	2580	CG	GLU	339	28.404	-14.185	81.843	1.00	30.73
	ATOM	2581	CD	GLU	339	28.942	-14.063	80.425	1.00	30.33
	ATOM	2582	OE1	GLU	339	30.121	-14.414	80.185	1.00	34.73
5	ATOM	2583	OE2	GLU	339	28.179	-13.619	79.548	1.00	29.50
	ATOM	2584	C	GLU	339	29.749	-13.085	85.311	1.00	26.93
	ATOM	2585	O	GLU	339	30.940	-13.345	85.209	1.00	27.69
	ATOM	2586	N	SER	340	29.264	-12.320	86.285	1.00	27.55
	ATOM	2587	CA	SER	340	30.140	-11.763	87.318	1.00	28.61
10	ATOM	2588	CB	SER	340	29.741	-10.323	87.667	1.00	29.40
	ATOM	2589	OG	SER	340	29.800	-9.485	86.528	1.00	35.97
	ATOM	2590	C	SER	340	30.029	-12.615	88.583	1.00	27.94
	ATOM	2591	O	SER	340	30.811	-12.448	89.526	1.00	24.04
	ATOM	2592	N	ASP	341	29.042	-13.511	88.600	1.00	28.02
15	ATOM	2593	CA	ASP	341	28.812	-14.387	89.748	1.00	29.66
	ATOM	2594	CB	ASP	341	27.808	-15.490	89.393	1.00	30.94
	ATOM	2595	CG	ASP	341	27.296	-16.227	90.620	1.00	33.11
	ATOM	2596	OD1	ASP	341	26.289	-15.778	91.217	1.00	28.78
	ATOM	2597	OD2	ASP	341	27.918	-17.247	90.991	1.00	32.82
20	ATOM	2598	C	ASP	341	30.137	-15.003	90.163	1.00	30.38
	ATOM	2599	O	ASP	341	30.853	-15.564	89.342	1.00	30.59
	ATOM	2600	N	THR	342	30.466	-14.886	91.443	1.00	33.59
	ATOM	2601	CA	THR	342	31.729	-15.405	91.953	1.00	37.01
	ATOM	2602	CB	THR	342	32.013	-14.836	93.350	1.00	38.81
25	ATOM	2603	OG1	THR	342	31.012	-15.304	94.265	1.00	43.90
	ATOM	2604	CG2	THR	342	31.972	-13.316	93.317	1.00	35.79
	ATOM	2605	C	THR	342	31.780	-16.929	92.027	1.00	37.87
	ATOM	2606	O	THR	342	32.853	-17.514	92.191	1.00	39.64
	ATOM	2607	N	GLY	343	30.625	-17.568	91.894	1.00	36.81

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	ATOM	2608	CA	GLY	343	30.578	-19.018	91.970	1.00	39.26
	ATOM	2609	C	GLY	343	29.631	-19.515	93.053	1.00	38.98
	ATOM	2610	O	GLY	343	29.293	-20.695	93.090	1.00	39.46
	ATOM	2611	N	ASP	344	29.204	-18.615	93.935	1.00	38.20
5	ATOM	2612	CA	ASP	344	28.287	-18.980	95.005	1.00	39.74
	ATOM	2613	CB	ASP	344	28.480	-18.071	96.231	1.00	39.14
	ATOM	2614	CG	ASP	344	28.267	-16.595	95.928	1.00	41.19
	ATOM	2615	OD1	ASP	344	27.733	-16.256	94.848	1.00	39.57
	ATOM	2616	OD2	ASP	344	28.627	-15.767	96.794	1.00	42.27
10	ATOM	2617	C	ASP	344	26.842	-18.926	94.516	1.00	40.25
	ATOM	2618	O	ASP	344	25.904	-19.235	95.257	1.00	39.36
	ATOM	2619	N	ARG	345	26.680	-18.525	93.259	1.00	38.45
	ATOM	2620	CA	ARG	345	25.374	-18.449	92.618	1.00	37.30
	ATOM	2621	CB	ARG	345	24.738	-19.847	92.587	1.00	37.49
15	ATOM	2622	CG	ARG	345	25.657	-20.935	92.044	1.00	38.81
	ATOM	2623	CD	ARG	345	24.976	-22.301	92.046	1.00	40.19
	ATOM	2624	NE	ARG	345	25.790	-23.327	91.397	1.00	42.18
	ATOM	2625	CZ	ARG	345	26.730	-24.051	91.999	1.00	43.19
	ATOM	2626	NH1	ARG	345	26.990	-23.880	93.288	1.00	43.31
20	ATOM	2627	NH2	ARG	345	27.421	-24.947	91.302	1.00	40.56
	ATOM	2628	C	ARG	345	24.397	-17.456	93.246	1.00	37.06
	ATOM	2629	O	ARG	345	23.231	-17.395	92.837	1.00	35.44
	ATOM	2630	N	LYS	346	24.855	-16.681	94.228	1.00	37.09
	ATOM	2631	CA	LYS	346	23.977	-15.704	94.876	1.00	39.61
25	ATOM	2632	CB	LYS	346	24.710	-14.964	96.005	1.00	43.18
	ATOM	2633	CG	LYS	346	25.084	-15.826	97.214	1.00	47.92
	ATOM	2634	CD	LYS	346	25.835	-15.009	98.285	1.00	50.48
	ATOM	2635	CE	LYS	346	26.274	-15.887	99.466	1.00	53.20
	ATOM	2636	NZ	LYS	346	27.039	-15.136	100.520	1.00	54.15

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	ATOM	2637	C	LYS	346	23.467	-14.690	93.858	1.00	39.25
	ATOM	2638	O	LYS	346	22.271	-14.400	93.795	1.00	38.51
	ATOM	2639	N	GLN	347	24.384	-14.158	93.055	1.00	40.01
	ATOM	2640	CA	GLN	347	24.036	-13.169	92.037	1.00	39.62
5	ATOM	2641	CB	GLN	347	25.301	-12.725	91.290	1.00	44.30
	ATOM	2642	CG	GLN	347	25.117	-11.507	90.403	1.00	50.12
	ATOM	2643	CD	GLN	347	24.996	-10.214	91.196	1.00	54.40
	ATOM	2644	OE1	GLN	347	24.699	-9.153	90.637	1.00	57.36
	ATOM	2645	NE2	GLN	347	25.234	-10.295	92.501	1.00	55.02
10	ATOM	2646	C	GLN	347	23.015	-13.735	91.046	1.00	36.71
	ATOM	2647	O	GLN	347	22.012	-13.087	90.732	1.00	35.38
	ATOM	2648	N	ILE	348	23.264	-14.949	90.563	1.00	33.61
	ATOM	2649	CA	ILE	348	22.360	-15.579	89.610	1.00	30.26
	ATOM	2650	CB	ILE	348	22.946	-16.906	89.103	1.00	31.09
15	ATOM	2651	CG2	ILE	348	21.983	-17.561	88.102	1.00	24.14
	ATOM	2652	CG1	ILE	348	24.315	-16.641	88.467	1.00	24.89
	ATOM	2653	CD1	ILE	348	25.016	-17.870	87.989	1.00	26.20
	ATOM	2654	C	ILE	348	20.990	-15.836	90.231	1.00	32.47
	ATOM	2655	O	ILE	348	19.946	-15.578	89.607	1.00	28.48
20	ATOM	2656	N	TYR	349	20.996	-16.330	91.468	1.00	33.64
	ATOM	2657	CA	TYR	349	19.757	-16.622	92.173	1.00	33.94
	ATOM	2658	CB	TYR	349	20.023	-17.189	93.566	1.00	35.19
	ATOM	2659	CG	TYR	349	18.728	-17.513	94.273	1.00	35.54
	ATOM	2660	CD1	TYR	349	18.085	-18.737	94.064	1.00	35.44
25	ATOM	2661	CE1	TYR	349	16.847	-19.009	94.647	1.00	35.96
	ATOM	2662	CD2	TYR	349	18.100	-16.569	95.083	1.00	34.28
	ATOM	2663	CE2	TYR	349	16.860	-16.833	95.665	1.00	34.50
	ATOM	2664	CZ	TYR	349	16.242	-18.053	95.441	1.00	34.82
	ATOM	2665	OH	TYR	349	15.007	-18.305	95.990	1.00	39.44



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	ATOM	2666	C	TYR	349	18.888	-15.390	92.339	1.00	35.45
	ATOM	2667	O	TYR	349	17.698	-15.419	92.042	1.00	37.11
	ATOM	2668	N	ASN	350	19.475	-14.312	92.846	1.00	37.18
	ATOM	2669	CA	ASN	350	18.722	-13.082	93.049	1.00	38.47
5	ATOM	2670	CB	ASN	350	19.617	-11.985	93.630	1.00	40.65
	ATOM	2671	CG	ASN	350	20.014	-12.263	95.065	1.00	45.75
	ATOM	2672	OD1	ASN	350	19.176	-12.638	95.893	1.00	45.11
	ATOM	2673	ND2	ASN	350	21.298	-12.075	95.373	1.00	46.81
	ATOM	2674	C	ASN	350	18.085	-12.585	91.768	1.00	37.56
10	ATOM	2675	O	ASN	350	16.924	-12.186	91.769	1.00	40.92
	ATOM	2676	N	ILE	351	18.839	-12.601	90.673	1.00	37.62
	ATOM	2677	CA	ILE	351	18.310	-12.139	89.395	1.00	37.09
	ATOM	2678	CB	ILE	351	19.401	-12.130	88.308	1.00	38.11
	ATOM	2679	CG2	ILE	351	18.771	-11.955	86.938	1.00	37.56
15	ATOM	2680	CG1	ILE	351	20.400	-11.004	88.588	1.00	38.11
	ATOM	2681	CD1	ILE	351	21.726	-11.178	87.879	1.00	36.24
	ATOM	2682	C	ILE	351	17.144	-12.997	88.921	1.00	36.57
	ATOM	2683	O	ILE	351	16.120	-12.474	88.479	1.00	38.22
	ATOM	2684	N	LEU	352	17.291	-14.314	89.012	1.00	35.96
20	ATOM	2685	CA	LEU	352	16.219	-15.206	88.577	1.00	36.28
	ATOM	2686	CB	LEU	352	16.740	-16.640	88.443	1.00	32.41
	ATOM	2687	CG	LEU	352	17.845	-16.828	87.395	1.00	30.66
	ATOM	2688	CD1	LEU	352	18.465	-18.226	87.496	1.00	25.83
	ATOM	2689	CD2	LEU	352	17.262	-16.597	86.025	1.00	27.66
25	ATOM	2690	C	LEU	352	15.039	-15.156	89.547	1.00	37.27
	ATOM	2691	O	LEU	352	13.896	-15.356	89.145	1.00	38.32
	ATOM	2692	N	SER	353	15.322	-14.888	90.819	1.00	39.41
	ATOM	2693	CA	SER	353	14.279	-14.794	91.838	1.00	42.13
	ATOM	2694	CB	SER	353	14.893	-14.708	93.237	1.00	43.72

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	ATOM	2695	OG	SER	353	13.883	-14.546	94.224	1.00	48.17
	ATOM	2696	C	SER	353	13.431	-13.557	91.590	1.00	43.61
	ATOM	2697	O	SER	353	12.229	-13.552	91.858	1.00	42.99
	ATOM	2698	N	THR	354	14.066	-12.506	91.081	1.00	44.80
5	ATOM	2699	CA	THR	354	13.363	-11.267	90.785	1.00	46.06
	ATOM	2700	CB	THR	354	14.356	-10.122	90.497	1.00	47.48
	ATOM	2701	OG1	THR	354	15.100	-9.820	91.687	1.00	47.39
	ATOM	2702	CG2	THR	354	13.615	-8.877	90.034	1.00	47.87
	ATOM	2703	C	THR	354	12.446	-11.455	89.579	1.00	46.06
10	ATOM	2704	O	THR	354	11.443	-10.757	89.436	1.00	47.23
	ATOM	2705	N	LEU	355	12.788	-12.406	88.717	1.00	46.03
	ATOM	2706	CA	LEU	355	11.983	-12.679	87.533	1.00	46.26
	ATOM	2707	CB	LEU	355	12.875	-13.157	86.390	1.00	46.43
	ATOM	2708	CG	LEU	355	14.030	-12.210	86.063	1.00	46.85
15	ATOM	2709	CD1	LEU	355	14.861	-12.813	84.950	1.00	47.00
	ATOM	2710	CD2	LEU	355	13.497	-10.844	85.660	1.00	45.99
	ATOM	2711	C	LEU	355	10.908	-13.722	87.821	1.00	46.88
	ATOM	2712	O	LEU	355	10.370	-14.346	86.902	1.00	47.28
	ATOM	2713	N	GLY	356	10.609	-13.912	89.105	1.00	47.29
20	ATOM	2714	CA	GLY	356	9.586	-14.858	89.511	1.00	44.74
	ATOM	2715	C	GLY	356	9.959	-16.321	89.396	1.00	44.45
	ATOM	2716	O	GLY	356	9.097	-17.163	89.146	1.00	45.09
	ATOM	2717	N	LEU	357	11.235	-16.635	89.575	1.00	43.26
	ATOM	2718	CA	LEU	357	11.681	-18.018	89.485	1.00	41.29
25	ATOM	2719	CB	LEU	357	12.653	-18.187	88.310	1.00	42.15
	ATOM	2720	CG	LEU	357	12.171	-17.833	86.896	1.00	41.21
	ATOM	2721	CD1	LEU	357	13.366	-17.781	85.972	1.00	39.61
	ATOM	2722	CD2	LEU	357	11.153	-18.849	86.393	1.00	39.50
	ATOM	2723	C	LEU	357	12.361	-18.455	90.780	1.00	40.57

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	ATOM	2724	O	LEU	357	12.780	-17.627	91.590	1.00	38.53
	ATOM	2725	N	ARG	358	12.448	-19.766	90.970	1.00	39.68
	ATOM	2726	CA	ARG	358	13.092	-20.355	92.139	1.00	40.04
	ATOM	2727	CB	ARG	358	12.048	-20.916	93.112	1.00	42.61
5	ATOM	2728	CG	ARG	358	11.172	-19.845	93.760	1.00	46.08
	ATOM	2729	CD	ARG	358	12.019	-18.871	94.560	1.00	49.74
	ATOM	2730	NE	ARG	358	11.355	-17.588	94.772	1.00	55.41
	ATOM	2731	CZ	ARG	358	10.588	-17.293	95.816	1.00	58.08
	ATOM	2732	NH1	ARG	358	10.376	-18.195	96.771	1.00	59.09
10	ATOM	2733	NH2	ARG	358	10.035	-16.087	95.906	1.00	58.98
	ATOM	2734	C	ARG	358	13.954	-21.471	91.576	1.00	38.39
	ATOM	2735	O	ARG	358	13.569	-22.641	91.586	1.00	37.47
	ATOM	2736	N	PRO	359	15.140	-21.109	91.065	1.00	36.51
	ATOM	2737	CD	PRO	359	15.664	-19.728	91.087	1.00	36.88
15	ATOM	2738	CA	PRO	359	16.123	-22.006	90.461	1.00	34.17
	ATOM	2739	CB	PRO	359	17.035	-21.039	89.722	1.00	35.29
	ATOM	2740	CG	PRO	359	17.135	-19.925	90.703	1.00	34.03
	ATOM	2741	C	PRO	359	16.915	-22.872	91.416	1.00	33.10
	ATOM	2742	O	PRO	359	17.140	-22.520	92.566	1.00	31.20
20	ATOM	2743	N	SER	360	17.365	-24.004	90.899	1.00	33.97
	ATOM	2744	CA	SER	360	18.183	-24.931	91.658	1.00	34.21
	ATOM	2745	CB	SER	360	17.912	-26.363	91.210	1.00	34.53
	ATOM	2746	OG	SER	360	18.287	-26.530	89.851	1.00	33.54
	ATOM	2747	C	SER	360	19.618	-24.568	91.307	1.00	34.99
25	ATOM	2748	O	SER	360	19.855	-23.673	90.495	1.00	35.49
	ATOM	2749	N	THR	361	20.564	-25.267	91.920	1.00	34.70
	ATOM	2750	CA	THR	361	21.977	-25.048	91.673	1.00	36.89
	ATOM	2751	CB	THR	361	22.838	-26.003	92.535	1.00	36.99
	ATOM	2752	OG1	THR	361	22.828	-25.558	93.898	1.00	38.93

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	ATOM	2753	CG2	THR	361	24.260	-26.041	92.033	1.00	38.24
	ATOM	2754	C	THR	361	22.303	-25.291	90.201	1.00	37.14
	ATOM	2755	O	THR	361	23.142	-24.606	89.616	1.00	37.81
	ATOM	2756	N	THR	362	21.635	-26.273	89.612	1.00	35.92
5	ATOM	2757	CA	THR	362	21.865	-26.614	88.223	1.00	34.91
	ATOM	2758	CB	THR	362	21.369	-28.037	87.914	1.00	36.12
	ATOM	2759	OG1	THR	362	19.969	-28.117	88.199	1.00	40.45
	ATOM	2760	CG2	THR	362	22.113	-29.063	88.771	1.00	34.62
	ATOM	2761	C	THR	362	21.181	-25.626	87.292	1.00	33.53
10	ATOM	2762	O	THR	362	21.684	-25.360	86.205	1.00	33.46
	ATOM	2763	N	ASP	363	20.034	-25.091	87.698	1.00	31.06
	ATOM	2764	CA	ASP	363	19.355	-24.115	86.860	1.00	32.46
	ATOM	2765	CB	ASP	363	18.018	-23.690	87.468	1.00	34.45
	ATOM	2766	CG	ASP	363	16.964	-24.783	87.409	1.00	37.91
15	ATOM	2767	OD1	ASP	363	16.889	-25.504	86.388	1.00	38.99
	ATOM	2768	OD2	ASP	363	16.194	-24.907	88.385	1.00	38.23
	ATOM	2769	C	ASP	363	20.254	-22.878	86.718	1.00	32.88
	ATOM	2770	O	ASP	363	20.419	-22.331	85.629	1.00	30.65
	ATOM	2771	N	CYS	364	20.833	-22.451	87.836	1.00	33.86
20	ATOM	2772	CA	CYS	364	21.712	-21.292	87.860	1.00	32.22
	ATOM	2773	CB	CYS	364	22.186	-21.015	89.289	1.00	31.35
	ATOM	2774	SG	CYS	364	20.915	-20.338	90.389	1.00	31.77
	ATOM	2775	C	CYS	364	22.914	-21.493	86.950	1.00	30.91
	ATOM	2776	O	CYS	364	23.207	-20.645	86.119	1.00	30.71
25	ATOM	2777	N	ASP	365	23.608	-22.614	87.107	1.00	31.25
	ATOM	2778	CA	ASP	365	24.774	-22.894	86.280	1.00	32.00
	ATOM	2779	CB	ASP	365	25.389	-24.243	86.659	1.00	32.78
	ATOM	2780	CG	ASP	365	26.037	-24.211	88.023	1.00	35.48
	ATOM	2781	OD1	ASP	365	26.017	-23.127	88.650	1.00	37.01

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	ATOM	2782	OD2	ASP	365	26.564	-25.251	88.466	1.00	35.21
	ATOM	2783	C	ASP	365	24.405	-22.886	84.810	1.00	30.41
	ATOM	2784	O	ASP	365	25.166	-22.407	83.966	1.00	31.73
	ATOM	2785	N	ILE	366	23.225	-23.408	84.514	1.00	29.17
5	ATOM	2786	CA	ILE	366	22.739	-23.462	83.148	1.00	30.58
	ATOM	2787	CB	ILE	366	21.456	-24.318	83.058	1.00	30.61
	ATOM	2788	CG2	ILE	366	20.779	-24.118	81.712	1.00	28.15
	ATOM	2789	CG1	ILE	366	21.808	-25.797	83.261	1.00	33.09
	ATOM	2790	CD1	ILE	366	20.577	-26.702	83.405	1.00	32.69
10	ATOM	2791	C	ILE	366	22.462	-22.066	82.576	1.00	29.08
	ATOM	2792	O	ILE	366	22.729	-21.815	81.405	1.00	28.78
	ATOM	2793	N	VAL	367	21.906	-21.170	83.386	1.00	27.52
	ATOM	2794	CA	VAL	367	21.632	-19.817	82.910	1.00	27.71
	ATOM	2795	CB	VAL	367	20.803	-19.021	83.943	1.00	26.66
15	ATOM	2796	CG1	VAL	367	20.812	-17.531	83.609	1.00	24.57
	ATOM	2797	CG2	VAL	367	19.373	-19.535	83.928	1.00	26.09
	ATOM	2798	C	VAL	367	22.979	-19.143	82.643	1.00	28.05
	ATOM	2799	O	VAL	367	23.144	-18.409	81.670	1.00	28.53
	ATOM	2800	N	ARG	368	23.940	-19.436	83.508	1.00	27.74
20	ATOM	2801	CA	ARG	368	25.300	-18.927	83.386	1.00	30.76
	ATOM	2802	CB	ARG	368	26.172	-19.575	84.458	1.00	31.66
	ATOM	2803	CG	ARG	368	27.023	-18.648	85.269	1.00	38.26
	ATOM	2804	CD	ARG	368	28.312	-18.282	84.579	1.00	41.00
	ATOM	2805	NE	ARG	368	29.272	-17.763	85.547	1.00	43.72
25	ATOM	2806	CZ	ARG	368	30.397	-17.135	85.226	1.00	46.75
	ATOM	2807	NH1	ARG	368	30.710	-16.938	83.954	1.00	48.06
	ATOM	2808	NH2	ARG	368	31.212	-16.708	86.179	1.00	47.96
	ATOM	2809	C	ARG	368	25.841	-19.317	82.003	1.00	30.63
	ATOM	2810	O	ARG	368	26.343	-18.469	81.256	1.00	27.84

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	ATOM	2811	N	ARG	369	25.735	-20.606	81.677	1.00	27.70
	ATOM	2812	CA	ARG	369	26.228	-21.115	80.399	1.00	28.24
	ATOM	2813	CB	ARG	369	26.077	-22.645	80.327	1.00	26.69
	ATOM	2814	CG	ARG	369	27.044	-23.429	81.224	1.00	29.04
5	ATOM	2815	CD	ARG	369	28.506	-23.228	80.815	1.00	31.91
	ATOM	2816	NE	ARG	369	28.752	-23.683	79.445	1.00	35.74
	ATOM	2817	CZ	ARG	369	29.117	-22.892	78.439	1.00	36.75
	ATOM	2818	NH1	ARG	369	29.291	-21.590	78.638	1.00	36.65
	ATOM	2819	NH2	ARG	369	29.291	-23.400	77.225	1.00	36.11
10	ATOM	2820	C	ARG	369	25.528	-20.472	79.208	1.00	27.14
	ATOM	2821	O	ARG	369	26.160	-20.188	78.189	1.00	28.06
	ATOM	2822	N	ALA	370	24.224	-20.252	79.327	1.00	25.64
	ATOM	2823	CA	ALA	370	23.480	-19.634	78.238	1.00	25.08
	ATOM	2824	CB	ALA	370	21.991	-19.587	78.574	1.00	25.47
15	ATOM	2825	C	ALA	370	24.015	-18.218	78.006	1.00	25.14
	ATOM	2826	O	ALA	370	24.196	-17.793	76.870	1.00	25.23
	ATOM	2827	N	CYS	371	24.268	-17.491	79.087	1.00	24.15
	ATOM	2828	CA	CYS	371	24.785	-16.135	78.965	1.00	25.09
	ATOM	2829	CB	CYS	371	24.855	-15.467	80.338	1.00	22.74
20	ATOM	2830	SG	CYS	371	23.239	-15.076	81.033	1.00	25.40
	ATOM	2831	C	CYS	371	26.161	-16.127	78.300	1.00	24.93
	ATOM	2832	O	CYS	371	26.392	-15.358	77.367	1.00	25.49
	ATOM	2833	N	GLU	372	27.062	-16.991	78.765	1.00	24.70
	ATOM	2834	CA	GLU	372	28.411	-17.073	78.207	1.00	26.69
25	ATOM	2835	CB	GLU	372	29.247	-18.105	78.975	1.00	27.07
	ATOM	2836	CG	GLU	372	29.232	-17.890	80.481	1.00	32.77
	ATOM	2837	CD	GLU	372	30.016	-18.945	81.243	1.00	33.87
	ATOM	2838	OE1	GLU	372	29.905	-20.139	80.892	1.00	36.95
	ATOM	2839	OE2	GLU	372	30.733	-18.583	82.200	1.00	35.18

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	ATOM	2840	C	GLU	372	28.418	-17.420	76.718	1.00	27.23
	ATOM	2841	O	GLU	372	29.259	-16.922	75.966	1.00	29.09
	ATOM	2842	N	SER	373	27.489	-18.273	76.296	1.00	25.93
	ATOM	2843	CA	SER	373	27.403	-18.664	74.894	1.00	27.07
5	ATOM	2844	CB	SER	373	26.393	-19.803	74.718	1.00	25.93
	ATOM	2845	OG	SER	373	26.784	-20.951	75.457	1.00	32.56
	ATOM	2846	C	SER	373	26.988	-17.471	74.034	1.00	25.31
	ATOM	2847	O	SER	373	27.585	-17.207	72.998	1.00	24.49
	ATOM	2848	N	VAL	374	25.962	-16.754	74.475	1.00	25.87
10	ATOM	2849	CA	VAL	374	25.473	-15.596	73.743	1.00	25.12
	ATOM	2850	CB	VAL	374	24.139	-15.103	74.319	1.00	26.07
	ATOM	2851	CG1	VAL	374	23.754	-13.766	73.682	1.00	29.29
	ATOM	2852	CG2	VAL	374	23.055	-16.127	74.061	1.00	25.56
	ATOM	2853	C	VAL	374	26.465	-14.429	73.742	1.00	24.54
15	ATOM	2854	O	VAL	374	26.657	-13.792	72.714	1.00	25.64
	ATOM	2855	N	SER	375	27.094	-14.144	74.878	1.00	21.70
	ATOM	2856	CA	SER	375	28.029	-13.034	74.922	1.00	23.89
	ATOM	2857	CB	SER	375	28.298	-12.585	76.365	1.00	23.28
	ATOM	2858	OG	SER	375	28.986	-13.565	77.120	1.00	29.71
20	ATOM	2859	C	SER	375	29.324	-13.391	74.210	1.00	24.77
	ATOM	2860	O	SER	375	29.873	-12.560	73.490	1.00	23.61
	ATOM	2861	N	THR	376	29.805	-14.623	74.386	1.00	23.54
	ATOM	2862	CA	THR	376	31.029	-15.052	73.707	1.00	23.38
	ATOM	2863	CB	THR	376	31.444	-16.501	74.096	1.00	23.76
25	ATOM	2864	OG1	THR	376	31.874	-16.527	75.458	1.00	26.36
	ATOM	2865	CG2	THR	376	32.594	-16.987	73.222	1.00	21.48
	ATOM	2866	C	THR	376	30.859	-14.996	72.189	1.00	22.33
	ATOM	2867	O	THR	376	31.810	-14.694	71.465	1.00	23.88
	ATOM	2868	N	ARG	377	29.660	-15.293	71.695	1.00	20.80

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	ATOM	2869	CA	ARG	377	29.452	-15.239	70.253	1.00	21.46
	ATOM	2870	CB	ARG	377	28.141	-15.918	69.839	1.00	22.21
	ATOM	2871	CG	ARG	377	27.958	-15.875	68.312	1.00	25.01
	ATOM	2872	CD	ARG	377	26.601	-16.377	67.827	1.00	27.70
5	ATOM	2873	NE	ARG	377	25.491	-15.558	68.302	1.00	25.17
	ATOM	2874	CZ	ARG	377	24.255	-15.637	67.825	1.00	26.42
	ATOM	2875	NH1	ARG	377	23.973	-16.492	66.850	1.00	25.23
	ATOM	2876	NH2	ARG	377	23.294	-14.877	68.339	1.00	26.96
	ATOM	2877	C	ARG	377	29.439	-13.773	69.787	1.00	21.55
10	ATOM	2878	O	ARG	377	29.856	-13.462	68.670	1.00	20.80
	ATOM	2879	N	ALA	378	28.951	-12.879	70.639	1.00	19.46
	ATOM	2880	CA	ALA	378	28.927	-11.463	70.302	1.00	21.17
	ATOM	2881	CB	ALA	378	28.239	-10.653	71.412	1.00	20.68
	ATOM	2882	C	ALA	378	30.374	-11.015	70.151	1.00	20.18
15	ATOM	2883	O	ALA	378	30.747	-10.420	69.145	1.00	20.36
	ATOM	2884	N	ALA	379	31.191	-11.326	71.153	1.00	19.41
	ATOM	2885	CA	ALA	379	32.600	-10.950	71.138	1.00	20.64
	ATOM	2886	CB	ALA	379	33.296	-11.515	72.371	1.00	20.04
	ATOM	2887	C	ALA	379	33.332	-11.405	69.869	1.00	22.79
20	ATOM	2888	O	ALA	379	34.054	-10.620	69.234	1.00	21.82
	ATOM	2889	N	HIS	380	33.139	-12.666	69.489	1.00	22.45
	ATOM	2890	CA	HIS	380	33.803	-13.208	68.305	1.00	22.78
	ATOM	2891	CB	HIS	380	33.726	-14.745	68.314	1.00	22.80
	ATOM	2892	CG	HIS	380	34.584	-15.384	69.364	1.00	26.52
25	ATOM	2893	CD2	HIS	380	35.557	-14.870	70.152	1.00	27.81
	ATOM	2894	ND1	HIS	380	34.499	-16.720	69.687	1.00	28.99
	ATOM	2895	CE1	HIS	380	35.383	-17.002	70.627	1.00	28.15
	ATOM	2896	NE2	HIS	380	36.039	-15.896	70.927	1.00	28.70
	ATOM	2897	C	HIS	380	33.242	-12.657	66.994	1.00	22.38



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	ATOM	2898	O	HIS	380	33.988	-12.368	66.073	1.00	20.71
	ATOM	2899	N	MET	381	31.926	-12.524	66.915	1.00	23.83
	ATOM	2900	CA	MET	381	31.285	-12.018	65.713	1.00	26.66
	ATOM	2901	CB	MET	381	29.760	-12.086	65.899	1.00	29.06
5	ATOM	2902	CG	MET	381	28.926	-12.031	64.622	1.00	34.34
	ATOM	2903	SD	MET	381	29.456	-13.157	63.312	1.00	33.69
	ATOM	2904	CE	MET	381	28.228	-14.472	63.429	1.00	34.64
	ATOM	2905	C	MET	381	31.781	-10.580	65.509	1.00	27.50
	ATOM	2906	O	MET	381	32.153	-10.188	64.406	1.00	26.70
10	ATOM	2907	N	CYS	382	31.830	-9.813	66.595	1.00	26.32
	ATOM	2908	CA	CYS	382	32.302	-8.441	66.536	1.00	24.87
	ATOM	2909	CB	CYS	382	32.102	-7.769	67.896	1.00	26.05
	ATOM	2910	SG	CYS	382	32.389	-5.962	67.931	1.00	26.70
	ATOM	2911	C	CYS	382	33.785	-8.355	66.122	1.00	24.60
15	ATOM	2912	O	CYS	382	34.187	-7.457	65.360	1.00	19.92
	ATOM	2913	N	SER	383	34.590	-9.288	66.623	1.00	22.62
	ATOM	2914	CA	SER	383	36.017	-9.302	66.327	1.00	22.35
	ATOM	2915	CB	SER	383	36.716	-10.439	67.096	1.00	23.03
	ATOM	2916	OG	SER	383	36.361	-11.712	66.571	1.00	24.25
20	ATOM	2917	C	SER	383	36.272	-9.463	64.834	1.00	23.77
	ATOM	2918	O	SER	383	37.202	-8.875	64.288	1.00	24.79
	ATOM	2919	N	ALA	384	35.448	-10.269	64.173	1.00	24.03
	ATOM	2920	CA	ALA	384	35.612	-10.480	62.743	1.00	25.52
	ATOM	2921	CB	ALA	384	34.649	-11.552	62.256	1.00	22.05
25	ATOM	2922	C	ALA	384	35.369	-9.182	61.980	1.00	25.61
	ATOM	2923	O	ALA	384	35.990	-8.942	60.947	1.00	25.37
	ATOM	2924	N	GLY	385	34.450	-8.360	62.490	1.00	25.67
	ATOM	2925	CA	GLY	385	34.134	-7.098	61.842	1.00	23.86
	ATOM	2926	C	GLY	385	35.289	-6.128	61.944	1.00	20.99

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	ATOM	2927	O	GLY	385	35.702	-5.531	60.960	1.00	22.47
	ATOM	2928	N	LEU	386	35.811	-5.962	63.148	1.00	22.82
	ATOM	2929	CA	LEU	386	36.937	-5.065	63.364	1.00	25.33
	ATOM	2930	CB	LEU	386	37.259	-4.971	64.850	1.00	23.48
5	ATOM	2931	CG	LEU	386	37.800	-3.658	65.425	1.00	27.75
	ATOM	2932	CD1	LEU	386	38.641	-4.007	66.641	1.00	26.18
	ATOM	2933	CD2	LEU	386	38.621	-2.865	64.428	1.00	25.52
	ATOM	2934	C	LEU	386	38.172	-5.584	62.616	1.00	26.01
	ATOM	2935	O	LEU	386	38.953	-4.794	62.067	1.00	26.60
10	ATOM	2936	N	ALA	387	38.356	-6.904	62.601	1.00	23.95
	ATOM	2937	CA	ALA	387	39.509	-7.482	61.902	1.00	24.13
	ATOM	2938	CB	ALA	387	39.585	-8.989	62.135	1.00	20.59
	ATOM	2939	C	ALA	387	39.405	-7.181	60.411	1.00	24.07
	ATOM	2940	O	ALA	387	40.419	-6.990	59.730	1.00	22.59
15	ATOM	2941	N	GLY	388	38.175	-7.141	59.904	1.00	24.30
	ATOM	2942	CA	GLY	388	37.975	-6.838	58.497	1.00	24.40
	ATOM	2943	C	GLY	388	38.380	-5.398	58.203	1.00	25.62
	ATOM	2944	O	GLY	388	39.048	-5.114	57.205	1.00	25.24
	ATOM	2945	N	VAL	389	37.974	-4.488	59.084	1.00	25.15
20	ATOM	2946	CA	VAL	389	38.294	-3.072	58.950	1.00	23.08
	ATOM	2947	CB	VAL	389	37.581	-2.259	60.057	1.00	21.38
	ATOM	2948	CG1	VAL	389	38.083	-0.820	60.076	1.00	21.90
	ATOM	2949	CG2	VAL	389	36.078	-2.303	59.819	1.00	20.64
	ATOM	2950	C	VAL	389	39.802	-2.858	59.034	1.00	24.13
25	ATOM	2951	O	VAL	389	40.402	-2.198	58.178	1.00	25.99
	ATOM	2952	N	ILE	390	40.424	-3.429	60.054	1.00	24.21
	ATOM	2953	CA	ILE	390	41.866	-3.289	60.209	1.00	25.31
	ATOM	2954	CB	ILE	390	42.317	-3.883	61.576	1.00	25.21
	ATOM	2955	CG2	ILE	390	43.831	-3.962	61.661	1.00	27.92

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	ATOM	2956	CG1	ILE	390	41.778	-2.993	62.708	1.00	26.03
	ATOM	2957	CD1	ILE	390	42.091	-3.476	64.094	1.00	27.41
	ATOM	2958	C	ILE	390	42.668	-3.899	59.040	1.00	26.27
	ATOM	2959	O	ILE	390	43.622	-3.287	58.563	1.00	25.08
5	ATOM	2960	N	ASN	391	42.286	-5.082	58.561	1.00	27.72
	ATOM	2961	CA	ASN	391	43.026	-5.689	57.448	1.00	29.87
	ATOM	2962	CB	ASN	391	42.649	-7.162	57.250	1.00	27.74
	ATOM	2963	CG	ASN	391	43.147	-8.044	58.375	1.00	29.54
	ATOM	2964	OD1	ASN	391	44.216	-7.804	58.939	1.00	28.68
10	ATOM	2965	ND2	ASN	391	42.383	-9.079	58.699	1.00	26.84
	ATOM	2966	C	ASN	391	42.805	-4.930	56.144	1.00	31.14
	ATOM	2967	O	ASN	391	43.688	-4.903	55.281	1.00	29.49
	ATOM	2968	N	ARG	392	41.627	-4.331	55.991	1.00	31.07
	ATOM	2969	CA	ARG	392	41.358	-3.553	54.795	1.00	33.43
15	ATOM	2970	CB	ARG	392	39.921	-3.018	54.780	1.00	35.04
	ATOM	2971	CG	ARG	392	39.597	-2.307	53.483	1.00	35.84
	ATOM	2972	CD	ARG	392	38.614	-1.173	53.650	1.00	37.18
	ATOM	2973	NE	ARG	392	38.804	-0.186	52.589	1.00	35.89
	ATOM	2974	CZ	ARG	392	38.518	-0.390	51.309	1.00	36.67
20	ATOM	2975	NH1	ARG	392	38.006	-1.550	50.911	1.00	38.42
	ATOM	2976	NH2	ARG	392	38.788	0.553	50.417	1.00	37.33
	ATOM	2977	C	ARG	392	42.335	-2.377	54.831	1.00	33.73
	ATOM	2978	O	ARG	392	43.028	-2.107	53.858	1.00	34.52
	ATOM	2979	N	MET	393	42.396	-1.691	55.967	1.00	34.05
25	ATOM	2980	CA	MET	393	43.298	-0.554	56.126	1.00	35.93
	ATOM	2981	CB	MET	393	43.119	0.073	57.517	1.00	32.21
	ATOM	2982	CG	MET	393	41.801	0.834	57.692	1.00	28.72
	ATOM	2983	SD	MET	393	41.530	1.348	59.400	1.00	27.28
	ATOM	2984	CE	MET	393	42.652	2.753	59.533	1.00	24.26

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	ATOM	2985	C	MET	393	44.751	-0.979	55.947	1.00	39.48
	ATOM	2986	O	MET	393	45.579	-0.216	55.448	1.00	39.63
	ATOM	2987	N	ARG	394	45.049	-2.205	56.364	1.00	43.20
	ATOM	2988	CA	ARG	394	46.391	-2.766	56.277	1.00	45.79
5	ATOM	2989	CB	ARG	394	46.381	-4.180	56.870	1.00	49.86
	ATOM	2990	CG	ARG	394	47.670	-4.595	57.551	1.00	53.76
	ATOM	2991	CD	ARG	394	48.587	-5.335	56.612	1.00	56.09
	ATOM	2992	NE	ARG	394	49.896	-5.554	57.217	1.00	60.36
	ATOM	2993	CZ	ARG	394	50.797	-4.596	57.411	1.00	60.35
10	ATOM	2994	NH1	ARG	394	50.528	-3.353	57.042	1.00	61.48
	ATOM	2995	NH2	ARG	394	51.964	-4.878	57.978	1.00	60.51
	ATOM	2996	C	ARG	394	46.912	-2.792	54.835	1.00	46.90
	ATOM	2997	O	ARG	394	48.117	-2.697	54.606	1.00	44.95
	ATOM	2998	N	GLU	395	46.005	-2.906	53.869	1.00	48.68
15	ATOM	2999	CA	GLU	395	46.387	-2.943	52.459	1.00	52.84
	ATOM	3000	CB	GLU	395	45.165	-3.275	51.590	1.00	54.51
	ATOM	3001	CG	GLU	395	44.388	-4.508	52.051	1.00	60.85
	ATOM	3002	CD	GLU	395	43.310	-4.952	51.061	1.00	64.84
	ATOM	3003	OE1	GLU	395	42.485	-4.105	50.642	1.00	65.83
20	ATOM	3004	OE2	GLU	395	43.286	-6.155	50.708	1.00	66.43
	ATOM	3005	C	GLU	395	47.008	-1.621	51.991	1.00	54.64
	ATOM	3006	O	GLU	395	47.791	-1.594	51.039	1.00	53.71
	ATOM	3007	N	SER	396	46.660	-0.528	52.666	1.00	56.54
	ATOM	3008	CA	SER	396	47.179	0.794	52.313	1.00	58.22
25	ATOM	3009	CB	SER	396	46.037	1.808	52.266	1.00	57.21
	ATOM	3010	OG	SER	396	44.980	1.340	51.448	1.00	59.52
	ATOM	3011	C	SER	396	48.221	1.268	53.318	1.00	60.22
	ATOM	3012	O	SER	396	48.394	2.468	53.527	1.00	60.38
	ATOM	3013	N	ARG	397	48.915	0.324	53.941	1.00	62.22

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	ATOM	3014	CA	ARG	397	49.924	0.663	54.933	1.00	64.67
	ATOM	3015	CB	ARG	397	49.430	0.260	56.324	1.00	65.24
	ATOM	3016	CG	ARG	397	49.798	1.218	57.444	1.00	67.16
	ATOM	3017	CD	ARG	397	49.178	2.596	57.244	1.00	68.03
5	ATOM	3018	NE	ARG	397	48.803	3.208	58.516	1.00	69.13
	ATOM	3019	CZ	ARG	397	47.681	2.933	59.178	1.00	70.58
	ATOM	3020	NH1	ARG	397	46.813	2.059	58.687	1.00	71.37
	ATOM	3021	NH2	ARG	397	47.429	3.521	60.340	1.00	70.29
	ATOM	3022	C	ARG	397	51.222	-0.063	54.611	1.00	65.54
10	ATOM	3023	O	ARG	397	51.416	-1.215	54.998	1.00	66.75
	ATOM	3024	N	SER	398	52.106	0.621	53.894	1.00	66.86
	ATOM	3025	CA	SER	398	53.388	0.052	53.508	1.00	67.48
	ATOM	3026	CB	SER	398	53.980	0.832	52.331	1.00	67.48
	ATOM	3027	OG	SER	398	53.155	0.725	51.181	1.00	66.93
15	ATOM	3028	C	SER	398	54.358	0.063	54.679	1.00	68.36
	ATOM	3029	O	SER	398	55.036	1.063	54.934	1.00	69.35
	ATOM	3030	N	GLU	399	54.413	-1.059	55.388	1.00	67.90
	ATOM	3031	CA	GLU	399	55.297	-1.206	56.533	1.00	68.16
	ATOM	3032	CB	GLU	399	55.002	-0.126	57.564	1.00	68.95
20	ATOM	3033	CG	GLU	399	53.540	0.020	57.889	1.00	71.05
	ATOM	3034	CD	GLU	399	53.261	1.318	58.598	1.00	71.37
	ATOM	3035	OE1	GLU	399	53.871	1.545	59.662	1.00	72.25
	ATOM	3036	OE2	GLU	399	52.443	2.111	58.089	1.00	71.32
	ATOM	3037	C	GLU	399	55.167	-2.581	57.168	1.00	67.57
25	ATOM	3038	O	GLU	399	54.078	-3.155	57.232	1.00	67.34
	ATOM	3039	N	ASP	400	56.301	-3.091	57.635	1.00	66.86
	ATOM	3040	CA	ASP	400	56.397	-4.400	58.265	1.00	65.75
	ATOM	3041	CB	ASP	400	57.739	-4.507	58.989	1.00	68.55
	ATOM	3042	CG	ASP	400	58.892	-3.961	58.157	1.00	71.49

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	ATOM	3043	OD1 ASP	400	59.015	-4.356	56.976	1.00	72.29
	ATOM	3044	OD2 ASP	400	59.675	-3.136	58.682	1.00	72.38
	ATOM	3045	C ASP	400	55.247	-4.676	59.233	1.00	63.41
	ATOM	3046	O ASP	400	54.385	-5.514	58.962	1.00	63.27
5	ATOM	3047	N VAL	401	55.241	-3.973	60.361	1.00	59.50
	ATOM	3048	CA VAL	401	54.193	-4.138	61.360	1.00	55.59
	ATOM	3049	CB VAL	401	54.789	-4.439	62.757	1.00	55.81
	ATOM	3050	CG1 VAL	401	53.698	-4.375	63.818	1.00	54.69
	ATOM	3051	CG2 VAL	401	55.442	-5.817	62.757	1.00	54.18
10	ATOM	3052	C VAL	401	53.345	-2.876	61.454	1.00	53.78
	ATOM	3053	O VAL	401	53.841	-1.807	61.820	1.00	53.39
	ATOM	3054	N MET	402	52.065	-2.991	61.114	1.00	50.91
	ATOM	3055	CA MET	402	51.190	-1.834	61.194	1.00	47.59
	ATOM	3056	CB MET	402	49.992	-1.958	60.250	1.00	46.98
15	ATOM	3057	CG MET	402	49.043	-0.768	60.387	1.00	47.22
	ATOM	3058	SD MET	402	47.505	-0.874	59.461	1.00	48.69
	ATOM	3059	CE MET	402	46.622	-2.099	60.439	1.00	48.15
	ATOM	3060	C MET	402	50.670	-1.643	62.605	1.00	44.98
	ATOM	3061	O MET	402	49.945	-2.483	63.134	1.00	43.92
20	ATOM	3062	N ARG	403	51.054	-0.533	63.219	1.00	43.27
	ATOM	3063	CA ARG	403	50.587	-0.229	64.556	1.00	41.71
	ATOM	3064	CB ARG	403	51.673	0.484	65.350	1.00	45.65
	ATOM	3065	CG ARG	403	52.903	-0.356	65.596	1.00	52.20
	ATOM	3066	CD ARG	403	53.973	0.474	66.262	1.00	57.99
25	ATOM	3067	NE ARG	403	55.137	-0.324	66.630	1.00	65.47
	ATOM	3068	CZ ARG	403	56.251	0.184	67.149	1.00	68.76
	ATOM	3069	NH1 ARG	403	56.349	1.493	67.357	1.00	69.34
	ATOM	3070	NH2 ARG	403	57.265	-0.615	67.468	1.00	69.59
	ATOM	3071	C ARG	403	49.388	0.685	64.372	1.00	37.99

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	ATOM	3072	O	ARG	403	49.471	1.692	63.679	1.00	37.13
	ATOM	3073	N	ILE	404	48.267	0.322	64.975	1.00	34.39
	ATOM	3074	CA	ILE	404	47.069	1.129	64.854	1.00	31.53
	ATOM	3075	CB	ILE	404	46.161	0.577	63.735	1.00	33.38
5	ATOM	3076	CG2	ILE	404	45.681	-0.829	64.096	1.00	32.57
	ATOM	3077	CG1	ILE	404	44.987	1.524	63.500	1.00	35.77
	ATOM	3078	CD1	ILE	404	44.144	1.153	62.300	1.00	38.45
	ATOM	3079	C	ILE	404	46.322	1.152	66.179	1.00	28.96
	ATOM	3080	O	ILE	404	46.393	0.204	66.956	1.00	29.35
10	ATOM	3081	N	THR	405	45.632	2.250	66.453	1.00	28.84
	ATOM	3082	CA	THR	405	44.874	2.359	67.693	1.00	27.84
	ATOM	3083	CB	THR	405	45.323	3.558	68.535	1.00	26.65
	ATOM	3084	OG1	THR	405	46.663	3.335	68.990	1.00	30.48
	ATOM	3085	CG2	THR	405	44.428	3.715	69.749	1.00	27.32
15	ATOM	3086	C	THR	405	43.387	2.460	67.408	1.00	27.13
	ATOM	3087	O	THR	405	42.964	3.127	66.462	1.00	24.36
	ATOM	3088	N	VAL	406	42.604	1.786	68.245	1.00	25.61
	ATOM	3089	CA	VAL	406	41.160	1.737	68.107	1.00	23.67
	ATOM	3090	CB	VAL	406	40.705	0.244	67.973	1.00	23.64
20	ATOM	3091	CG1	VAL	406	39.189	0.138	67.798	1.00	24.19
	ATOM	3092	CG2	VAL	406	41.405	-0.399	66.783	1.00	21.36
	ATOM	3093	C	VAL	406	40.493	2.392	69.320	1.00	26.21
	ATOM	3094	O	VAL	406	40.763	2.018	70.469	1.00	26.86
	ATOM	3095	N	GLY	407	39.644	3.389	69.072	1.00	25.61
25	ATOM	3096	CA	GLY	407	38.943	4.044	70.168	1.00	23.09
	ATOM	3097	C	GLY	407	37.645	3.285	70.387	1.00	21.77
	ATOM	3098	O	GLY	407	36.919	3.011	69.426	1.00	23.17
	ATOM	3099	N	VAL	408	37.334	2.943	71.632	1.00	20.52
	ATOM	3100	CA	VAL	408	36.128	2.167	71.907	1.00	21.51

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	ATOM	3101	CB	VAL	408	36.500	0.684	72.252	1.00	23.04
	ATOM	3102	CG1	VAL	408	35.237	-0.176	72.351	1.00	19.52
	ATOM	3103	CG2	VAL	408	37.436	0.121	71.201	1.00	20.49
	ATOM	3104	C	VAL	408	35.282	2.704	73.060	1.00	23.66
5	ATOM	3105	O	VAL	408	35.814	3.223	74.045	1.00	23.60
	ATOM	3106	N	ASP	409	33.963	2.580	72.923	1.00	24.58
	ATOM	3107	CA	ASP	409	33.040	2.992	73.975	1.00	26.70
	ATOM	3108	CB	ASP	409	32.612	4.455	73.803	1.00	30.78
	ATOM	3109	CG	ASP	409	31.909	4.998	75.041	1.00	31.51
10	ATOM	3110	OD1	ASP	409	32.322	4.625	76.156	1.00	31.70
	ATOM	3111	OD2	ASP	409	30.955	5.794	74.910	1.00	35.70
	ATOM	3112	C	ASP	409	31.824	2.083	73.898	1.00	25.68
	ATOM	3113	O	ASP	409	31.639	1.396	72.901	1.00	27.99
	ATOM	3114	N	GLY	410	30.999	2.079	74.943	1.00	28.67
15	ATOM	3115	CA	GLY	410	29.807	1.233	74.964	1.00	29.54
	ATOM	3116	C	GLY	410	29.755	0.355	76.212	1.00	30.09
	ATOM	3117	O	GLY	410	30.787	-0.138	76.657	1.00	28.57
	ATOM	3118	N	SER	411	28.560	0.150	76.767	1.00	30.89
	ATOM	3119	CA	SER	411	28.392	-0.649	77.983	1.00	32.71
20	ATOM	3120	CB	SER	411	26.941	-0.554	78.490	1.00	32.88
	ATOM	3121	OG	SER	411	26.011	-0.884	77.473	1.00	36.82
	ATOM	3122	C	SER	411	28.804	-2.121	77.840	1.00	31.25
	ATOM	3123	O	SER	411	29.480	-2.661	78.712	1.00	29.96
	ATOM	3124	N	VAL	412	28.398	-2.768	76.754	1.00	29.78
25	ATOM	3125	CA	VAL	412	28.780	-4.158	76.535	1.00	28.59
	ATOM	3126	CB	VAL	412	28.264	-4.665	75.174	1.00	29.68
	ATOM	3127	CG1	VAL	412	28.772	-6.088	74.908	1.00	27.25
	ATOM	3128	CG2	VAL	412	26.739	-4.642	75.173	1.00	29.93
	ATOM	3129	C	VAL	412	30.307	-4.320	76.584	1.00	29.24



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	ATOM	3130	O	VAL	412	30.831	-5.145	77.340	1.00	28.78
	ATOM	3131	N	TYR	413	31.023	-3.522	75.796	1.00	27.57
	ATOM	3132	CA	TYR	413	32.482	-3.602	75.763	1.00	24.60
	ATOM	3133	CB	TYR	413	33.049	-2.730	74.645	1.00	19.87
5	ATOM	3134	CG	TYR	413	34.568	-2.710	74.587	1.00	20.22
	ATOM	3135	CD1	TYR	413	35.270	-3.566	73.735	1.00	21.52
	ATOM	3136	CE1	TYR	413	36.667	-3.519	73.655	1.00	19.93
	ATOM	3137	CD2	TYR	413	35.300	-1.819	75.363	1.00	14.63
	ATOM	3138	CE2	TYR	413	36.690	-1.770	75.294	1.00	17.31
10	ATOM	3139	CZ	TYR	413	37.364	-2.616	74.439	1.00	19.92
	ATOM	3140	OH	TYR	413	38.737	-2.547	74.362	1.00	23.08
	ATOM	3141	C	TYR	413	33.151	-3.193	77.072	1.00	26.48
	ATOM	3142	O	TYR	413	34.085	-3.849	77.534	1.00	26.86
	ATOM	3143	N	LYS	414	32.690	-2.108	77.669	1.00	26.13
15	ATOM	3144	CA	LYS	414	33.309	-1.640	78.902	1.00	29.80
	ATOM	3145	CB	LYS	414	33.001	-0.147	79.117	1.00	29.42
	ATOM	3146	CG	LYS	414	33.882	0.802	78.302	1.00	32.94
	ATOM	3147	CD	LYS	414	33.558	2.275	78.559	1.00	34.12
	ATOM	3148	CE	LYS	414	34.553	3.179	77.833	1.00	36.09
20	ATOM	3149	NZ	LYS	414	34.170	4.626	77.859	1.00	35.28
	ATOM	3150	C	LYS	414	32.966	-2.400	80.181	1.00	29.74
	ATOM	3151	O	LYS	414	33.850	-2.677	80.988	1.00	28.77
	ATOM	3152	N	LEU	415	31.696	-2.749	80.357	1.00	30.99
	ATOM	3153	CA	LEU	415	31.255	-3.395	81.591	1.00	34.39
25	ATOM	3154	CB	LEU	415	29.942	-2.738	82.041	1.00	34.94
	ATOM	3155	CG	LEU	415	29.964	-1.195	82.012	1.00	38.17
	ATOM	3156	CD1	LEU	415	28.610	-0.647	82.469	1.00	38.59
	ATOM	3157	CD2	LEU	415	31.080	-0.660	82.901	1.00	34.42
	ATOM	3158	C	LEU	415	31.113	-4.923	81.657	1.00	34.46

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	ATOM	3159	O	LEU	415	31.202	-5.493	82.741	1.00	33.89
	ATOM	3160	N	HIS	416	30.886	-5.586	80.531	1.00	34.56
	ATOM	3161	CA	HIS	416	30.746	-7.041	80.561	1.00	36.94
	ATOM	3162	CB	HIS	416	30.394	-7.572	79.175	1.00	39.81
5	ATOM	3163	CG	HIS	416	29.811	-8.949	79.192	1.00	44.04
	ATOM	3164	CD2	HIS	416	28.536	-9.375	79.038	1.00	43.02
	ATOM	3165	ND1	HIS	416	30.573	-10.080	79.402	1.00	44.57
	ATOM	3166	CE1	HIS	416	29.791	-11.144	79.374	1.00	44.76
	ATOM	3167	NE2	HIS	416	28.550	-10.744	79.156	1.00	46.14
10	ATOM	3168	C	HIS	416	32.046	-7.673	81.060	1.00	35.57
	ATOM	3169	O	HIS	416	33.103	-7.483	80.471	1.00	37.06
	ATOM	3170	N	PRO	417	31.973	-8.445	82.153	1.00	33.55
	ATOM	3171	CD	PRO	417	30.727	-8.999	82.700	1.00	32.04
	ATOM	3172	CA	PRO	417	33.134	-9.109	82.757	1.00	33.47
15	ATOM	3173	CB	PRO	417	32.504	-10.219	83.614	1.00	31.67
	ATOM	3174	CG	PRO	417	31.142	-10.410	83.016	1.00	32.88
	ATOM	3175	C	PRO	417	34.252	-9.628	81.849	1.00	32.70
	ATOM	3176	O	PRO	417	35.428	-9.411	82.146	1.00	36.28
	ATOM	3177	N	SER	418	33.929	-10.302	80.752	1.00	29.70
20	ATOM	3178	CA	SER	418	35.015	-10.808	79.915	1.00	28.37
	ATOM	3179	CB	SER	418	35.215	-12.314	80.163	1.00	30.65
	ATOM	3180	OG	SER	418	35.798	-12.555	81.439	1.00	35.61
	ATOM	3181	C	SER	418	34.895	-10.560	78.418	1.00	25.27
	ATOM	3182	O	SER	418	35.730	-11.028	77.648	1.00	23.69
25	ATOM	3183	N	PHE	419	33.856	-9.846	78.004	1.00	21.86
	ATOM	3184	CA	PHE	419	33.673	-9.543	76.587	1.00	24.13
	ATOM	3185	CB	PHE	419	32.551	-8.522	76.407	1.00	22.03
	ATOM	3186	CG	PHE	419	32.270	-8.187	74.978	1.00	24.42
	ATOM	3187	CD1	PHE	419	31.273	-8.860	74.276	1.00	23.32

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	ATOM	3188	CD2	PHE	419	33.033	-7.231	74.312	1.00	22.16
	ATOM	3189	CE1	PHE	419	31.038	-8.593	72.932	1.00	23.49
	ATOM	3190	CE2	PHE	419	32.808	-6.961	72.967	1.00	25.91
	ATOM	3191	CZ	PHE	419	31.806	-7.645	72.275	1.00	24.70
5	ATOM	3192	C	PHE	419	34.961	-8.965	76.000	1.00	24.09
	ATOM	3193	O	PHE	419	35.491	-9.455	75.009	1.00	26.51
	ATOM	3194	N	LYS	420	35.432	-7.899	76.628	1.00	25.00
	ATOM	3195	CA	LYS	420	36.641	-7.179	76.238	1.00	26.79
	ATOM	3196	CB	LYS	420	36.984	-6.207	77.370	1.00	28.35
10	ATOM	3197	CG	LYS	420	38.241	-5.396	77.229	1.00	30.04
	ATOM	3198	CD	LYS	420	38.433	-4.537	78.497	1.00	33.98
	ATOM	3199	CE	LYS	420	37.170	-3.740	78.832	1.00	31.09
	ATOM	3200	NZ	LYS	420	37.322	-2.923	80.067	1.00	36.69
	ATOM	3201	C	LYS	420	37.819	-8.118	75.968	1.00	25.76
15	ATOM	3202	O	LYS	420	38.446	-8.064	74.911	1.00	25.94
	ATOM	3203	N	GLU	421	38.111	-8.961	76.951	1.00	24.13
	ATOM	3204	CA	GLU	421	39.195	-9.929	76.887	1.00	26.26
	ATOM	3205	CB	GLU	421	39.204	-10.781	78.155	1.00	32.38
	ATOM	3206	CG	GLU	421	39.547	-10.043	79.417	1.00	38.45
20	ATOM	3207	CD	GLU	421	38.700	-8.798	79.664	1.00	41.54
	ATOM	3208	OE1	GLU	421	37.458	-8.844	79.501	1.00	42.17
	ATOM	3209	OE2	GLU	421	39.300	-7.767	80.053	1.00	42.62
	ATOM	3210	C	GLU	421	39.075	-10.864	75.699	1.00	24.57
	ATOM	3211	O	GLU	421	40.017	-11.023	74.930	1.00	25.86
25	ATOM	3212	N	ARG	422	37.921	-11.509	75.576	1.00	24.00
	ATOM	3213	CA	ARG	422	37.682	-12.439	74.480	1.00	26.01
	ATOM	3214	CB	ARG	422	36.284	-13.063	74.610	1.00	27.36
	ATOM	3215	CG	ARG	422	36.076	-13.878	75.887	1.00	31.58
	ATOM	3216	CD	ARG	422	34.600	-14.053	76.188	1.00	35.39

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	ATOM	3217	NE	ARG	422	34.390	-14.834	77.397	1.00	40.58
	ATOM	3218	CZ	ARG	422	33.232	-14.911	78.046	1.00	44.53
	ATOM	3219	NH1	ARG	422	32.171	-14.243	77.596	1.00	41.79
	ATOM	3220	NH2	ARG	422	33.141	-15.651	79.150	1.00	41.67
5	ATOM	3221	C	ARG	422	37.794	-11.691	73.160	1.00	24.48
	ATOM	3222	O	ARG	422	38.439	-12.148	72.221	1.00	22.97
	ATOM	3223	N	PHE	423	37.153	-10.531	73.094	1.00	24.48
	ATOM	3224	CA	PHE	423	37.189	-9.737	71.879	1.00	22.97
	ATOM	3225	CB	PHE	423	36.403	-8.442	72.089	1.00	24.98
10	ATOM	3226	CG	PHE	423	36.494	-7.484	70.939	1.00	25.21
	ATOM	3227	CD1	PHE	423	37.468	-6.490	70.926	1.00	25.04
	ATOM	3228	CD2	PHE	423	35.618	-7.584	69.861	1.00	23.47
	ATOM	3229	CE1	PHE	423	37.568	-5.607	69.857	1.00	24.77
	ATOM	3230	CE2	PHE	423	35.710	-6.708	68.784	1.00	25.48
15	ATOM	3231	CZ	PHE	423	36.684	-5.715	68.780	1.00	24.31
	ATOM	3232	C	PHE	423	38.629	-9.442	71.456	1.00	21.03
	ATOM	3233	O	PHE	423	38.989	-9.680	70.308	1.00	19.38
	ATOM	3234	N	HIS	424	39.454	-8.952	72.381	1.00	20.46
	ATOM	3235	CA	HIS	424	40.846	-8.631	72.054	1.00	23.40
20	ATOM	3236	CB	HIS	424	41.602	-8.128	73.293	1.00	24.89
	ATOM	3237	CG	HIS	424	41.133	-6.803	73.808	1.00	25.28
	ATOM	3238	CD2	HIS	424	40.391	-5.828	73.230	1.00	24.67
	ATOM	3239	ND1	HIS	424	41.419	-6.361	75.083	1.00	25.18
	ATOM	3240	CE1	HIS	424	40.869	-5.174	75.269	1.00	22.64
25	ATOM	3241	NE2	HIS	424	40.239	-4.829	74.161	1.00	24.12
	ATOM	3242	C	HIS	424	41.604	-9.834	71.486	1.00	24.51
	ATOM	3243	O	HIS	424	42.239	-9.741	70.432	1.00	23.58
	ATOM	3244	N	ALA	425	41.540	-10.962	72.191	1.00	24.51
	ATOM	3245	CA	ALA	425	42.242	-12.164	71.746	1.00	26.94

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	ATOM	3246	CB	ALA	425	42.068	-13.306	72.774	1.00	27.10
	ATOM	3247	C	ALA	425	41.759	-12.605	70.370	1.00	25.71
	ATOM	3248	O	ALA	425	42.559	-12.937	69.505	1.00	27.02
	ATOM	3249	N	SER	426	40.453	-12.600	70.151	1.00	24.30
5	ATOM	3250	CA	SER	426	39.967	-13.003	68.850	1.00	23.93
	ATOM	3251	CB	SER	426	38.450	-13.142	68.863	1.00	20.85
	ATOM	3252	OG	SER	426	38.007	-13.582	67.596	1.00	21.86
	ATOM	3253	C	SER	426	40.394	-12.039	67.743	1.00	25.72
	ATOM	3254	O	SER	426	40.760	-12.483	66.660	1.00	25.40
10	ATOM	3255	N	VAL	427	40.363	-10.727	68.007	1.00	27.03
	ATOM	3256	CA	VAL	427	40.761	-9.750	66.983	1.00	27.43
	ATOM	3257	CB	VAL	427	40.591	-8.269	67.450	1.00	28.91
	ATOM	3258	CG1	VAL	427	40.999	-7.323	66.314	1.00	29.57
	ATOM	3259	CG2	VAL	427	39.150	-7.990	67.852	1.00	27.73
15	ATOM	3260	C	VAL	427	42.226	-9.919	66.601	1.00	28.67
	ATOM	3261	O	VAL	427	42.582	-9.858	65.424	1.00	27.30
	ATOM	3262	N	ARG	428	43.076	-10.119	67.603	1.00	28.43
	ATOM	3263	CA	ARG	428	44.498	-10.281	67.350	1.00	31.91
	ATOM	3264	CB	ARG	428	45.273	-10.231	68.670	1.00	31.80
20	ATOM	3265	CG	ARG	428	45.449	-8.793	69.130	1.00	31.90
	ATOM	3266	CD	ARG	428	45.662	-8.639	70.617	1.00	34.40
	ATOM	3267	NE	ARG	428	45.867	-7.231	70.971	1.00	34.78
	ATOM	3268	CZ	ARG	428	45.668	-6.728	72.186	1.00	38.69
	ATOM	3269	NH1	ARG	428	45.251	-7.516	73.172	1.00	38.56
25	ATOM	3270	NH2	ARG	428	45.901	-5.442	72.424	1.00	39.08
	ATOM	3271	C	ARG	428	44.797	-11.548	66.572	1.00	33.56
	ATOM	3272	O	ARG	428	45.694	-11.558	65.731	1.00	32.81
	ATOM	3273	N	ARG	429	44.037	-12.609	66.837	1.00	34.25
	ATOM	3274	CA	ARG	429	44.224	-13.859	66.115	1.00	33.42

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	ATOM	3275	CB	ARG	429	43.252	-14.941	66.601	1.00	36.36
	ATOM	3276	CG	ARG	429	43.756	-15.769	67.760	1.00	43.73
	ATOM	3277	CD	ARG	429	42.930	-17.038	67.939	1.00	47.67
	ATOM	3278	NE	ARG	429	41.561	-16.789	68.398	1.00	51.58
5	ATOM	3279	CZ	ARG	429	41.222	-16.467	69.646	1.00	51.70
	ATOM	3280	NH1	ARG	429	42.154	-16.345	70.585	1.00	50.85
	ATOM	3281	NH2	ARG	429	39.945	-16.288	69.962	1.00	49.95
	ATOM	3282	C	ARG	429	43.960	-13.618	64.639	1.00	32.81
	ATOM	3283	O	ARG	429	44.610	-14.215	63.783	1.00	32.29
10	ATOM	3284	N	LEU	430	43.001	-12.741	64.345	1.00	30.18
	ATOM	3285	CA	LEU	430	42.623	-12.455	62.965	1.00	29.19
	ATOM	3286	CB	LEU	430	41.132	-12.109	62.904	1.00	29.15
	ATOM	3287	CG	LEU	430	40.173	-13.164	63.453	1.00	31.83
	ATOM	3288	CD1	LEU	430	38.746	-12.629	63.437	1.00	28.32
15	ATOM	3289	CD2	LEU	430	40.281	-14.441	62.613	1.00	32.03
	ATOM	3290	C	LEU	430	43.407	-11.355	62.251	1.00	27.64
	ATOM	3291	O	LEU	430	43.244	-11.151	61.048	1.00	28.08
	ATOM	3292	N	THR	431	44.261	-10.645	62.966	1.00	28.04
	ATOM	3293	CA	THR	431	44.988	-9.567	62.326	1.00	31.15
20	ATOM	3294	CB	THR	431	44.569	-8.201	62.934	1.00	30.03
	ATOM	3295	OG1	THR	431	44.666	-8.254	64.363	1.00	31.84
	ATOM	3296	CG2	THR	431	43.137	-7.879	62.561	1.00	26.93
	ATOM	3297	C	THR	431	46.507	-9.719	62.367	1.00	34.65
	ATOM	3298	O	THR	431	47.190	-9.015	63.101	1.00	34.08
25	ATOM	3299	N	PRO	432	47.049	-10.655	61.566	1.00	37.36
	ATOM	3300	CD	PRO	432	46.296	-11.603	60.726	1.00	37.91
	ATOM	3301	CA	PRO	432	48.489	-10.923	61.484	1.00	38.59
	ATOM	3302	CB	PRO	432	48.572	-12.080	60.487	1.00	38.98
	ATOM	3303	CG	PRO	432	47.245	-12.758	60.630	1.00	40.10

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	ATOM	3304	C	PRO	432	49.224	-9.689	60.969	1.00	39.65
	ATOM	3305	O	PRO	432	48.712	-8.968	60.113	1.00	39.80
	ATOM	3306	N	SER	433	50.420	-9.461	61.495	1.00	39.94
	ATOM	3307	CA	SER	433	51.254	-8.326	61.112	1.00	42.47
5	ATOM	3308	CB	SER	433	51.467	-8.280	59.586	1.00	44.12
	ATOM	3309	OG	SER	433	50.363	-7.707	58.898	1.00	48.10
	ATOM	3310	C	SER	433	50.687	-6.996	61.598	1.00	42.26
	ATOM	3311	O	SER	433	51.085	-5.932	61.121	1.00	42.50
	ATOM	3312	N	CYS	434	49.756	-7.053	62.544	1.00	40.68
10	ATOM	3313	CA	CYS	434	49.184	-5.831	63.092	1.00	40.64
	ATOM	3314	CB	CYS	434	47.679	-5.735	62.826	1.00	39.36
	ATOM	3315	SG	CYS	434	47.196	-5.674	61.111	1.00	39.36
	ATOM	3316	C	CYS	434	49.398	-5.789	64.590	1.00	40.17
	ATOM	3317	O	CYS	434	49.258	-6.801	65.281	1.00	40.51
15	ATOM	3318	N	GLU	435	49.743	-4.609	65.081	1.00	38.91
	ATOM	3319	CA	GLU	435	49.945	-4.388	66.504	1.00	39.30
	ATOM	3320	CB	GLU	435	51.302	-3.733	66.738	1.00	42.29
	ATOM	3321	CG	GLU	435	51.779	-3.766	68.162	1.00	49.24
	ATOM	3322	CD	GLU	435	53.072	-2.993	68.340	1.00	53.77
20	ATOM	3323	OE1	GLU	435	54.106	-3.421	67.781	1.00	56.24
	ATOM	3324	OE2	GLU	435	53.047	-1.950	69.032	1.00	54.88
	ATOM	3325	C	GLU	435	48.801	-3.430	66.839	1.00	37.06
	ATOM	3326	O	GLU	435	48.866	-2.241	66.532	1.00	34.30
	ATOM	3327	N	ILE	436	47.749	-3.971	67.449	1.00	36.39
25	ATOM	3328	CA	ILE	436	46.552	-3.203	67.786	1.00	34.47
	ATOM	3329	CB	ILE	436	45.280	-4.040	67.508	1.00	34.15
	ATOM	3330	CG2	ILE	436	44.024	-3.166	67.639	1.00	33.64
	ATOM	3331	CG1	ILE	436	45.357	-4.633	66.100	1.00	36.06
	ATOM	3332	CD1	ILE	436	44.166	-5.487	65.719	1.00	36.35

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	ATOM	3333	C	ILE	436	46.492	-2.717	69.228	1.00	34.50
	ATOM	3334	O	ILE	436	46.612	-3.506	70.164	1.00	35.88
	ATOM	3335	N	THR	437	46.308	-1.411	69.405	1.00	32.66
	ATOM	3336	CA	THR	437	46.196	-0.837	70.741	1.00	30.32
5	ATOM	3337	CB	THR	437	47.134	0.370	70.930	1.00	29.83
	ATOM	3338	OG1	THR	437	48.496	-0.060	70.833	1.00	33.74
	ATOM	3339	CG2	THR	437	46.925	0.996	72.294	1.00	28.96
	ATOM	3340	C	THR	437	44.759	-0.377	70.949	1.00	29.92
	ATOM	3341	O	THR	437	44.177	0.293	70.090	1.00	28.24
10	ATOM	3342	N	PHE	438	44.179	-0.750	72.083	1.00	29.43
	ATOM	3343	CA	PHE	438	42.807	-0.359	72.390	1.00	29.35
	ATOM	3344	CB	PHE	438	41.991	-1.567	72.853	1.00	27.92
	ATOM	3345	CG	PHE	438	41.794	-2.614	71.789	1.00	27.95
	ATOM	3346	CD1	PHE	438	42.695	-3.661	71.648	1.00	27.90
15	ATOM	3347	CD2	PHE	438	40.703	-2.549	70.930	1.00	24.76
	ATOM	3348	CE1	PHE	438	42.505	-4.634	70.662	1.00	29.21
	ATOM	3349	CE2	PHE	438	40.506	-3.505	69.950	1.00	28.87
	ATOM	3350	CZ	PHE	438	41.408	-4.554	69.814	1.00	28.70
	ATOM	3351	C	PHE	438	42.772	0.712	73.467	1.00	30.41
20	ATOM	3352	O	PHE	438	43.469	0.601	74.474	1.00	30.53
	ATOM	3353	N	ILE	439	41.968	1.752	73.250	1.00	30.35
	ATOM	3354	CA	ILE	439	41.839	2.832	74.220	1.00	31.89
	ATOM	3355	CB	ILE	439	42.544	4.124	73.751	1.00	33.03
	ATOM	3356	CG2	ILE	439	42.233	5.269	74.721	1.00	36.00
25	ATOM	3357	CG1	ILE	439	44.053	3.916	73.704	1.00	33.82
	ATOM	3358	CD1	ILE	439	44.818	5.165	73.296	1.00	36.93
	ATOM	3359	C	ILE	439	40.373	3.158	74.420	1.00	32.85
	ATOM	3360	O	ILE	439	39.603	3.157	73.467	1.00	33.09
	ATOM	3361	N	GLU	440	39.991	3.442	75.659	1.00	35.09



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	ATOM	3362	CA	GLU	440	38.608	3.789	75.956	1.00	39.34
	ATOM	3363	CB	GLU	440	38.133	3.041	77.199	1.00	37.95
	ATOM	3364	CG	GLU	440	38.213	1.526	77.038	1.00	39.96
	ATOM	3365	CD	GLU	440	37.837	0.773	78.298	1.00	40.82
5	ATOM	3366	OE1	GLU	440	38.058	-0.456	78.340	1.00	41.23
	ATOM	3367	OE2	GLU	440	37.318	1.403	79.245	1.00	41.08
	ATOM	3368	C	GLU	440	38.495	5.298	76.156	1.00	41.28
	ATOM	3369	O	GLU	440	39.356	5.918	76.769	1.00	42.10
	ATOM	3370	N	SER	441	37.431	5.886	75.627	1.00	43.99
10	ATOM	3371	CA	SER	441	37.231	7.327	75.738	1.00	48.53
	ATOM	3372	CB	SER	441	36.390	7.823	74.550	1.00	47.96
	ATOM	3373	OG	SER	441	35.196	7.066	74.390	1.00	48.42
	ATOM	3374	C	SER	441	36.577	7.752	77.051	1.00	50.20
	ATOM	3375	O	SER	441	35.654	7.087	77.531	1.00	51.01
15	ATOM	3376	N	GLU	442	37.060	8.852	77.634	1.00	53.24
	ATOM	3377	CA	GLU	442	36.490	9.359	78.885	1.00	55.51
	ATOM	3378	CB	GLU	442	37.362	10.454	79.507	1.00	60.16
	ATOM	3379	CG	GLU	442	36.822	10.936	80.859	1.00	65.44
	ATOM	3380	CD	GLU	442	37.596	12.107	81.450	1.00	69.63
20	ATOM	3381	OE1	GLU	442	38.824	11.984	81.667	1.00	71.27
	ATOM	3382	OE2	GLU	442	36.965	13.155	81.709	1.00	72.91
	ATOM	3383	C	GLU	442	35.118	9.938	78.579	1.00	54.68
	ATOM	3384	O	GLU	442	34.104	9.495	79.126	1.00	56.30
	ATOM	3385	N	GLU	443	35.094	10.942	77.714	1.00	51.73
25	ATOM	3386	CA	GLU	443	33.840	11.555	77.307	1.00	51.12
	ATOM	3387	CB	GLU	443	33.706	12.960	77.888	1.00	51.77
	ATOM	3388	CG	GLU	443	32.561	13.086	78.869	1.00	49.05
	ATOM	3389	CD	GLU	443	31.202	12.812	78.239	1.00	48.41
	ATOM	3390	OE1	GLU	443	30.245	12.572	79.006	1.00	48.06

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	ATOM	3391	OE2	GLU	443	31.084	12.842	76.990	1.00	44.46
	ATOM	3392	C	GLU	443	33.851	11.614	75.793	1.00	50.48
	ATOM	3393	O	GLU	443	33.624	12.662	75.191	1.00	50.61
	ATOM	3394	N	GLY	444	34.131	10.458	75.199	1.00	49.69
5	ATOM	3395	CA	GLY	444	34.213	10.321	73.760	1.00	46.29
	ATOM	3396	C	GLY	444	33.300	11.190	72.928	1.00	45.39
	ATOM	3397	O	GLY	444	33.786	12.031	72.181	1.00	44.10
	ATOM	3398	N	SER	445	31.990	10.996	73.052	1.00	44.40
	ATOM	3399	CA	SER	445	31.035	11.765	72.263	1.00	45.82
10	ATOM	3400	CB	SER	445	29.614	11.258	72.505	1.00	43.70
	ATOM	3401	OG	SER	445	29.248	11.396	73.860	1.00	51.13
	ATOM	3402	C	SER	445	31.108	13.265	72.523	1.00	45.79
	ATOM	3403	O	SER	445	31.381	14.043	71.607	1.00	46.62
	ATOM	3404	N	GLY	446	30.867	13.666	73.766	1.00	45.46
15	ATOM	3405	CA	GLY	446	30.924	15.075	74.112	1.00	44.61
	ATOM	3406	C	GLY	446	32.176	15.778	73.615	1.00	44.65
	ATOM	3407	O	GLY	446	32.085	16.754	72.872	1.00	45.17
	ATOM	3408	N	ARG	447	33.344	15.286	74.024	1.00	44.10
	ATOM	3409	CA	ARG	447	34.615	15.878	73.615	1.00	44.23
20	ATOM	3410	CB	ARG	447	35.765	15.244	74.396	1.00	44.71
	ATOM	3411	CG	ARG	447	36.079	15.917	75.720	1.00	46.63
	ATOM	3412	CD	ARG	447	36.405	14.896	76.794	1.00	48.87
	ATOM	3413	NE	ARG	447	37.226	13.804	76.286	1.00	53.97
	ATOM	3414	CZ	ARG	447	38.507	13.915	75.956	1.00	55.65
25	ATOM	3415	NH1	ARG	447	39.130	15.076	76.085	1.00	56.71
	ATOM	3416	NH2	ARG	447	39.161	12.862	75.486	1.00	58.00
	ATOM	3417	C	ARG	447	34.891	15.739	72.122	1.00	45.53
	ATOM	3418	O	ARG	447	35.506	16.617	71.508	1.00	45.95
	ATOM	3419	N	GLY	448	34.444	14.630	71.543	1.00	45.12

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	ATOM	3420	CA	GLY	448	34.667	14.395	70.129	1.00	43.75
	ATOM	3421	C	GLY	448	33.915	15.390	69.275	1.00	44.42
	ATOM	3422	O	GLY	448	34.497	16.033	68.401	1.00	43.25
	ATOM	3423	N	ALA	449	32.617	15.508	69.530	1.00	44.33
5	ATOM	3424	CA	ALA	449	31.764	16.435	68.798	1.00	46.02
	ATOM	3425	CB	ALA	449	30.349	16.393	69.362	1.00	44.02
	ATOM	3426	C	ALA	449	32.334	17.852	68.901	1.00	47.27
	ATOM	3427	O	ALA	449	32.388	18.585	67.910	1.00	46.99
	ATOM	3428	N	ALA	450	32.771	18.226	70.100	1.00	47.32
10	ATOM	3429	CA	ALA	450	33.337	19.549	70.320	1.00	48.93
	ATOM	3430	CB	ALA	450	33.590	19.771	71.803	1.00	48.70
	ATOM	3431	C	ALA	450	34.630	19.752	69.537	1.00	49.10
	ATOM	3432	O	ALA	450	34.795	20.770	68.864	1.00	51.55
	ATOM	3433	N	LEU	451	35.546	18.792	69.625	1.00	47.13
15	ATOM	3434	CA	LEU	451	36.828	18.889	68.923	1.00	46.08
	ATOM	3435	CB	LEU	451	37.693	17.661	69.226	1.00	43.72
	ATOM	3436	CG	LEU	451	38.376	17.636	70.598	1.00	44.07
	ATOM	3437	CD1	LEU	451	38.798	16.218	70.955	1.00	41.74
	ATOM	3438	CD2	LEU	451	39.577	18.574	70.574	1.00	40.23
20	ATOM	3439	C	LEU	451	36.672	19.055	67.410	1.00	45.46
	ATOM	3440	O	LEU	451	37.495	19.708	66.760	1.00	46.36
	ATOM	3441	N	VAL	452	35.618	18.465	66.857	1.00	43.95
	ATOM	3442	CA	VAL	452	35.348	18.552	65.428	1.00	44.38
	ATOM	3443	CB	VAL	452	34.426	17.376	64.959	1.00	43.85
25	ATOM	3444	CG1	VAL	452	33.998	17.576	63.513	1.00	41.59
	ATOM	3445	CG2	VAL	452	35.169	16.040	65.087	1.00	40.86
	ATOM	3446	C	VAL	452	34.687	19.905	65.125	1.00	45.31
	ATOM	3447	O	VAL	452	34.881	20.482	64.056	1.00	42.97
	ATOM	3448	N	SER	453	33.912	20.411	66.077	1.00	46.60

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	ATOM	3449	CA	SER	453	33.253	21.693	65.900	1.00	49.07
	ATOM	3450	CB	SER	453	32.204	21.902	66.986	1.00	47.21
	ATOM	3451	OG	SER	453	31.146	20.972	66.845	1.00	44.37
	ATOM	3452	C	SER	453	34.293	22.806	65.951	1.00	51.53
5	ATOM	3453	O	SER	453	34.150	23.820	65.281	1.00	52.56
	ATOM	3454	N	ALA	454	35.352	22.593	66.728	1.00	54.40
	ATOM	3455	CA	ALA	454	36.430	23.567	66.881	1.00	56.39
	ATOM	3456	CB	ALA	454	37.336	23.158	68.031	1.00	55.74
	ATOM	3457	C	ALA	454	37.259	23.751	65.614	1.00	58.75
10	ATOM	3458	O	ALA	454	37.863	24.807	65.408	1.00	59.45
	ATOM	3459	N	VAL	455	37.310	22.719	64.779	1.00	60.29
	ATOM	3460	CA	VAL	455	38.063	22.796	63.535	1.00	61.78
	ATOM	3461	CB	VAL	455	38.603	21.416	63.112	1.00	61.44
	ATOM	3462	CG1	VAL	455	39.090	21.464	61.672	1.00	60.81
15	ATOM	3463	CG2	VAL	455	39.737	21.005	64.031	1.00	60.68
	ATOM	3464	C	VAL	455	37.152	23.330	62.442	1.00	63.56
	ATOM	3465	O	VAL	455	37.550	24.176	61.643	1.00	63.25
	ATOM	3466	N	ALA	456	35.921	22.835	62.416	1.00	65.38
	ATOM	3467	CA	ALA	456	34.959	23.275	61.422	1.00	69.39
20	ATOM	3468	CB	ALA	456	33.751	22.354	61.423	1.00	68.17
	ATOM	3469	C	ALA	456	34.522	24.709	61.710	1.00	73.10
	ATOM	3470	O	ALA	456	33.975	25.382	60.837	1.00	73.04
	ATOM	3471	N	CYS	457	34.771	25.170	62.935	1.00	77.06
	ATOM	3472	CA	CYS	457	34.390	26.521	63.341	1.00	81.01
25	ATOM	3473	CB	CYS	457	34.192	26.599	64.856	1.00	80.51
	ATOM	3474	SG	CYS	457	33.478	28.151	65.432	1.00	81.75
	ATOM	3475	C	CYS	457	35.420	27.554	62.916	1.00	83.65
	ATOM	3476	O	CYS	457	35.312	28.726	63.275	1.00	85.11
	ATOM	3477	N	LYS	458	36.430	27.118	62.172	1.00	86.29

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	ATOM	3478	CA	LYS	458	37.441	28.041	61.683	1.00	89.14
	ATOM	3479	CB	LYS	458	38.843	27.441	61.803	1.00	88.60
	ATOM	3480	CG	LYS	458	39.932	28.486	61.632	1.00	89.51
	ATOM	3481	CD	LYS	458	41.276	27.992	62.130	1.00	89.70
5	ATOM	3482	CE	LYS	458	42.257	29.146	62.269	1.00	89.22
	ATOM	3483	NZ	LYS	458	41.718	30.194	63.180	1.00	88.81
	ATOM	3484	C	LYS	458	37.096	28.310	60.232	1.00	91.26
	ATOM	3485	O	LYS	458	37.936	28.733	59.438	1.00	91.56
	ATOM	3486	N	LYS	459	35.834	28.043	59.901	1.00	93.94
10	ATOM	3487	CA	LYS	459	35.302	28.240	58.548	1.00	96.28
	ATOM	3488	CB	LYS	459	35.323	26.923	57.765	1.00	96.25
	ATOM	3489	CG	LYS	459	36.719	26.409	57.421	1.00	96.30
	ATOM	3490	CD	LYS	459	37.458	27.348	56.475	1.00	96.73
	ATOM	3491	CE	LYS	459	38.833	26.801	56.111	1.00	97.12
15	ATOM	3492	NZ	LYS	459	39.577	27.717	55.197	1.00	97.75
	ATOM	3493	C	LYS	459	33.863	28.759	58.624	1.00	97.78
	ATOM	3494	O	LYS	459	33.417	29.516	57.758	1.00	98.11
	ATOM	3495	N	ALA	460	33.153	28.327	59.666	1.00	99.29
	ATOM	3496	CA	ALA	460	31.778	28.738	59.916	1.00	100.54
20	ATOM	3497	CB	ALA	460	31.028	27.644	60.681	1.00	100.58
	ATOM	3498	C	ALA	460	31.765	30.042	60.719	1.00	101.56
	ATOM	3499	O	ALA	460	30.755	30.750	60.777	1.00	101.79
	ATOM	3500	N	CYS	461	32.899	30.360	61.338	1.00	102.59
	ATOM	3501	CA	CYS	461	33.033	31.572	62.156	1.00	103.00
25	ATOM	3502	CB	CYS	461	33.145	31.169	63.624	1.00	103.05
	ATOM	3503	SG	CYS	461	33.354	32.536	64.774	1.00	103.32
	ATOM	3504	C	CYS	461	34.265	32.367	61.753	1.00	103.21
	ATOM	3505	O	CYS	461	34.788	33.098	62.620	1.00	103.54
	ATOM	3506	OXT	CYS	461	34.665	32.248	60.578	1.00	103.24

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	TER 3507	CYS	461							
	ATOM	3508	C1	GLC	500	23.469	1.767	65.521	1.00	30.82
	ATOM	3509	C2	GLC	500	23.418	3.122	64.706	1.00	29.40
	ATOM	3510	C3	GLC	500	24.837	3.619	64.445	1.00	29.78
5	ATOM	3511	C4	GLC	500	25.496	3.860	65.778	1.00	28.77
	ATOM	3512	C5	GLC	500	25.529	2.514	66.593	1.00	27.72
	ATOM	3513	C6	GLC	500	26.162	2.717	67.936	1.00	26.98
	ATOM	3514	01	GLC	500	24.127	0.765	64.857	1.00	36.62
	ATOM	3515	02	GLC	500	22.756	2.872	63.483	1.00	32.75
10	ATOM	3516	03	GLC	500	24.786	4.837	63.698	1.00	29.31
	ATOM	3517	04	GLC	500	26.853	4.253	65.639	1.00	29.10
	ATOM	3518	05	GLC	500	24.152	2.040	66.770	1.00	29.59
	ATOM	3519	06	GLC	500	25.517	3.687	68.814	1.00	30.98
	TER 3520	GLC	500							
15	ATOM	3521	S1	CP1	501	36.312	19.051	60.824	1.00	50.83
	ATOM	3522	C2	CP1	501	35.720	19.405	59.240	1.00	49.96
	ATOM	3523	C3	CP1	501	36.398	18.662	58.318	1.00	49.96
	ATOM	3524	N4	CP1	501	37.363	17.829	58.827	1.00	49.99
	ATOM	3525	C5	CP1	501	37.429	17.932	60.162	1.00	49.39
20	ATOM	3526	N6	CP1	501	38.317	17.183	60.878	1.00	48.07
	ATOM	3527	C7	CP1	501	38.575	17.220	62.294	1.00	46.71
	ATOM	3528	08	CP1	501	37.968	18.001	63.039	1.00	47.48
	ATOM	3529	C9	CP1	501	40.386	16.405	64.107	1.00	46.71
	ATOM	3530	C10	CP1	501	39.620	16.253	62.884	1.00	47.34
25	ATOM	3531	C11	CP1	501	39.831	15.053	62.110	1.00	46.39
	ATOM	3532	C12	CP1	501	40.749	14.066	62.520	1.00	46.34
	ATOM	3533	C13	CP1	501	41.496	14.237	63.722	1.00	47.57
	ATOM	3534	F	CP1	501	42.392	13.310	64.155	1.00	48.24
	ATOM	3535	C15	CP1	501	41.306	15.404	64.502	1.00	46.98

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	ATOM	3536	S16	CP1	501	40.907	12.638	61.485	1.00	44.61
	ATOM	3537	N17	CP1	501	42.782	10.864	62.327	1.00	40.11
	ATOM	3538	C18	CP1	501	42.525	11.942	61.488	1.00	41.49
	ATOM	3539	N19	CP1	501	43.528	12.436	60.686	1.00	42.95
5	ATOM	3540	C20	CP1	501	44.549	11.571	61.054	1.00	43.00
	ATOM	3541	C21	CP1	501	44.116	10.651	62.014	1.00	39.24
	ATOM	3542	C22	CP1	501	41.894	10.152	63.276	1.00	32.83
	ATOM	3543	N23	CP1	501	40.279	17.465	64.913	1.00	46.10
	TER	3544	CP1	501		JJJJ				
10	ATOM	3545	NA+1	NA1	600	36.903	10.609	46.484	1.00	48.71
	ATOM	3546	O	HOH	601	20.332	-23.624	70.208	1.00	45.57
	ATOM	3547	O	HOH	602	18.766	-22.456	65.630	1.00	41.87
	ATOM	3548	O	HOH	603	13.471	-20.599	70.297	1.00	45.83
	ATOM	3549	O	HOH	604	11.104	-30.408	72.307	1.00	48.61
15	ATOM	3550	O	HOH	605	6.606	-26.352	79.319	1.00	59.47
	ATOM	3551	O	HOH	606	15.315	-28.400	85.522	1.00	48.85
	ATOM	3552	O	HOH	607	18.765	-29.705	82.807	1.00	55.60
	ATOM	3553	O	HOH	608	27.649	-22.465	84.914	1.00	39.29
	ATOM	3554	O	HOH	609	28.890	-18.936	88.942	1.00	38.24
20	ATOM	3555	O	HOH	610	31.397	-19.437	88.300	1.00	44.33
	ATOM	3556	O	HOH	611	33.495	-12.487	88.943	1.00	40.63
	ATOM	3557	O	HOH	612	28.110	-14.193	93.119	1.00	37.41
	ATOM	3558	O	HOH	613	22.501	-9.921	93.883	1.00	55.62
	ATOM	3559	O	HOH	614	18.084	-9.259	91.966	1.00	48.69
25	ATOM	3560	O	HOH	615	19.985	-7.585	89.518	1.00	54.30
	ATOM	3561	O	HOH	616	18.162	-4.982	77.583	1.00	42.44
	ATOM	3562	O	HOH	617	15.728	-5.792	77.752	1.00	49.61
	ATOM	3563	O	HOH	618	17.869	-7.338	75.263	1.00	52.43
	ATOM	3564	O	HOH	619	14.631	-9.827	77.339	1.00	27.38

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	ATOM	3565	0	HOH	620	14.305	-5.926	69.446	1.00	38.14
	ATOM	3566	0	HOH	621	13.616	-3.087	68.452	1.00	51.29
	ATOM	3567	0	HOH	622	15.537	-2.602	66.865	1.00	35.42
	ATOM	3568	0	HOH	623	18.821	-1.831	65.405	1.00	31.67
5	ATOM	3569	0	HOH	624	17.261	0.174	60.996	1.00	34.87
	ATOM	3570	0	HOH	625	18.895	-0.653	58.995	1.00	41.82
	ATOM	3571	0	HOH	626	20.053	-2.478	55.373	1.00	35.91
	ATOM	3572	0	HOH	627	22.217	-1.019	55.062	1.00	36.64
	ATOM	3573	0	HOH	628	25.137	-0.153	56.470	1.00	24.69
10	ATOM	3574	0	HOH	629	22.562	1.498	59.774	1.00	31.68
	ATOM	3575	0	HOH	630	24.912	0.122	62.135	1.00	25.12
	ATOM	3576	0	HOH	631	25.071	2.179	71.129	1.00	26.49
	ATOM	3577	0	HOH	632	27.157	5.888	71.903	1.00	41.05
	ATOM	3578	0	HOH	633	29.481	7.227	73.290	1.00	47.52
15	ATOM	3579	0	HOH	634	31.223	8.383	71.417	1.00	44.33
	ATOM	3580	0	HOH	635	32.517	7.788	77.983	1.00	44.30
	ATOM	3581	0	HOH	636	35.945	15.748	80.298	1.00	32.85
	ATOM	3582	0	HOH	637	41.395	13.522	74.250	1.00	52.40
	ATOM	3583	0	HOH	638	41.454	16.603	73.492	1.00	35.38
20	ATOM	3584	0	HOH	639	44.238	18.657	64.621	1.00	57.41
	ATOM	3585	0	HOH	640	48.524	12.679	62.857	1.00	55.80
	ATOM	3586	0	HOH	641	50.088	10.035	69.707	1.00	37.86
	ATOM	3587	0	HOH	642	47.834	4.897	73.654	1.00	43.91
	ATOM	3588	0	HOH	643	47.658	2.456	75.515	1.00	46.89
25	ATOM	3589	0	HOH	644	45.862	0.872	75.793	1.00	36.22
	ATOM	3590	0	HOH	645	42.167	-0.401	77.407	1.00	46.09
	ATOM	3591	0	HOH	646	39.939	-1.664	76.818	1.00	28.80
	ATOM	3592	0	HOH	647	41.804	2.590	77.672	1.00	30.06
	ATOM	3593	0	HOH	648	35.946	-0.230	81.704	1.00	44.47



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	ATOM	3594	0	HOH	649	35.692	-3.832	84.533	1.00	48.68
	ATOM	3595	0	HOH	650	35.503	-5.648	82.602	1.00	39.36
	ATOM	3596	0	HOH	651	34.249	-6.282	78.743	1.00	28.80
	ATOM	3597	0	HOH	652	41.570	-6.014	79.114	1.00	41.31
5	ATOM	3598	0	HOH	653	42.725	-8.259	76.851	1.00	34.12
	ATOM	3599	0	HOH	654	42.400	-10.619	75.649	1.00	32.12
	ATOM	3600	0	HOH	655	44.745	-10.112	73.414	1.00	30.95
	ATOM	3601	0	HOH	656	44.977	-6.287	75.709	1.00	54.82
	ATOM	3602	0	HOH	657	49.536	-3.896	71.639	1.00	46.68
10	ATOM	3603	0	HOH	658	47.500	-6.424	68.659	1.00	37.00
	ATOM	3604	0	HOH	659	46.887	-8.289	65.948	1.00	35.73
	ATOM	3605	0	HOH	660	45.007	-14.004	70.403	1.00	31.53
	ATOM	3606	0	HOH	661	44.785	-16.666	70.958	1.00	39.67
	ATOM	3607	0	HOH	662	39.546	-15.899	74.666	1.00	38.86
15	ATOM	3608	0	HOH	663	38.539	-14.985	72.232	1.00	34.80
	ATOM	3609	0	HOH	664	38.252	-17.032	68.208	1.00	47.76
	ATOM	3610	0	HOH	665	39.836	-15.454	66.437	1.00	38.55
	ATOM	3611	0	HOH	666	36.975	-19.549	67.636	1.00	43.12
	ATOM	3612	0	HOH	667	37.200	-20.262	70.388	1.00	51.64
20	ATOM	3613	0	HOH	668	33.328	-20.695	70.543	1.00	49.91
	ATOM	3614	0	HOH	669	32.877	-18.716	69.209	1.00	30.69
	ATOM	3615	0	HOH	670	30.463	-18.228	69.770	1.00	29.35
	ATOM	3616	0	HOH	671	29.403	-18.862	72.028	1.00	29.94
	ATOM	3617	0	HOH	672	31.677	-19.876	75.929	1.00	57.83
25	ATOM	3618	0	HOH	673	32.105	-15.120	81.811	1.00	56.36
	ATOM	3619	0	HOH	674	25.408	-13.262	70.399	1.00	19.73
	ATOM	3620	0	HOH	675	20.199	-11.770	66.567	1.00	31.95
	ATOM	3621	0	HOH	676	20.589	-11.169	63.684	1.00	28.18
	ATOM	3622	0	HOH	677	18.416	-12.169	62.695	1.00	34.73

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	ATOM	3623	0	HOH	678	18.037	-12.657	56.097	1.00	62.31
	ATOM	3624	0	HOH	679	15.700	-10.616	55.942	1.00	49.61
	ATOM	3625	0	HOH	680	17.485	-8.240	55.372	1.00	37.91
	ATOM	3626	0	HOH	681	22.370	-12.555	56.733	1.00	27.53
5	ATOM	3627	0	HOH	682	21.048	-16.039	51.265	1.00	53.09
	ATOM	3628	0	HOH	683	25.649	-8.890	49.620	1.00	43.30
	ATOM	3629	0	HOH	684	25.472	-5.908	50.031	1.00	43.23
	ATOM	3630	0	HOH	685	27.841	-3.633	51.119	1.00	34.64
	ATOM	3631	0	HOH	686	23.209	1.359	50.792	1.00	44.06
10	ATOM	3632	0	HOH	687	26.198	3.711	50.151	1.00	38.65
	ATOM	3633	0	HOH	688	27.728	6.416	50.494	1.00	39.66
	ATOM	3634	0	HOH	689	30.171	5.238	50.152	1.00	36.90
	ATOM	3635	0	HOH	690	32.248	6.334	48.750	1.00	33.36
	ATOM	3636	0	HOH	691	36.665	2.495	46.196	1.00	32.68
15	ATOM	3637	0	HOH	692	37.821	0.573	47.634	1.00	47.42
	ATOM	3638	0	HOH	693	42.794	0.201	52.097	1.00	44.65
	ATOM	3639	0	HOH	694	41.559	1.725	53.810	1.00	38.52
	ATOM	3640	0	HOH	695	43.105	3.662	55.242	1.00	34.89
	ATOM	3641	0	HOH	696	45.510	2.836	56.086	1.00	40.92
20	ATOM	3642	0	HOH	697	50.206	2.510	60.598	1.00	45.86
	ATOM	3643	0	HOH	698	52.258	1.308	61.720	1.00	45.43
	ATOM	3644	0	HOH	699	48.954	1.961	67.618	1.00	35.43
	ATOM	3645	0	HOH	700	49.694	-0.399	68.442	1.00	39.38
	ATOM	3646	0	HOH	701	40.015	-5.106	51.960	1.00	36.49
25	ATOM	3647	0	HOH	702	34.048	-12.903	50.839	1.00	37.87
	ATOM	3648	0	HOH	703	33.190	-14.541	52.882	1.00	51.09
	ATOM	3649	0	HOH	704	34.961	-16.254	52.067	1.00	35.42
	ATOM	3650	0	HOH	705	30.397	-15.105	52.902	1.00	39.69
	ATOM	3651	0	HOH	706	31.770	-20.985	57.467	1.00	48.16

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	ATOM	3652	0	HOH	707	37.192	-19.637	55.866	1.00	46.43
	ATOM	3653	0	HOH	708	38.187	-23.567	61.924	1.00	40.92
	ATOM	3654	0	HOH	709	38.470	-23.126	65.456	1.00	45.43
	ATOM	3655	0	HOH	710	30.533	-23.844	62.578	1.00	37.90
5	ATOM	3656	0	HOH	711	26.515	-21.678	62.544	1.00	39.08
	ATOM	3657	0	HOH	712	27.242	-20.400	65.671	1.00	33.60
	ATOM	3658	0	HOH	713	25.907	-18.116	65.171	1.00	24.64
	ATOM	3659	0	HOH	714	28.226	-26.567	74.622	1.00	44.93
	ATOM	3660	0	HOH	715	31.091	-28.151	73.632	1.00	39.43
10	ATOM	3661	0	HOH	716	28.020	-32.685	74.512	1.00	48.35
	ATOM	3662	0	HOH	717	28.401	-36.363	77.956	1.00	47.24
	ATOM	3663	0	HOH	718	26.796	-22.733	95.375	1.00	34.50
	ATOM	3664	0	HOH	719	23.506	-18.729	96.532	1.00	46.50
	ATOM	3665	0	HOH	720	7.193	-13.392	87.134	1.00	48.33
15	ATOM	3666	0	HOH	721	23.769	-2.393	77.130	1.00	39.79
	ATOM	3667	0	HOH	722	21.538	6.141	76.432	1.00	52.58
	ATOM	3668	0	HOH	723	26.038	13.552	80.579	1.00	47.60
	ATOM	3669	0	HOH	724	25.460	9.823	62.329	1.00	33.10
	ATOM	3670	0	HOH	725	27.321	10.443	60.403	1.00	39.23
20	ATOM	3671	0	HOH	726	26.658	8.602	58.871	1.00	32.16
	ATOM	3672	0	HOH	727	29.670	11.059	61.417	1.00	24.95
	ATOM	3673	0	HOH	728	30.585	13.937	60.932	1.00	41.90
	ATOM	3674	0	HOH	729	34.591	18.790	55.094	1.00	40.47
	ATOM	3675	0	HOH	730	34.117	19.353	52.182	1.00	54.62
25	ATOM	3676	0	HOH	731	31.428	16.535	48.224	1.00	37.06
	ATOM	3677	0	HOH	732	31.432	15.488	46.047	1.00	33.85
	ATOM	3678	0	HOH	733	27.660	11.291	51.289	1.00	40.74
	ATOM	3679	0	HOH	734	27.629	10.029	53.857	1.00	30.56
	ATOM	3680	0	HOH	735	22.996	7.311	45.724	1.00	57.65

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	ATOM	3681	0	HOH	736	25.532	2.038	43.263	1.00	34.43
	ATOM	3682	0	HOH	737	33.508	3.221	40.211	1.00	45.05
	ATOM	3683	0	HOH	738	35.525	1.426	41.242	1.00	44.71
	ATOM	3684	0	HOH	739	37.227	9.576	44.352	1.00	31.96
5	ATOM	3685	0	HOH	740	39.858	15.804	52.237	1.00	43.41
	ATOM	3686	0	HOH	741	42.053	15.415	53.940	1.00	47.39
	ATOM	3687	0	HOH	742	32.200	24.148	58.683	1.00	45.42
	ATOM	3688	0	HOH	743	28.016	21.804	51.201	1.00	44.12
	ATOM	3689	0	HOH	744	22.797	26.498	63.763	1.00	53.69
10	ATOM	3690	0	HOH	745	10.552	26.073	62.119	1.00	43.13
	ATOM	3691	0	HOH	746	11.190	7.673	68.338	1.00	57.06
	ATOM	3692	0	HOH	747	20.818	-3.881	51.225	1.00	56.55
	ATOM	3693	0	HOH	748	29.885	-6.633	43.981	1.00	46.17
	ATOM	3694	0	HOH	749	40.811	30.945	68.309	1.00	45.88
15	TER	3695		HOH						

なお、表 1 は、当業者によって慣用されているプロテイン・データ・バンク  
 の表記方法に準拠して作成されている。表 1 中、GLC はグルコース分子を表  
 し、CP1 は式 I I I a で表される化合物を表し、HOH は水分子を表す。

また、本発明においては、配列番号 8 に示す GK タンパク質の結晶を調製す  
 ることに成功している（後述の実施例参照）。そしてこのようにして得られた  
 GK タンパク質の結晶は、格子定数が、下記式（5）～（8）：

25  $a=b=103.2\pm5$  オングストローム … (5)

$c=281.0\pm7$  オングストローム … (6)

$\alpha=\beta=90^\circ$  … (7)

$\gamma=120^\circ$  … (8)

を満たすものであった。また、この結晶は、空間群が  $P6_322$  であることが

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解明された。ここで、前記  $a=b$  は  $103.2 \pm 3$  オングストロームであることが好ましく、 $103.2 \pm 2$  オングストロームであることがより好ましく、 $103.2 \pm 1$  オングストロームであることがさらに好ましい。また、前記  $c$  は  $281.0 \pm 6$  オングストロームであることが好ましく、 $281.0 \pm 4$  オングストロームであることがより好ましく、 $281.0 \pm 2$  オングストロームであることがさらに好ましい。

5 このようにして得られたGKタンパク質結晶の3次元構造座標を表2に示す。

表2

	ATOM	1	CB	MET	15	54.150	5.972	67.103	1.00	55.10
10	ATOM	2	CG	MET	15	55.594	5.943	67.591	1.00	55.46
	ATOM	3	SD	MET	15	56.013	4.505	68.603	1.00	52.92
	ATOM	4	CE	MET	15	56.517	5.326	70.108	1.00	51.73
	ATOM	5	C	MET	15	52.357	4.955	65.669	1.00	56.87
	ATOM	6	O	MET	15	52.057	4.609	64.524	1.00	57.60
15	ATOM	7	N	MET	15	54.770	4.766	65.028	1.00	55.00
	ATOM	8	CA	MET	15	53.800	4.813	66.167	1.00	56.04
	ATOM	9	N	VAL	16	51.468	5.456	66.525	1.00	55.58
	ATOM	10	CA	VAL	16	50.065	5.625	66.154	1.00	52.87
	ATOM	11	CB	VAL	16	49.141	4.862	67.129	1.00	49.32
20	ATOM	12	CG1	VAL	16	47.696	5.016	66.716	1.00	48.26
	ATOM	13	CG2	VAL	16	49.508	3.394	67.126	1.00	47.28
	ATOM	14	C	VAL	16	49.666	7.097	66.085	1.00	53.26
	ATOM	15	O	VAL	16	49.218	7.563	65.040	1.00	52.32
	ATOM	16	N	GLU	17	49.845	7.828	67.182	1.00	56.12
25	ATOM	17	CA	GLU	17	49.511	9.253	67.210	1.00	59.41
	ATOM	18	CB	GLU	17	50.102	9.921	68.456	1.00	63.35
	ATOM	19	CG	GLU	17	49.063	10.373	69.484	1.00	68.69
	ATOM	20	CD	GLU	17	48.174	11.525	69.004	1.00	72.00
	ATOM	21	OE1	GLU	17	47.314	11.964	69.805	1.00	74.22

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	ATOM	22	OE2	GLU	17	48.328	11.992	67.847	1.00	72.36
	ATOM	23	C	GLU	17	50.035	9.963	65.967	1.00	59.05
	ATOM	24	O	GLU	17	49.521	11.011	65.566	1.00	57.70
	ATOM	25	N	GLN	18	51.070	9.389	65.367	1.00	60.75
5	ATOM	26	CA	GLN	18	51.661	9.960	64.170	1.00	61.70
	ATOM	27	CB	GLN	18	53.038	9.329	63.895	1.00	66.55
	ATOM	28	CG	GLN	18	54.001	9.219	65.110	1.00	72.22
	ATOM	29	CD	GLN	18	54.509	10.566	65.654	1.00	75.87
	ATOM	30	OE1	GLN	18	55.317	10.605	66.595	1.00	75.55
10	ATOM	31	NE2	GLN	18	54.037	11.669	65.067	1.00	77.63
	ATOM	32	C	GLN	18	50.709	9.682	63.004	1.00	59.33
	ATOM	33	O	GLN	18	50.322	10.601	62.287	1.00	59.09
	ATOM	34	N	ILE	19	50.321	8.418	62.832	1.00	55.64
	ATOM	35	CA	ILE	19	49.416	8.029	61.747	1.00	53.41
15	ATOM	36	CB	ILE	19	49.113	6.529	61.778	1.00	52.34
	ATOM	37	CG2	ILE	19	47.964	6.211	60.832	1.00	50.69
	ATOM	38	CG1	ILE	19	50.374	5.754	61.389	1.00	52.73
	ATOM	39	CD1	ILE	19	50.186	4.256	61.274	1.00	53.73
	ATOM	40	C	ILE	19	48.088	8.774	61.741	1.00	53.03
20	ATOM	41	O	ILE	19	47.791	9.528	60.812	1.00	52.86
	ATOM	42	N	LEU	20	47.279	8.548	62.766	1.00	52.38
	ATOM	43	CA	LEU	20	45.997	9.228	62.861	1.00	51.95
	ATOM	44	CB	LEU	20	45.336	8.937	64.195	1.00	50.70
	ATOM	45	CG	LEU	20	44.563	7.632	64.212	1.00	51.65
25	ATOM	46	CD1	LEU	20	45.450	6.454	63.803	1.00	51.77
	ATOM	47	CD2	LEU	20	44.010	7.463	65.599	1.00	51.02
	ATOM	48	C	LEU	20	46.158	10.723	62.727	1.00	52.33
	ATOM	49	O	LEU	20	45.204	11.427	62.401	1.00	54.11
	ATOM	50	N	ALA	21	47.366	11.207	62.990	1.00	51.49

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	ATOM	51	CA	ALA 21	47.643	12.628	62.907	1.00	49.87
	ATOM	52	CB	ALA 21	49.066	12.899	63.342	1.00	50.58
	ATOM	53	C	ALA 21	47.414	13.133	61.491	1.00	48.63
	ATOM	54	O	ALA 21	47.090	14.301	61.286	1.00	47.74
5	ATOM	55	N	GLU 22	47.571	12.243	60.517	1.00	47.60
	ATOM	56	CA	GLU 22	47.383	12.605	59.121	1.00	48.69
	ATOM	57	CB	GLU 22	47.818	11.457	58.215	1.00	51.49
	ATOM	58	CG	GLU 22	49.282	11.520	57.838	1.00	59.47
	ATOM	59	CD	GLU 22	49.738	10.335	57.003	1.00	64.78
10	ATOM	60	OE1	GLU 22	50.896	10.369	56.519	1.00	66.47
	ATOM	61	OE2	GLU 22	48.948	9.373	56.839	1.00	68.05
	ATOM	62	C	GLU 22	45.954	12.999	58.794	1.00	48.26
	ATOM	63	O	GLU 22	45.683	13.538	57.721	1.00	48.86
	ATOM	64	N	PHE 23	45.036	12.733	59.715	1.00	47.14
15	ATOM	65	CA	PHE 23	43.641	13.076	59.490	1.00	45.51
	ATOM	66	CB	PHE 23	42.722	12.045	60.147	1.00	41.36
	ATOM	67	CG	PHE 23	42.544	10.783	59.347	1.00	37.96
	ATOM	68	CD1	PHE 23	43.208	9.613	59.697	1.00	35.23
	ATOM	69	CD2	PHE 23	41.687	10.758	58.255	1.00	37.67
20	ATOM	70	CE1	PHE 23	43.016	8.435	58.968	1.00	32.67
	ATOM	71	CE2	PHE 23	41.492	9.583	57.523	1.00	37.15
	ATOM	72	CZ	PHE 23	42.158	8.423	57.883	1.00	33.48
	ATOM	73	C	PHE 23	43.310	14.468	60.013	1.00	47.24
	ATOM	74	O	PHE 23	42.227	14.993	59.767	1.00	46.34
25	ATOM	75	N	GLN 24	44.245	15.068	60.735	1.00	50.44
	ATOM	76	CA	GLN 24	44.028	16.400	61.279	1.00	55.06
	ATOM	77	CB	GLN 24	45.306	16.882	61.979	1.00	59.10
	ATOM	78	CG	GLN 24	45.715	16.023	63.168	1.00	62.03
	ATOM	79	CD	GLN 24	44.686	16.075	64.277	1.00	65.56

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	ATOM	80	OE1	GLN	24	44.653	15.207	65.156	1.00	66.95
	ATOM	81	NE2	GLN	24	43.834	17.103	64.245	1.00	65.89
	ATOM	82	C	GLN	24	43.644	17.359	60.149	1.00	56.09
	ATOM	83	O	GLN	24	43.892	17.073	58.979	1.00	57.63
5	ATOM	84	N	LEU	25	43.016	18.476	60.504	1.00	55.99
	ATOM	85	CA	LEU	25	42.616	19.501	59.540	1.00	55.27
	ATOM	86	CB	LEU	25	41.303	19.128	58.841	1.00	54.71
	ATOM	87	CG	LEU	25	41.325	17.896	57.922	1.00	53.30
	ATOM	88	CD1	LEU	25	39.928	17.618	57.419	1.00	53.18
10	ATOM	89	CD2	LEU	25	42.264	18.113	56.755	1.00	51.55
	ATOM	90	C	LEU	25	42.444	20.786	60.336	1.00	56.31
	ATOM	91	O	LEU	25	41.377	21.061	60.889	1.00	55.85
	ATOM	92	N	GLN	26	43.519	21.563	60.399	1.00	58.22
	ATOM	93	CA	GLN	26	43.527	22.807	61.153	1.00	58.31
15	ATOM	94	CB	GLN	26	44.980	23.280	61.361	1.00	63.03
	ATOM	95	CG	GLN	26	45.118	24.480	62.313	1.00	69.87
	ATOM	96	CD	GLN	26	46.490	25.161	62.245	1.00	73.70
	ATOM	97	OE1	GLN	26	47.009	25.446	61.158	1.00	74.68
	ATOM	98	NE2	GLN	26	47.067	25.446	63.411	1.00	74.99
20	ATOM	99	C	GLN	26	42.702	23.903	60.485	1.00	55.29
	ATOM	100	O	GLN	26	42.358	23.811	59.308	1.00	51.30
	ATOM	101	N	GLU	27	42.389	24.931	61.267	1.00	55.08
	ATOM	102	CA	GLU	27	41.617	26.083	60.824	1.00	55.66
	ATOM	103	CB	GLU	27	41.940	27.280	61.709	1.00	57.13
25	ATOM	104	CG	GLU	27	41.029	28.469	61.523	1.00	59.64
	ATOM	105	CD	GLU	27	39.694	28.272	62.208	1.00	62.00
	ATOM	106	OE1	GLU	27	39.685	27.840	63.382	1.00	62.44
	ATOM	107	OE2	GLU	27	38.653	28.559	61.581	1.00	64.27
	ATOM	108	C	GLU	27	41.905	26.454	59.380	1.00	55.70



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	ATOM	109	O	GLU 27	41.025	26.416	58.531	1.00	56.30
	ATOM	110	N	GLU 28	43.147	26.828	59.113	1.00	56.74
	ATOM	111	CA	GLU 28	43.571	27.208	57.770	1.00	58.34
	ATOM	112	CB	GLU 28	45.102	27.226	57.714	1.00	63.94
5	ATOM	113	CG	GLU 28	45.704	28.026	56.573	1.00	70.36
	ATOM	114	CD	GLU 28	45.615	29.524	56.806	1.00	74.74
	ATOM	115	OE1	GLU 28	46.245	30.289	56.040	1.00	77.18
	ATOM	116	OE2	GLU 28	44.912	29.938	57.755	1.00	77.44
	ATOM	117	C	GLU 28	43.032	26.231	56.721	1.00	56.56
10	ATOM	118	O	GLU 28	42.375	26.641	55.764	1.00	54.38
	ATOM	119	N	ASP 29	43.316	24.942	56.921	1.00	55.20
	ATOM	120	CA	ASP 29	42.893	23.869	56.015	1.00	53.13
	ATOM	121	CB	ASP 29	43.106	22.499	56.667	1.00	56.36
	ATOM	122	CG	ASP 29	44.570	22.116	56.758	1.00	59.69
15	ATOM	123	OD1	ASP 29	45.263	22.198	55.717	1.00	61.07
	ATOM	124	OD2	ASP 29	45.021	21.727	57.863	1.00	60.92
	ATOM	125	C	ASP 29	41.439	23.995	55.607	1.00	49.74
	ATOM	126	O	ASP 29	41.100	23.924	54.424	1.00	47.81
	ATOM	127	N	LEU 30	40.579	24.156	56.603	1.00	46.04
20	ATOM	128	CA	LEU 30	39.167	24.309	56.344	1.00	43.06
	ATOM	129	CB	LEU 30	38.393	24.491	57.649	1.00	39.08
	ATOM	130	CG	LEU 30	38.026	23.218	58.404	1.00	36.61
	ATOM	131	CD1	LEU 30	39.280	22.441	58.756	1.00	37.28
	ATOM	132	CD2	LEU 30	37.233	23.576	59.642	1.00	35.29
25	ATOM	133	C	LEU 30	38.948	25.516	55.452	1.00	44.18
	ATOM	134	O	LEU 30	38.410	25.388	54.354	1.00	45.60
	ATOM	135	N	LYS 31	39.381	26.685	55.920	1.00	44.63
	ATOM	136	CA	LYS 31	39.206	27.927	55.170	1.00	43.67
	ATOM	137	CB	LYS 31	40.136	29.020	55.695	1.00	45.23

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	ATOM	138	CG	LYS	31	39.968	29.361	57.165	1.00	46.98
	ATOM	139	CD	LYS	31	38.743	30.221	57.440	1.00	45.54
	ATOM	140	CE	LYS	31	38.695	30.675	58.915	1.00	45.82
	ATOM	141	NZ	LYS	31	39.836	31.545	59.387	1.00	42.73
5	ATOM	142	C	LYS	31	39.483	27.725	53.697	1.00	42.23
	ATOM	143	O	LYS	31	38.759	28.241	52.855	1.00	41.29
	ATOM	144	N	LYS	32	40.535	26.976	53.385	1.00	41.79
	ATOM	145	CA	LYS	32	40.877	26.737	51.994	1.00	43.47
	ATOM	146	CB	LYS	32	42.171	25.928	51.888	1.00	45.16
10	ATOM	147	CG	LYS	32	42.811	25.974	50.499	1.00	50.49
	ATOM	148	CD	LYS	32	44.302	25.565	50.510	1.00	54.48
	ATOM	149	CE	LYS	32	44.505	24.086	50.900	1.00	57.45
	ATOM	150	NZ	LYS	32	45.934	23.610	51.002	1.00	56.65
	ATOM	151	C	LYS	32	39.740	25.995	51.308	1.00	43.99
15	ATOM	152	O	LYS	32	39.260	26.407	50.246	1.00	43.34
	ATOM	153	N	VAL	33	39.306	24.901	51.925	1.00	43.47
	ATOM	154	CA	VAL	33	38.218	24.100	51.382	1.00	40.87
	ATOM	155	CB	VAL	33	37.895	22.927	52.310	1.00	40.53
	ATOM	156	CG1	VAL	33	36.977	21.939	51.604	1.00	40.20
20	ATOM	157	CG2	VAL	33	39.183	22.248	52.729	1.00	40.29
	ATOM	158	C	VAL	33	36.994	24.981	51.226	1.00	39.39
	ATOM	159	O	VAL	33	36.370	25.011	50.165	1.00	37.22
	ATOM	160	N	MET	34	36.675	25.707	52.290	1.00	39.46
	ATOM	161	CA	MET	34	35.539	26.609	52.288	1.00	42.17
25	ATOM	162	CB	MET	34	35.515	27.460	53.555	1.00	43.81
	ATOM	163	CG	MET	34	34.259	28.305	53.656	1.00	48.81
	ATOM	164	SD	MET	34	34.302	29.606	54.908	1.00	56.60
	ATOM	165	CE	MET	34	34.576	31.074	53.859	1.00	55.54
	ATOM	166	C	MET	34	35.612	27.535	51.086	1.00	43.35

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	ATOM	167	O	MET 34	34.626	27.735	50.383	1.00	43.86
	ATOM	168	N	ARG 35	36.785	28.104	50.847	1.00	44.90
	ATOM	169	CA	ARG 35	36.938	29.015	49.729	1.00	45.60
	ATOM	170	CB	ARG 35	38.286	29.727	49.815	1.00	49.40
5	ATOM	171	CG	ARG 35	38.459	30.563	51.075	1.00	53.81
	ATOM	172	CD	ARG 35	38.231	32.052	50.851	1.00	57.78
	ATOM	173	NE	ARG 35	38.483	32.807	52.077	1.00	63.20
	ATOM	174	CZ	ARG 35	39.587	32.696	52.820	1.00	65.30
	ATOM	175	NH1	ARG 35	40.557	31.854	52.466	1.00	64.80
10	ATOM	176	NH2	ARG 35	39.720	33.425	53.925	1.00	66.89
	ATOM	177	C	ARG 35	36.814	28.262	48.418	1.00	44.08
	ATOM	178	O	ARG 35	35.977	28.605	47.586	1.00	43.75
	ATOM	179	N	ARG 36	37.633	27.227	48.245	1.00	43.43
	ATOM	180	CA	ARG 36	37.612	26.418	47.026	1.00	43.94
15	ATOM	181	CB	ARG 36	38.547	25.212	47.174	1.00	44.76
	ATOM	182	CG	ARG 36	40.020	25.580	47.244	1.00	44.66
	ATOM	183	CD	ARG 36	40.898	24.392	47.617	1.00	44.20
	ATOM	184	NE	ARG 36	41.728	23.919	46.512	1.00	44.66
	ATOM	185	CZ	ARG 36	42.890	23.292	46.678	1.00	45.10
20	ATOM	186	NH1	ARG 36	43.350	23.075	47.900	1.00	44.34
	ATOM	187	NH2	ARG 36	43.590	22.870	45.631	1.00	45.47
	ATOM	188	C	ARG 36	36.202	25.941	46.660	1.00	43.73
	ATOM	189	O	ARG 36	35.921	25.645	45.497	1.00	43.31
	ATOM	190	N	MET 37	35.324	25.851	47.656	1.00	42.87
25	ATOM	191	CA	MET 37	33.946	25.440	47.413	1.00	41.30
	ATOM	192	CB	MET 37	33.222	25.136	48.726	1.00	43.30
	ATOM	193	CG	MET 37	31.782	24.636	48.556	1.00	45.16
	ATOM	194	SD	MET 37	31.646	22.826	48.280	1.00	52.61
	ATOM	195	CE	MET 37	31.892	22.708	46.492	1.00	46.47

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	ATOM	196	C	MET 37	33.249	26.603	46.723	1.00	39.52
	ATOM	197	O	MET 37	32.702	26.458	45.635	1.00	39.06
	ATOM	198	N	GLN 38	33.275	27.767	47.359	1.00	37.22
	ATOM	199	CA	GLN 38	32.637	28.927	46.776	1.00	35.67
5	ATOM	200	CB	GLN 38	32.874	30.155	47.643	1.00	36.29
	ATOM	201	CG	GLN 38	32.128	30.122	48.950	1.00	37.44
	ATOM	202	CD	GLN 38	32.689	31.108	49.950	1.00	41.99
	ATOM	203	OE1	GLN 38	33.841	30.992	50.376	1.00	44.33
	ATOM	204	NE2	GLN 38	31.880	32.091	50.331	1.00	44.58
10	ATOM	205	C	GLN 38	33.184	29.155	45.382	1.00	35.21
	ATOM	206	O	GLN 38	32.454	29.557	44.486	1.00	34.82
	ATOM	207	N	LYS 39	34.467	28.884	45.188	1.00	36.41
	ATOM	208	CA	LYS 39	35.069	29.081	43.875	1.00	38.60
	ATOM	209	CB	LYS 39	36.560	28.708	43.888	1.00	42.47
15	ATOM	210	CG	LYS 39	37.395	29.263	42.714	1.00	45.02
	ATOM	211	CD	LYS 39	37.638	30.775	42.861	1.00	49.54
	ATOM	212	CE	LYS 39	38.523	31.365	41.752	1.00	51.65
	ATOM	213	NZ	LYS 39	38.621	32.865	41.821	1.00	53.58
	ATOM	214	C	LYS 39	34.339	28.196	42.884	1.00	38.31
20	ATOM	215	O	LYS 39	34.229	28.534	41.710	1.00	40.28
	ATOM	216	N	GLU 40	33.827	27.066	43.369	1.00	37.21
	ATOM	217	CA	GLU 40	33.117	26.107	42.525	1.00	34.69
	ATOM	218	CB	GLU 40	33.329	24.705	43.072	1.00	32.80
	ATOM	219	CG	GLU 40	34.742	24.245	42.900	1.00	33.53
25	ATOM	220	CD	GLU 40	35.164	24.348	41.459	1.00	36.48
	ATOM	221	OE1	GLU 40	34.318	24.044	40.589	1.00	39.36
	ATOM	222	OE2	GLU 40	36.326	24.720	41.187	1.00	37.18
	ATOM	223	C	GLU 40	31.632	26.387	42.375	1.00	34.48
	ATOM	224	O	GLU 40	31.040	26.110	41.332	1.00	32.30

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	ATOM	225	N	MET 41	31.030	26.928	43.425	1.00	35.61
	ATOM	226	CA	MET 41	29.621	27.256	43.373	1.00	39.30
	ATOM	227	CB	MET 41	29.155	27.852	44.692	1.00	39.16
	ATOM	228	CG	MET 41	29.146	26.910	45.867	1.00	40.71
5	ATOM	229	SD	MET 41	27.930	27.569	47.040	1.00	46.34
	ATOM	230	CE	MET 41	28.978	28.338	48.243	1.00	46.54
	ATOM	231	C	MET 41	29.336	28.258	42.251	1.00	42.24
	ATOM	232	O	MET 41	28.358	28.113	41.517	1.00	44.97
	ATOM	233	N	ASP 42	30.173	29.284	42.118	1.00	43.47
10	ATOM	234	CA	ASP 42	29.952	30.274	41.069	1.00	42.69
	ATOM	235	CB	ASP 42	30.848	31.497	41.249	1.00	44.70
	ATOM	236	CG	ASP 42	30.548	32.254	42.523	1.00	49.63
	ATOM	237	OD1	ASP 42	31.352	32.128	43.477	1.00	52.14
	ATOM	238	OD2	ASP 42	29.510	32.968	42.572	1.00	49.66
15	ATOM	239	C	ASP 42	30.248	29.641	39.739	1.00	41.40
	ATOM	240	O	ASP 42	29.550	29.880	38.759	1.00	41.06
	ATOM	241	N	ARG 43	31.289	28.826	39.707	1.00	39.70
	ATOM	242	CA	ARG 43	31.668	28.171	38.477	1.00	39.99
	ATOM	243	CB	ARG 43	32.835	27.227	38.739	1.00	43.98
20	ATOM	244	CG	ARG 43	33.329	26.482	37.516	1.00	49.72
	ATOM	245	CD	ARG 43	34.636	25.777	37.831	1.00	55.67
	ATOM	246	NE	ARG 43	34.962	24.746	36.854	1.00	62.98
	ATOM	247	CZ	ARG 43	36.062	24.002	36.899	1.00	67.95
	ATOM	248	NH1	ARG 43	36.950	24.178	37.877	1.00	69.41
25	ATOM	249	NH2	ARG 43	36.269	23.075	35.969	1.00	70.32
	ATOM	250	C	ARG 43	30.488	27.417	37.881	1.00	38.35
	ATOM	251	O	ARG 43	30.253	27.493	36.677	1.00	38.07
	ATOM	252	N	GLY 44	29.739	26.709	38.728	1.00	36.44
	ATOM	253	CA	GLY 44	28.592	25.938	38.262	1.00	32.80

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	ATOM	254	C	GLY 44	27.344	26.772	38.062	1.00	31.71
	ATOM	255	O	GLY 44	26.483	26.448	37.251	1.00	30.43
	ATOM	256	N	LEU 45	27.258	27.854	38.820	1.00	31.23
	ATOM	257	CA	LEU 45	26.144	28.774	38.761	1.00	31.72
5	ATOM	258	CB	LEU 45	26.168	29.638	40.010	1.00	30.96
	ATOM	259	CG	LEU 45	25.063	29.363	41.013	1.00	34.38
	ATOM	260	CD1	LEU 45	25.346	30.066	42.334	1.00	34.74
	ATOM	261	CD2	LEU 45	23.750	29.849	40.413	1.00	37.12
	ATOM	262	C	LEU 45	26.204	29.666	37.517	1.00	33.39
10	ATOM	263	O	LEU 45	25.184	30.211	37.086	1.00	34.01
	ATOM	264	N	ARG 46	27.402	29.813	36.955	1.00	34.39
	ATOM	265	CA	ARG 46	27.628	30.651	35.774	1.00	37.39
	ATOM	266	CB	ARG 46	29.092	31.140	35.744	1.00	42.80
	ATOM	267	CG	ARG 46	29.463	32.067	34.562	1.00	48.17
15	ATOM	268	CD	ARG 46	30.951	32.487	34.546	1.00	49.35
	ATOM	269	NE	ARG 46	31.250	33.400	33.441	1.00	54.04
	ATOM	270	CZ	ARG 46	30.599	34.542	33.216	1.00	57.98
	ATOM	271	NH1	ARG 46	29.608	34.915	34.019	1.00	56.34
	ATOM	272	NH2	ARG 46	30.936	35.316	32.187	1.00	59.91
20	ATOM	273	C	ARG 46	27.301	29.920	34.477	1.00	37.53
	ATOM	274	O	ARG 46	27.773	28.804	34.243	1.00	38.11
	ATOM	275	N	LEU 47	26.515	30.573	33.623	1.00	36.42
	ATOM	276	CA	LEU 47	26.089	29.993	32.350	1.00	35.82
	ATOM	277	CB	LEU 47	25.151	30.957	31.617	1.00	31.45
25	ATOM	278	CG	LEU 47	24.771	30.548	30.196	1.00	29.68
	ATOM	279	CD1	LEU 47	24.031	29.240	30.230	1.00	28.93
	ATOM	280	CD2	LEU 47	23.929	31.622	29.559	1.00	28.83
	ATOM	281	C	LEU 47	27.223	29.578	31.418	1.00	37.14
	ATOM	282	O	LEU 47	27.152	28.534	30.764	1.00	36.41

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	ATOM	283	N	GLU 48	28.272	30.383	31.347	1.00	39.28
	ATOM	284	CA	GLU 48	29.371	30.034	30.462	1.00	42.38
	ATOM	285	CB	GLU 48	30.448	31.126	30.473	1.00	43.91
	ATOM	286	CG	GLU 48	30.126	32.354	29.631	1.00	46.02
5	ATOM	287	CD	GLU 48	29.022	33.215	30.221	1.00	48.71
	ATOM	288	OE1	GLU 48	28.581	34.157	29.524	1.00	48.10
	ATOM	289	OE2	GLU 48	28.600	32.959	31.375	1.00	49.31
	ATOM	290	C	GLU 48	30.005	28.691	30.809	1.00	43.42
	ATOM	291	O	GLU 48	30.593	28.045	29.939	1.00	43.61
10	ATOM	292	N	THR 49	29.873	28.262	32.066	1.00	44.28
	ATOM	293	CA	THR 49	30.484	26.999	32.508	1.00	46.81
	ATOM	294	CB	THR 49	31.761	27.267	33.366	1.00	47.70
	ATOM	295	OG1	THR 49	31.477	28.265	34.356	1.00	45.18
	ATOM	296	CG2	THR 49	32.921	27.739	32.486	1.00	48.17
15	ATOM	297	C	THR 49	29.595	26.024	33.293	1.00	46.50
	ATOM	298	O	THR 49	30.043	24.932	33.683	1.00	45.72
	ATOM	299	N	HIS 50	28.340	26.405	33.508	1.00	44.18
	ATOM	300	CA	HIS 50	27.416	25.565	34.262	1.00	41.93
	ATOM	301	CB	HIS 50	25.980	26.129	34.190	1.00	38.83
20	ATOM	302	CG	HIS 50	25.217	25.754	32.953	1.00	35.50
	ATOM	303	CD2	HIS 50	23.950	25.304	32.795	1.00	33.70
	ATOM	304	ND1	HIS 50	25.730	25.894	31.682	1.00	36.24
	ATOM	305	CE1	HIS 50	24.812	25.550	30.796	1.00	33.56
	ATOM	306	NE2	HIS 50	23.722	25.189	31.446	1.00	32.06
25	ATOM	307	C	HIS 50	27.447	24.117	33.804	1.00	41.73
	ATOM	308	O	HIS 50	27.144	23.212	34.572	1.00	41.14
	ATOM	309	N	GLU 51	27.848	23.883	32.566	1.00	42.00
	ATOM	310	CA	GLU 51	27.863	22.519	32.103	1.00	45.79
	ATOM	311	CB	GLU 51	27.573	22.463	30.617	1.00	46.76

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	ATOM	312	CG	GLU 51	27.523	21.048	30.100	1.00	50.98
	ATOM	313	CD	GLU 51	26.521	20.885	28.989	1.00	53.94
	ATOM	314	OE1	GLU 51	25.313	21.082	29.253	1.00	55.61
	ATOM	315	OE2	GLU 51	26.940	20.560	27.857	1.00	55.48
5	ATOM	316	C	GLU 51	29.139	21.757	32.402	1.00	48.17
	ATOM	317	O	GLU 51	29.094	20.657	32.953	1.00	49.35
	ATOM	318	N	GLU 52	30.276	22.331	32.034	1.00	50.75
	ATOM	319	CA	GLU 52	31.565	21.681	32.264	1.00	52.07
	ATOM	320	CB	GLU 52	32.633	22.321	31.352	1.00	56.66
10	ATOM	321	CG	GLU 52	32.768	23.854	31.476	1.00	63.81
	ATOM	322	CD	GLU 52	33.420	24.528	30.253	1.00	67.84
	ATOM	323	OE1	GLU 52	33.601	25.770	30.278	1.00	68.83
	ATOM	324	OE2	GLU 52	33.742	23.826	29.266	1.00	70.00
	ATOM	325	C	GLU 52	31.982	21.760	33.738	1.00	49.95
15	ATOM	326	O	GLU 52	33.013	21.215	34.132	1.00	47.47
	ATOM	327	N	ALA 53	31.162	22.429	34.548	1.00	48.46
	ATOM	328	CA	ALA 53	31.449	22.594	35.972	1.00	47.88
	ATOM	329	CB	ALA 53	30.418	23.510	36.615	1.00	47.30
	ATOM	330	C	ALA 53	31.510	21.278	36.731	1.00	46.84
20	ATOM	331	O	ALA 53	31.287	20.206	36.172	1.00	48.51
	ATOM	332	N	SER 54	31.816	21.353	38.016	1.00	44.67
	ATOM	333	CA	SER 54	31.895	20.133	38.792	1.00	42.38
	ATOM	334	CB	SER 54	33.201	20.090	39.581	1.00	44.26
	ATOM	335	OG	SER 54	33.290	18.883	40.316	1.00	45.49
25	ATOM	336	C	SER 54	30.712	20.059	39.734	1.00	39.72
	ATOM	337	O	SER 54	30.058	19.028	39.841	1.00	41.09
	ATOM	338	N	VAL 55	30.440	21.165	40.411	1.00	34.77
	ATOM	339	CA	VAL 55	29.326	21.239	41.343	1.00	30.58
	ATOM	340	CB	VAL 55	29.682	22.186	42.498	1.00	28.73



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	ATOM	341	CG1	VAL	55	28.480	22.433	43.383	1.00	30.75
	ATOM	342	CG2	VAL	55	30.814	21.596	43.297	1.00	25.80
	ATOM	343	C	VAL	55	28.094	21.760	40.597	1.00	30.28
	ATOM	344	O	VAL	55	27.704	22.920	40.745	1.00	32.16
5	ATOM	345	N	LYS	56	27.482	20.887	39.803	1.00	26.82
	ATOM	346	CA	LYS	56	26.323	21.235	38.986	1.00	21.66
	ATOM	347	CB	LYS	56	25.362	20.046	38.891	1.00	26.53
	ATOM	348	CG	LYS	56	25.936	18.737	38.337	1.00	29.32
	ATOM	349	CD	LYS	56	26.311	18.836	36.875	1.00	29.86
10	ATOM	350	CE	LYS	56	27.609	19.592	36.698	1.00	29.73
	ATOM	351	NZ	LYS	56	27.932	19.759	35.259	1.00	32.80
	ATOM	352	C	LYS	56	25.520	22.470	39.374	1.00	17.56
	ATOM	353	O	LYS	56	25.133	23.236	38.498	1.00	15.95
	ATOM	354	N	MET	57	25.257	22.660	40.665	1.00	14.30
15	ATOM	355	CA	MET	57	24.462	23.803	41.128	1.00	12.73
	ATOM	356	CB	MET	57	25.277	25.089	41.059	1.00	9.92
	ATOM	357	CG	MET	57	26.515	25.090	41.930	1.00	6.47
	ATOM	358	SD	MET	57	26.219	25.164	43.694	1.00	8.00
	ATOM	359	CE	MET	57	25.523	26.842	43.905	1.00	1.00
20	ATOM	360	C	MET	57	23.207	23.953	40.270	1.00	14.05
	ATOM	361	O	MET	57	23.000	24.972	39.610	1.00	12.36
	ATOM	362	N	LEU	58	22.371	22.923	40.290	1.00	17.80
	ATOM	363	CA	LEU	58	21.154	22.914	39.498	1.00	19.02
	ATOM	364	CB	LEU	58	20.710	21.466	39.245	1.00	18.03
25	ATOM	365	CG	LEU	58	21.726	20.444	38.720	1.00	16.28
	ATOM	366	CD1	LEU	58	21.193	19.068	39.021	1.00	20.44
	ATOM	367	CD2	LEU	58	21.999	20.608	37.233	1.00	15.03
	ATOM	368	C	LEU	58	20.005	23.696	40.134	1.00	20.20
	ATOM	369	O	LEU	58	19.752	23.602	41.340	1.00	19.91

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	ATOM	370	N	PRO 59	19.316	24.507	39.320	1.00	20.57
	ATOM	371	CD	PRO 59	19.856	24.939	38.022	1.00	20.39
	ATOM	372	CA	PRO 59	18.171	25.342	39.694	1.00	22.50
	ATOM	373	CB	PRO 59	17.939	26.168	38.437	1.00	22.07
5	ATOM	374	CG	PRO 59	19.306	26.329	37.906	1.00	21.92
	ATOM	375	C	PRO 59	16.975	24.437	40.010	1.00	23.49
	ATOM	376	O	PRO 59	16.698	23.504	39.264	1.00	25.36
	ATOM	377	N	THR 60	16.258	24.714	41.092	1.00	22.35
	ATOM	378	CA	THR 60	15.133	23.871	41.469	1.00	20.99
10	ATOM	379	CB	THR 60	15.097	23.607	42.964	1.00	22.35
	ATOM	380	OG1	THR 60	14.823	24.837	43.647	1.00	24.53
	ATOM	381	CG2	THR 60	16.408	23.049	43.441	1.00	24.88
	ATOM	382	C	THR 60	13.815	24.516	41.160	1.00	20.21
	ATOM	383	O	THR 60	12.793	23.848	41.119	1.00	24.18
15	ATOM	384	N	TYR 61	13.839	25.822	40.973	1.00	19.09
	ATOM	385	CA	TYR 61	12.628	26.595	40.715	1.00	20.03
	ATOM	386	CB	TYR 61	11.955	26.172	39.427	1.00	13.50
	ATOM	387	CG	TYR 61	12.581	26.830	38.234	1.00	13.18
	ATOM	388	CD1	TYR 61	12.028	27.983	37.666	1.00	8.00
20	ATOM	389	CE1	TYR 61	12.596	28.551	36.536	1.00	4.24
	ATOM	390	CD2	TYR 61	13.725	26.281	37.647	1.00	14.04
	ATOM	391	CE2	TYR 61	14.296	26.843	36.529	1.00	10.05
	ATOM	392	CZ	TYR 61	13.730	27.963	35.976	1.00	5.80
	ATOM	393	OH	TYR 61	14.307	28.423	34.828	1.00	4.54
25	ATOM	394	C	TYR 61	11.620	26.572	41.833	1.00	21.95
	ATOM	395	O	TYR 61	10.437	26.816	41.609	1.00	22.47
	ATOM	396	N	VAL 62	12.102	26.293	43.037	1.00	24.47
	ATOM	397	CA	VAL 62	11.265	26.288	44.218	1.00	29.86
	ATOM	398	CB	VAL 62	11.750	25.231	45.207	1.00	28.92

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	ATOM	399	CG1	VAL	62	10.780	25.091	46.370	1.00	28.30
	ATOM	400	CG2	VAL	62	11.909	23.926	44.480	1.00	28.58
	ATOM	401	C	VAL	62	11.494	27.680	44.786	1.00	34.67
	ATOM	402	O	VAL	62	11.584	27.879	45.993	1.00	39.01
5	ATOM	403	N	ARG	63	11.589	28.638	43.874	1.00	38.40
	ATOM	404	CA	ARG	63	11.847	30.038	44.182	1.00	41.10
	ATOM	405	CB	ARG	63	12.041	30.804	42.874	1.00	42.02
	ATOM	406	CG	ARG	63	10.794	30.798	41.996	1.00	44.76
	ATOM	407	CD	ARG	63	11.072	31.197	40.550	1.00	46.61
10	ATOM	408	NE	ARG	63	9.827	31.366	39.804	1.00	48.56
	ATOM	409	CZ	ARG	63	8.972	30.381	39.541	1.00	50.39
	ATOM	410	NH1	ARG	63	9.225	29.145	39.955	1.00	50.83
	ATOM	411	NH2	ARG	63	7.854	30.635	38.875	1.00	51.11
	ATOM	412	C	ARG	63	10.788	30.751	45.004	1.00	42.71
15	ATOM	413	O	ARG	63	9.790	30.167	45.424	1.00	41.58
	ATOM	414	N	SER	64	11.047	32.036	45.224	1.00	46.12
	ATOM	415	CA	SER	64	10.155	32.922	45.954	1.00	49.96
	ATOM	416	CB	SER	64	10.400	32.826	47.454	1.00	50.57
	ATOM	417	OG	SER	64	9.374	33.507	48.157	1.00	53.70
20	ATOM	418	C	SER	64	10.435	34.340	45.458	1.00	51.04
	ATOM	419	O	SER	64	11.300	35.047	45.985	1.00	50.38
	ATOM	420	N	THR	65	9.690	34.728	44.425	1.00	53.23
	ATOM	421	CA	THR	65	9.827	36.031	43.791	1.00	54.89
	ATOM	422	CB	THR	65	10.151	35.871	42.281	1.00	56.21
25	ATOM	423	OG1	THR	65	9.094	35.158	41.622	1.00	55.23
	ATOM	424	CG2	THR	65	11.461	35.112	42.103	1.00	56.71
	ATOM	425	C	THR	65	8.582	36.911	43.939	1.00	56.01
	ATOM	426	O	THR	65	7.503	36.430	44.291	1.00	56.26
	ATOM	427	N	PRO	66	8.728	38.222	43.676	1.00	56.49

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	ATOM	428	CD	PRO 66	10.019	38.866	43.377	1.00	56.96
	ATOM	429	CA	PRO 66	7.666	39.228	43.758	1.00	56.28
	ATOM	430	CB	PRO 66	8.369	40.502	43.313	1.00	57.08
	ATOM	431	CG	PRO 66	9.759	40.287	43.786	1.00	58.08
5	ATOM	432	C	PRO 66	6.487	38.901	42.864	1.00	56.75
	ATOM	433	O	PRO 66	5.477	39.604	42.874	1.00	57.23
	ATOM	434	N	GLU 67	6.631	37.849	42.072	1.00	56.42
	ATOM	435	CA	GLU 67	5.540	37.445	41.193	1.00	56.82
	ATOM	436	CB	GLU 67	6.048	36.487	40.115	1.00	61.19
10	ATOM	437	CG	GLU 67	6.421	35.108	40.637	1.00	66.99
	ATOM	438	CD	GLU 67	7.123	34.261	39.594	1.00	69.61
	ATOM	439	OE1	GLU 67	8.253	34.618	39.201	1.00	70.19
	ATOM	440	OE2	GLU 67	6.541	33.241	39.168	1.00	70.18
	ATOM	441	C	GLU 67	4.406	36.803	41.984	1.00	54.30
15	ATOM	442	O	GLU 67	3.241	36.940	41.633	1.00	54.25
	ATOM	443	N	GLY 68	4.753	36.116	43.076	1.00	50.50
	ATOM	444	CA	GLY 68	3.741	35.478	43.901	1.00	45.77
	ATOM	445	C	GLY 68	4.166	34.087	44.316	1.00	43.04
	ATOM	446	O	GLY 68	3.626	33.503	45.259	1.00	40.69
20	ATOM	447	N	SER 69	5.154	33.564	43.599	1.00	42.30
	ATOM	448	CA	SER 69	5.690	32.230	43.845	1.00	41.02
	ATOM	449	CB	SER 69	6.769	31.902	42.804	1.00	41.03
	ATOM	450	OG	SER 69	6.438	32.404	41.517	1.00	42.34
	ATOM	451	C	SER 69	6.301	32.126	45.240	1.00	39.68
25	ATOM	452	O	SER 69	7.163	32.920	45.607	1.00	38.89
	ATOM	453	N	GLU 70	5.857	31.143	46.014	1.00	39.96
	ATOM	454	CA	GLU 70	6.388	30.942	47.355	1.00	40.53
	ATOM	455	CB	GLU 70	5.265	31.074	48.391	1.00	44.80
	ATOM	456	CG	GLU 70	4.675	32.483	48.492	1.00	52.74

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	ATOM	457	CD	GLU 70	5.705	33.554	48.900	1.00	58.55
	ATOM	458	OE1	GLU 70	5.362	34.763	48.866	1.00	59.55
	ATOM	459	OE2	GLU 70	6.852	33.192	49.258	1.00	60.30
	ATOM	460	C	GLU 70	7.075	29.583	47.483	1.00	38.65
5	ATOM	461	O	GLU 70	6.807	28.660	46.704	1.00	37.89
	ATOM	462	N	VAL 71	7.962	29.459	48.466	1.00	35.96
	ATOM	463	CA	VAL 71	8.670	28.207	48.653	1.00	34.46
	ATOM	464	CB	VAL 71	9.723	28.319	49.755	1.00	33.00
	ATOM	465	CG1	VAL 71	10.236	26.949	50.120	1.00	33.91
10	ATOM	466	CG2	VAL 71	10.885	29.152	49.249	1.00	32.56
	ATOM	467	C	VAL 71	7.730	27.042	48.931	1.00	34.75
	ATOM	468	O	VAL 71	7.851	25.985	48.310	1.00	37.23
	ATOM	469	N	GLY 72	6.783	27.219	49.841	1.00	33.37
	ATOM	470	CA	GLY 72	5.842	26.139	50.105	1.00	32.39
15	ATOM	471	C	GLY 72	5.066	25.644	48.879	1.00	31.10
	ATOM	472	O	GLY 72	4.631	24.493	48.859	1.00	28.98
	ATOM	473	N	ASP 73	4.878	26.503	47.870	1.00	31.05
	ATOM	474	CA	ASP 73	4.156	26.129	46.650	1.00	31.14
	ATOM	475	CB	ASP 73	4.389	27.147	45.532	1.00	34.00
20	ATOM	476	CG	ASP 73	3.759	28.491	45.817	1.00	38.43
	ATOM	477	OD1	ASP 73	3.758	29.355	44.907	1.00	41.88
	ATOM	478	OD2	ASP 73	3.262	28.690	46.945	1.00	41.23
	ATOM	479	C	ASP 73	4.675	24.785	46.189	1.00	30.89
	ATOM	480	O	ASP 73	5.875	24.544	46.256	1.00	32.81
25	ATOM	481	N	PHE 74	3.796	23.921	45.694	1.00	28.84
	ATOM	482	CA	PHE 74	4.233	22.595	45.271	1.00	27.21
	ATOM	483	CB	PHE 74	4.728	21.834	46.502	1.00	26.13
	ATOM	484	CG	PHE 74	5.407	20.551	46.185	1.00	25.61
	ATOM	485	CD1	PHE 74	6.641	20.546	45.547	1.00	29.29

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	ATOM	486	CD2	PHE 74	4.805	19.344	46.496	1.00	24.94
	ATOM	487	CE1	PHE 74	7.259	19.354	45.213	1.00	31.36
	ATOM	488	CE2	PHE 74	5.408	18.149	46.168	1.00	27.38
	ATOM	489	CZ	PHE 74	6.640	18.149	45.527	1.00	30.18
5	ATOM	490	C	PHE 74	3.080	21.837	44.604	1.00	27.31
	ATOM	491	O	PHE 74	1.912	22.034	44.951	1.00	28.04
	ATOM	492	N	LEU 75	3.402	20.965	43.654	1.00	23.99
	ATOM	493	CA	LEU 75	2.370	20.214	42.958	1.00	20.00
	ATOM	494	CB	LEU 75	2.222	20.725	41.534	1.00	19.88
10	ATOM	495	CG	LEU 75	0.868	20.487	40.865	1.00	21.27
	ATOM	496	CD1	LEU 75	1.083	20.282	39.354	1.00	19.58
	ATOM	497	CD2	LEU 75	0.190	19.279	41.474	1.00	18.85
	ATOM	498	C	LEU 75	2.755	18.758	42.911	1.00	18.82
	ATOM	499	O	LEU 75	3.587	18.369	42.102	1.00	19.49
15	ATOM	500	N	SER 76	2.143	17.957	43.774	1.00	21.08
	ATOM	501	CA	SER 76	2.434	16.530	43.834	1.00	22.49
	ATOM	502	CB	SER 76	2.333	16.001	45.261	1.00	22.74
	ATOM	503	OG	SER 76	2.591	14.612	45.292	1.00	20.37
	ATOM	504	C	SER 76	1.507	15.720	42.967	1.00	23.58
20	ATOM	505	O	SER 76	0.309	15.980	42.866	1.00	23.06
	ATOM	506	N	LEU 77	2.064	14.686	42.378	1.00	25.35
	ATOM	507	CA	LEU 77	1.280	13.862	41.509	1.00	27.55
	ATOM	508	CB	LEU 77	1.758	14.122	40.089	1.00	29.38
	ATOM	509	CG	LEU 77	1.176	13.275	38.980	1.00	32.75
25	ATOM	510	CD1	LEU 77	-0.334	13.434	38.974	1.00	34.55
	ATOM	511	CD2	LEU 77	1.796	13.695	37.661	1.00	32.83
	ATOM	512	C	LEU 77	1.445	12.402	41.913	1.00	28.86
	ATOM	513	O	LEU 77	2.527	11.826	41.760	1.00	26.84
	ATOM	514	N	ASP 78	0.386	11.811	42.465	1.00	29.41

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	ATOM	515	CA	ASP 78	0.457	10.407	42.865	1.00	30.41
	ATOM	516	CB	ASP 78	-0.150	10.186	44.255	1.00	31.87
	ATOM	517	CG	ASP 78	-0.286	8.702	44.606	1.00	33.99
	ATOM	518	OD1	ASP 78	-1.025	7.993	43.894	1.00	35.38
5	ATOM	519	OD2	ASP 78	0.338	8.241	45.586	1.00	33.31
	ATOM	520	C	ASP 78	-0.270	9.530	41.860	1.00	29.41
	ATOM	521	O	ASP 78	-1.484	9.587	41.732	1.00	29.74
	ATOM	522	N	LEU 79	0.472	8.710	41.143	1.00	27.93
	ATOM	523	CA	LEU 79	-0.169	7.858	40.184	1.00	28.08
10	ATOM	524	CB	LEU 79	0.323	8.173	38.781	1.00	25.78
	ATOM	525	CG	LEU 79	1.676	7.627	38.371	1.00	24.57
	ATOM	526	CD1	LEU 79	1.845	7.871	36.904	1.00	25.82
	ATOM	527	CD2	LEU 79	2.779	8.274	39.166	1.00	26.37
	ATOM	528	C	LEU 79	0.114	6.420	40.548	1.00	31.25
15	ATOM	529	O	LEU 79	1.265	6.017	40.712	1.00	32.14
	ATOM	530	N	GLY 80	-0.955	5.652	40.699	1.00	34.99
	ATOM	531	CA	GLY 80	-0.812	4.259	41.056	1.00	38.29
	ATOM	532	C	GLY 80	-2.088	3.499	40.776	1.00	40.81
	ATOM	533	O	GLY 80	-3.100	3.686	41.452	1.00	40.77
20	ATOM	534	N	GLY 81	-2.038	2.642	39.765	1.00	43.19
	ATOM	535	CA	GLY 81	-3.197	1.850	39.422	1.00	45.84
	ATOM	536	C	GLY 81	-3.936	2.428	38.244	1.00	49.22
	ATOM	537	O	GLY 81	-3.328	2.825	37.241	1.00	49.20
	ATOM	538	N	THR 82	-5.260	2.465	38.365	1.00	51.93
25	ATOM	539	CA	THR 82	-6.117	3.003	37.312	1.00	54.41
	ATOM	540	CB	THR 82	-7.344	2.090	37.060	1.00	56.74
	ATOM	541	OG1	THR 82	-6.908	0.727	36.952	1.00	60.43
	ATOM	542	CG2	THR 82	-8.043	2.473	35.752	1.00	58.23
	ATOM	543	C	THR 82	-6.584	4.382	37.759	1.00	52.48

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	ATOM	544	O	THR 82	-7.308	5.077	37.046	1.00	52.21
	ATOM	545	N	ASN 83	-6.148	4.778	38.946	1.00	50.63
	ATOM	546	CA	ASN 83	-6.523	6.071	39.466	1.00	50.52
	ATOM	547	CB	ASN 83	-7.574	5.911	40.568	1.00	53.97
5	ATOM	548	CG	ASN 83	-8.955	5.560	40.020	1.00	58.88
	ATOM	549	OD1	ASN 83	-9.508	6.290	39.190	1.00	60.51
	ATOM	550	ND2	ASN 83	-9.521	4.444	40.489	1.00	60.30
	ATOM	551	C	ASN 83	-5.338	6.861	39.997	1.00	48.79
	ATOM	552	O	ASN 83	-4.682	6.442	40.956	1.00	48.09
10	ATOM	553	N	PHE 84	-5.068	8.003	39.356	1.00	45.51
	ATOM	554	CA	PHE 84	-3.995	8.907	39.772	1.00	40.32
	ATOM	555	CB	PHE 84	-2.998	9.145	38.644	1.00	39.20
	ATOM	556	CG	PHE 84	-3.436	10.175	37.652	1.00	39.52
	ATOM	557	CD1	PHE 84	-4.096	9.802	36.494	1.00	40.87
15	ATOM	558	CD2	PHE 84	-3.159	11.524	37.860	1.00	39.69
	ATOM	559	CE1	PHE 84	-4.479	10.758	35.549	1.00	41.79
	ATOM	560	CE2	PHE 84	-3.540	12.490	36.922	1.00	40.16
	ATOM	561	CZ	PHE 84	-4.198	12.105	35.762	1.00	40.38
	ATOM	562	C	PHE 84	-4.604	10.246	40.176	1.00	37.84
20	ATOM	563	O	PHE 84	-5.405	10.806	39.439	1.00	37.11
	ATOM	564	N	ARG 85	-4.216	10.762	41.338	1.00	36.37
	ATOM	565	CA	ARG 85	-4.738	12.032	41.840	1.00	35.14
	ATOM	566	CB	ARG 85	-5.496	11.779	43.136	1.00	39.80
	ATOM	567	CG	ARG 85	-4.888	10.677	43.970	1.00	47.71
25	ATOM	568	CD	ARG 85	-5.948	9.964	44.805	1.00	55.73
	ATOM	569	NE	ARG 85	-5.391	8.801	45.493	1.00	62.76
	ATOM	570	CZ	ARG 85	-4.799	7.772	44.883	1.00	65.65
	ATOM	571	NH1	ARG 85	-4.684	7.749	43.557	1.00	63.79
	ATOM	572	NH2	ARG 85	-4.314	6.765	45.605	1.00	66.67



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	ATOM	573	C	ARG 85	-3.664	13.088	42.075	1.00	32.14
	ATOM	574	O	ARG 85	-2.561	12.772	42.522	1.00	32.77
	ATOM	575	N	VAL 86	-3.977	14.345	41.778	1.00	27.45
	ATOM	576	CA	VAL 86	-2.997	15.405	41.983	1.00	26.49
5	ATOM	577	CB	VAL 86	-2.975	16.400	40.821	1.00	24.77
	ATOM	578	CG1	VAL 86	-3.033	15.655	39.510	1.00	26.70
	ATOM	579	CG2	VAL 86	-4.109	17.373	40.948	1.00	24.73
	ATOM	580	C	VAL 86	-3.292	16.177	43.257	1.00	26.66
	ATOM	581	O	VAL 86	-4.401	16.121	43.779	1.00	28.06
10	ATOM	582	N	MET 87	-2.289	16.888	43.757	1.00	26.93
	ATOM	583	CA	MET 87	-2.427	17.677	44.973	1.00	25.08
	ATOM	584	CB	MET 87	-1.748	16.979	46.138	1.00	25.05
	ATOM	585	CG	MET 87	-1.674	17.833	47.375	1.00	24.83
	ATOM	586	SD	MET 87	-0.509	17.090	48.503	1.00	30.68
15	ATOM	587	CE	MET 87	-1.544	16.749	49.894	1.00	29.41
	ATOM	588	C	MET 87	-1.768	19.021	44.774	1.00	24.52
	ATOM	589	O	MET 87	-0.638	19.097	44.298	1.00	27.12
	ATOM	590	N	LEU 88	-2.455	20.087	45.146	1.00	22.16
	ATOM	591	CA	LEU 88	-1.872	21.398	44.975	1.00	20.70
20	ATOM	592	CB	LEU 88	-2.825	22.309	44.230	1.00	20.34
	ATOM	593	CG	LEU 88	-2.178	23.663	43.991	1.00	23.49
	ATOM	594	CD1	LEU 88	-0.806	23.470	43.354	1.00	24.39
	ATOM	595	CD2	LEU 88	-3.078	24.493	43.094	1.00	25.91
	ATOM	596	C	LEU 88	-1.535	22.021	46.301	1.00	19.94
25	ATOM	597	O	LEU 88	-2.225	21.794	47.282	1.00	21.18
	ATOM	598	N	VAL 89	-0.463	22.799	46.343	1.00	20.16
	ATOM	599	CA	VAL 89	-0.082	23.462	47.580	1.00	21.15
	ATOM	600	CB	VAL 89	0.984	22.676	48.357	1.00	14.95
	ATOM	601	CG1	VAL 89	1.292	23.385	49.657	1.00	7.73

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	ATOM	602	CG2	VAL	89	0.515	21.268	48.609	1.00	10.59
	ATOM	603	C	VAL	89	0.491	24.829	47.254	1.00	27.10
	ATOM	604	O	VAL	89	1.410	24.939	46.442	1.00	27.22
	ATOM	605	N	LYS	90	-0.066	25.866	47.875	1.00	33.21
5	ATOM	606	CA	LYS	90	0.401	27.235	47.671	1.00	40.01
	ATOM	607	CB	LYS	90	-0.443	27.962	46.604	1.00	41.03
	ATOM	608	CG	LYS	90	-1.941	27.979	46.850	1.00	47.19
	ATOM	609	CD	LYS	90	-2.749	28.454	45.622	1.00	52.33
	ATOM	610	CE	LYS	90	-4.274	28.393	45.899	1.00	55.73
10	ATOM	611	NZ	LYS	90	-5.161	28.724	44.731	1.00	56.02
	ATOM	612	C	LYS	90	0.384	28.009	48.981	1.00	43.61
	ATOM	613	O	LYS	90	-0.577	27.943	49.747	1.00	44.04
	ATOM	614	N	VAL	91	1.469	28.728	49.241	1.00	47.88
	ATOM	615	CA	VAL	91	1.587	29.513	50.458	1.00	51.82
15	ATOM	616	CB	VAL	91	3.059	29.780	50.788	1.00	51.29
	ATOM	617	CG1	VAL	91	3.160	30.748	51.947	1.00	54.88
	ATOM	618	CG2	VAL	91	3.749	28.479	51.137	1.00	48.18
	ATOM	619	C	VAL	91	0.849	30.846	50.355	1.00	55.01
	ATOM	620	O	VAL	91	0.994	31.569	49.369	1.00	54.57
20	ATOM	621	N	GLY	92	0.060	31.157	51.382	1.00	59.16
	ATOM	622	CA	GLY	92	-0.696	32.396	51.401	1.00	64.58
	ATOM	623	C	GLY	92	-0.305	33.297	52.558	1.00	68.39
	ATOM	624	O	GLY	92	0.637	32.992	53.295	1.00	66.92
	ATOM	625	N	GLU	93	-1.025	34.410	52.712	1.00	73.13
25	ATOM	626	CA	GLU	93	-0.751	35.351	53.792	1.00	78.27
	ATOM	627	CB	GLU	93	-0.623	36.780	53.248	1.00	79.11
	ATOM	628	CG	GLU	93	0.334	37.635	54.077	1.00	82.44
	ATOM	629	CD	GLU	93	0.218	39.120	53.795	1.00	84.34
	ATOM	630	OE1	GLU	93	-0.877	39.688	54.018	1.00	84.71

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	ATOM	631	OE2	GLU	93	1.228	39.718	53.359	1.00	85.45
	ATOM	632	C	GLU	93	-1.813	35.309	54.904	1.00	80.72
	ATOM	633	O	GLU	93	-1.469	35.340	56.086	1.00	81.42
	ATOM	634	N	GLY	94	-3.093	35.240	54.536	1.00	83.03
5	ATOM	635	CA	GLY	94	-4.153	35.182	55.538	1.00	85.37
	ATOM	636	C	GLY	94	-4.867	36.502	55.792	1.00	87.51
	ATOM	637	O	GLY	94	-4.356	37.562	55.430	1.00	88.65
	ATOM	638	N	GLU	95	-6.041	36.447	56.427	1.00	88.43
	ATOM	639	CA	GLU	95	-6.831	37.653	56.716	1.00	88.66
10	ATOM	640	CB	GLU	95	-8.192	37.281	57.328	1.00	89.61
	ATOM	641	CG	GLU	95	-9.077	36.406	56.448	1.00	90.41
	ATOM	642	CD	GLU	95	-8.620	34.958	56.408	1.00	91.01
	ATOM	643	OE1	GLU	95	-9.089	34.211	55.523	1.00	90.26
	ATOM	644	OE2	GLU	95	-7.800	34.565	57.266	1.00	91.81
15	ATOM	645	C	GLU	95	-6.115	38.625	57.652	1.00	88.62
	ATOM	646	O	GLU	95	-6.576	39.748	57.868	1.00	88.29
	ATOM	647	N	GLU	96	-4.991	38.182	58.208	1.00	89.03
	ATOM	648	CA	GLU	96	-4.200	38.995	59.124	1.00	88.80
	ATOM	649	CB	GLU	96	-4.065	38.282	60.476	1.00	88.55
20	ATOM	650	CG	GLU	96	-5.368	38.155	61.268	1.00	89.59
	ATOM	651	CD	GLU	96	-6.400	37.262	60.593	1.00	90.56
	ATOM	652	OE1	GLU	96	-6.163	36.040	60.481	1.00	90.53
	ATOM	653	OE2	GLU	96	-7.452	37.785	60.172	1.00	90.67
	ATOM	654	C	GLU	96	-2.810	39.327	58.519	1.00	88.40
25	ATOM	655	O	GLU	96	-2.097	40.166	59.052	1.00	89.12
	ATOM	656	N	GLY	97	-2.431	38.700	57.404	1.00	86.87
	ATOM	657	CA	GLY	97	-1.133	38.917	56.789	1.00	85.05
	ATOM	658	C	GLY	97	-0.161	37.976	57.494	1.00	84.17
	ATOM	659	O	GLY	97	1.044	38.179	57.605	1.00	83.49

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	ATOM	660	N	GLN 98	-0.820	36.901	57.977	1.00	83.07
	ATOM	661	CA	GLN 98	-0.253	35.810	58.769	1.00	82.28
	ATOM	662	CB	GLN 98	-1.346	34.825	59.250	1.00	82.41
	ATOM	663	CG	GLN 98	-2.647	35.462	59.699	1.00	83.61
5	ATOM	664	CD	GLN 98	-3.740	34.427	60.007	1.00	84.16
	ATOM	665	OE1	GLN 98	-3.606	33.239	59.714	1.00	84.01
	ATOM	666	NE2	GLN 98	-4.905	34.685	60.592	1.00	84.46
	ATOM	667	C	GLN 98	0.735	34.981	58.011	1.00	81.85
	ATOM	668	O	GLN 98	1.955	35.200	57.956	1.00	83.51
10	ATOM	669	N	TRP 99	0.118	33.962	57.470	1.00	79.05
	ATOM	670	CA	TRP 99	0.703	32.914	56.706	1.00	75.85
	ATOM	671	CB	TRP 99	1.993	32.398	57.308	1.00	73.88
	ATOM	672	CG	TRP 99	2.968	31.780	56.325	1.00	71.82
	ATOM	673	CD2	TRP 99	3.211	30.386	56.075	1.00	70.49
15	ATOM	674	CE2	TRP 99	4.222	30.308	55.123	1.00	69.72
	ATOM	675	CE3	TRP 99	2.671	29.200	56.550	1.00	69.52
	ATOM	676	CD1	TRP 99	3.832	32.464	55.525	1.00	71.99
	ATOM	677	NE1	TRP 99	4.598	31.589	54.790	1.00	71.07
	ATOM	678	CZ2	TRP 99	4.692	29.089	54.624	1.00	67.81
20	ATOM	679	CZ3	TRP 99	3.136	27.984	56.080	1.00	67.31
	ATOM	680	CH2	TRP 99	4.151	27.945	55.111	1.00	67.77
	ATOM	681	C	TRP 99	-0.247	31.793	56.673	1.00	74.58
	ATOM	682	O	TRP 99	-1.060	31.567	57.556	1.00	75.00
	ATOM	683	N	SER 100	-0.090	31.087	55.647	1.00	72.11
25	ATOM	684	CA	SER 100	-0.948	29.999	55.517	1.00	68.48
	ATOM	685	CB	SER 100	-2.376	30.466	55.232	1.00	68.40
	ATOM	686	OG	SER 100	-2.467	31.128	53.985	1.00	68.76
	ATOM	687	C	SER 100	-0.522	29.152	54.382	1.00	66.28
	ATOM	688	O	SER 100	0.405	29.473	53.632	1.00	65.13

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	ATOM	689	N	VAL 101	-1.225	28.028	54.291	1.00	64.27
	ATOM	690	CA	VAL 101	-0.982	27.030	53.262	1.00	62.66
	ATOM	691	CB	VAL 101	0.090	26.023	53.715	1.00	62.98
	ATOM	692	CG1	VAL 101	1.493	26.554	53.459	1.00	66.77
5	ATOM	693	CG2	VAL 101	-0.075	25.688	55.198	1.00	63.17
	ATOM	694	C	VAL 101	-2.219	26.243	52.878	1.00	60.88
	ATOM	695	O	VAL 101	-2.561	25.258	53.530	1.00	60.62
	ATOM	696	N	LYS 102	-2.880	26.671	51.810	1.00	58.24
	ATOM	697	CA	LYS 102	-4.066	25.981	51.337	1.00	56.12
10	ATOM	698	CB	LYS 102	-4.887	26.880	50.410	1.00	57.06
	ATOM	699	CG	LYS 102	-5.884	27.806	51.111	1.00	60.55
	ATOM	700	CD	LYS 102	-7.056	27.038	51.748	1.00	63.17
	ATOM	701	CE	LYS 102	-8.282	27.944	52.036	1.00	64.70
	ATOM	702	NZ	LYS 102	-8.021	29.150	52.899	1.00	63.52
15	ATOM	703	C	LYS 102	-3.677	24.710	50.596	1.00	54.04
	ATOM	704	O	LYS 102	-2.599	24.609	50.007	1.00	52.35
	ATOM	705	N	THR 103	-4.576	23.738	50.631	1.00	52.24
	ATOM	706	CA	THR 103	-4.345	22.474	49.972	1.00	49.72
	ATOM	707	CB	THR 103	-4.139	21.385	51.010	1.00	49.49
20	ATOM	708	OG1	THR 103	-3.399	20.316	50.422	1.00	53.11
	ATOM	709	CG2	THR 103	-5.475	20.861	51.517	1.00	48.32
	ATOM	710	C	THR 103	-5.563	22.158	49.106	1.00	49.61
	ATOM	711	O	THR 103	-6.693	22.435	49.507	1.00	50.24
	ATOM	712	N	LYS 104	-5.330	21.587	47.924	1.00	48.56
25	ATOM	713	CA	LYS 104	-6.404	21.251	46.983	1.00	48.50
	ATOM	714	CB	LYS 104	-6.469	22.298	45.864	1.00	49.98
	ATOM	715	CG	LYS 104	-6.753	23.737	46.313	1.00	56.05
	ATOM	716	CD	LYS 104	-8.195	23.932	46.814	1.00	60.38
	ATOM	717	CE	LYS 104	-8.456	25.383	47.254	1.00	62.32

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	ATOM	718	NZ	LYS	104	-9.845	25.649	47.761	1.00	61.31
	ATOM	719	C	LYS	104	-6.224	19.878	46.332	1.00	48.13
	ATOM	720	O	LYS	104	-5.286	19.685	45.563	1.00	49.60
	ATOM	721	N	HIS	105	-7.127	18.936	46.606	1.00	47.57
5	ATOM	722	CA	HIS	105	-7.023	17.601	46.010	1.00	47.23
	ATOM	723	CB	HIS	105	-7.165	16.529	47.074	1.00	47.40
	ATOM	724	CG	HIS	105	-6.241	16.709	48.228	1.00	49.37
	ATOM	725	CD2	HIS	105	-5.098	16.066	48.563	1.00	49.55
	ATOM	726	ND1	HIS	105	-6.459	17.648	49.212	1.00	50.43
10	ATOM	727	CE1	HIS	105	-5.493	17.571	50.110	1.00	51.38
	ATOM	728	NE2	HIS	105	-4.655	16.619	49.740	1.00	50.58
	ATOM	729	C	HIS	105	-8.030	17.304	44.907	1.00	46.39
	ATOM	730	O	HIS	105	-9.195	17.692	44.985	1.00	49.62
	ATOM	731	N	GLN	106	-7.575	16.580	43.894	1.00	42.98
15	ATOM	732	CA	GLN	106	-8.419	16.226	42.771	1.00	40.44
	ATOM	733	CB	GLN	106	-8.284	17.285	41.685	1.00	40.41
	ATOM	734	CG	GLN	106	-9.546	17.548	40.908	1.00	40.59
	ATOM	735	CD	GLN	106	-10.428	16.324	40.813	1.00	40.54
	ATOM	736	OE1	GLN	106	-11.061	15.927	41.795	1.00	39.16
20	ATOM	737	NE2	GLN	106	-10.475	15.712	39.631	1.00	40.06
	ATOM	738	C	GLN	106	-7.940	14.878	42.249	1.00	40.70
	ATOM	739	O	GLN	106	-6.745	14.699	42.012	1.00	41.69
	ATOM	740	N	MET	107	-8.867	13.937	42.066	1.00	41.01
	ATOM	741	CA	MET	107	-8.532	12.588	41.599	1.00	40.17
25	ATOM	742	CB	MET	107	-9.083	11.551	42.588	1.00	42.07
	ATOM	743	CG	MET	107	-8.772	10.094	42.249	1.00	44.67
	ATOM	744	SD	MET	107	-10.185	9.202	41.551	1.00	50.71
	ATOM	745	CE	MET	107	-10.688	8.056	42.927	1.00	43.37
	ATOM	746	C	MET	107	-9.059	12.294	40.204	1.00	38.93

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	ATOM	747	O	MET 107	-10.264	12.285	39.979	1.00	41.30
	ATOM	748	N	TYR 108	-8.161	12.044	39.264	1.00	37.96
	ATOM	749	CA	TYR 108	-8.588	11.750	37.907	1.00	38.48
	ATOM	750	CB	TYR 108	-7.670	12.454	36.900	1.00	35.63
5	ATOM	751	CG	TYR 108	-7.732	13.972	36.977	1.00	35.18
	ATOM	752	CD1	TYR 108	-7.492	14.645	38.180	1.00	37.21
	ATOM	753	CE1	TYR 108	-7.550	16.047	38.268	1.00	34.81
	ATOM	754	CD2	TYR 108	-8.031	14.735	35.857	1.00	34.14
	ATOM	755	CE2	TYR 108	-8.092	16.134	35.931	1.00	35.09
10	ATOM	756	CZ	TYR 108	-7.852	16.783	37.139	1.00	35.25
	ATOM	757	OH	TYR 108	-7.937	18.158	37.211	1.00	33.27
	ATOM	758	C	TYR 108	-8.583	10.241	37.689	1.00	40.17
	ATOM	759	O	TYR 108	-7.817	9.514	38.325	1.00	38.04
	ATOM	760	N	SER 109	-9.469	9.765	36.818	1.00	42.63
15	ATOM	761	CA	SER 109	-9.524	8.341	36.530	1.00	44.60
	ATOM	762	CB	SER 109	-10.929	7.787	36.736	1.00	43.05
	ATOM	763	OG	SER 109	-10.926	6.385	36.522	1.00	41.66
	ATOM	764	C	SER 109	-9.090	8.106	35.097	1.00	46.74
	ATOM	765	O	SER 109	-9.531	8.799	34.182	1.00	44.65
20	ATOM	766	N	ILE 110	-8.217	7.120	34.918	1.00	50.31
	ATOM	767	CA	ILE 110	-7.686	6.782	33.608	1.00	55.29
	ATOM	768	CB	ILE 110	-6.326	6.060	33.731	1.00	54.32
	ATOM	769	CG2	ILE 110	-5.690	5.932	32.364	1.00	56.16
	ATOM	770	CG1	ILE 110	-5.373	6.844	34.626	1.00	53.30
25	ATOM	771	CD1	ILE 110	-4.067	6.117	34.869	1.00	51.57
	ATOM	772	C	ILE 110	-8.621	5.882	32.799	1.00	59.70
	ATOM	773	O	ILE 110	-8.906	4.749	33.199	1.00	58.82
	ATOM	774	N	PRO 111	-9.114	6.381	31.650	1.00	64.10
	ATOM	775	CD	PRO 111	-8.972	7.759	31.142	1.00	64.05

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	ATOM	776	CA	PRO	111	-10.012	5.608	30.788	1.00	68.40
	ATOM	777	CB	PRO	111	-10.118	6.484	29.547	1.00	67.29
	ATOM	778	CG	PRO	111	-10.105	7.860	30.144	1.00	63.88
	ATOM	779	C	PRO	111	-9.416	4.231	30.494	1.00	72.88
5	ATOM	780	O	PRO	111	-8.195	4.065	30.506	1.00	73.72
	ATOM	781	N	GLU	112	-10.280	3.250	30.239	1.00	77.60
	ATOM	782	CA	GLU	112	-9.845	1.879	29.958	1.00	80.79
	ATOM	783	CB	GLU	112	-11.072	0.968	29.798	1.00	82.29
	ATOM	784	CG	GLU	112	-10.748	-0.498	29.524	1.00	83.62
10	ATOM	785	CD	GLU	112	-11.896	-1.247	28.851	1.00	85.04
	ATOM	786	OE1	GLU	112	-11.697	-2.423	28.470	1.00	85.60
	ATOM	787	OE2	GLU	112	-12.995	-0.665	28.700	1.00	85.42
	ATOM	788	C	GLU	112	-8.971	1.806	28.702	1.00	82.21
	ATOM	789	O	GLU	112	-7.936	1.137	28.693	1.00	82.17
15	ATOM	790	N	ASP	113	-9.394	2.501	27.649	1.00	83.97
	ATOM	791	CA	ASP	113	-8.660	2.522	26.385	1.00	85.79
	ATOM	792	CB	ASP	113	-9.506	3.221	25.302	1.00	86.45
	ATOM	793	CG	ASP	113	-9.961	4.624	25.712	1.00	87.32
	ATOM	794	OD1	ASP	113	-10.655	4.756	26.748	1.00	86.75
20	ATOM	795	OD2	ASP	113	-9.629	5.595	24.991	1.00	87.18
	ATOM	796	C	ASP	113	-7.297	3.215	26.533	1.00	86.44
	ATOM	797	O	ASP	113	-6.467	3.195	25.617	1.00	86.35
	ATOM	798	N	ALA	114	-7.075	3.813	27.701	1.00	86.34
	ATOM	799	CA	ALA	114	-5.837	4.533	28.000	1.00	85.22
25	ATOM	800	CB	ALA	114	-6.174	5.904	28.585	1.00	84.46
	ATOM	801	C	ALA	114	-4.928	3.768	28.963	1.00	83.67
	ATOM	802	O	ALA	114	-3.716	3.692	28.762	1.00	83.48
	ATOM	803	N	MET	115	-5.528	3.212	30.012	1.00	81.79
	ATOM	804	CA	MET	115	-4.802	2.457	31.023	1.00	78.70



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	ATOM	805	CB	MET	115	-5.776	2.050	32.135	1.00	81.16
	ATOM	806	CG	MET	115	-5.148	1.863	33.503	1.00	84.52
	ATOM	807	SD	MET	115	-3.978	0.492	33.553	1.00	90.44
	ATOM	808	CE	MET	115	-5.060	-0.891	34.119	1.00	88.49
5	ATOM	809	C	MET	115	-4.145	1.224	30.391	1.00	76.27
	ATOM	810	O	MET	115	-3.066	0.809	30.813	1.00	74.47
	ATOM	811	N	THR	116	-4.796	0.658	29.372	1.00	74.50
	ATOM	812	CA	THR	116	-4.282	-0.518	28.666	1.00	72.46
	ATOM	813	CB	THR	116	-5.399	-1.524	28.309	1.00	72.22
10	ATOM	814	OG1	THR	116	-6.200	-0.993	27.244	1.00	71.17
	ATOM	815	CG2	THR	116	-6.275	-1.805	29.516	1.00	71.94
	ATOM	816	C	THR	116	-3.621	-0.110	27.356	1.00	71.75
	ATOM	817	O	THR	116	-3.562	-0.899	26.412	1.00	71.39
	ATOM	818	N	GLY	117	-3.142	1.131	27.301	1.00	71.09
15	ATOM	819	CA	GLY	117	-2.477	1.639	26.110	1.00	68.62
	ATOM	820	C	GLY	117	-0.961	1.651	26.260	1.00	66.70
	ATOM	821	O	GLY	117	-0.384	0.702	26.798	1.00	67.20
	ATOM	822	N	THR	118	-0.313	2.716	25.783	1.00	63.05
	ATOM	823	CA	THR	118	1.142	2.844	25.876	1.00	59.92
20	ATOM	824	CB	THR	118	1.796	3.020	24.502	1.00	59.06
	ATOM	825	OG1	THR	118	1.013	3.926	23.718	1.00	57.88
	ATOM	826	CG2	THR	118	1.917	1.688	23.794	1.00	59.21
	ATOM	827	C	THR	118	1.548	4.038	26.721	1.00	58.97
	ATOM	828	O	THR	118	0.764	4.971	26.912	1.00	58.11
25	ATOM	829	N	ALA	119	2.782	4.001	27.218	1.00	56.72
	ATOM	830	CA	ALA	119	3.313	5.071	28.052	1.00	52.86
	ATOM	831	CB	ALA	119	4.807	4.938	28.177	1.00	51.30
	ATOM	832	C	ALA	119	2.972	6.399	27.421	1.00	51.58
	ATOM	833	O	ALA	119	2.456	7.301	28.080	1.00	52.70

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	ATOM	834	N	GLU 120	3.260	6.502	26.131	1.00	48.02
	ATOM	835	CA	GLU 120	2.994	7.716	25.386	1.00	46.07
	ATOM	836	CB	GLU 120	3.194	7.471	23.894	1.00	49.10
	ATOM	837	CG	GLU 120	4.210	6.381	23.550	1.00	52.89
5	ATOM	838	CD	GLU 120	5.630	6.736	23.945	1.00	53.64
	ATOM	839	OE1	GLU 120	5.962	6.621	25.141	1.00	55.30
	ATOM	840	OE2	GLU 120	6.411	7.139	23.057	1.00	52.83
	ATOM	841	C	GLU 120	1.557	8.140	25.630	1.00	44.27
	ATOM	842	O	GLU 120	1.295	9.257	26.070	1.00	44.84
10	ATOM	843	N	MET 121	0.627	7.235	25.351	1.00	41.37
	ATOM	844	CA	MET 121	-0.791	7.525	25.513	1.00	38.57
	ATOM	845	CB	MET 121	-1.626	6.358	24.990	1.00	41.30
	ATOM	846	CG	MET 121	-1.721	6.328	23.479	1.00	46.24
	ATOM	847	SD	MET 121	-2.483	4.835	22.838	1.00	50.88
15	ATOM	848	CE	MET 121	-3.908	4.669	23.961	1.00	50.02
	ATOM	849	C	MET 121	-1.190	7.820	26.937	1.00	34.60
	ATOM	850	O	MET 121	-1.910	8.780	27.204	1.00	31.69
	ATOM	851	N	LEU 122	-0.719	6.985	27.852	1.00	32.63
	ATOM	852	CA	LEU 122	-1.051	7.141	29.263	1.00	30.24
20	ATOM	853	CB	LEU 122	-0.256	6.140	30.108	1.00	27.33
	ATOM	854	CG	LEU 122	-0.778	5.923	31.533	1.00	21.99
	ATOM	855	CD1	LEU 122	-0.279	4.601	32.031	1.00	22.53
	ATOM	856	CD2	LEU 122	-0.366	7.034	32.456	1.00	17.78
	ATOM	857	C	LEU 122	-0.759	8.551	29.746	1.00	28.67
25	ATOM	858	O	LEU 122	-1.619	9.228	30.326	1.00	25.21
	ATOM	859	N	PHE 123	0.469	8.987	29.502	1.00	26.83
	ATOM	860	CA	PHE 123	0.871	10.306	29.929	1.00	25.29
	ATOM	861	CB	PHE 123	2.387	10.398	29.908	1.00	20.22
	ATOM	862	CG	PHE 123	3.015	9.772	31.112	1.00	15.51

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	ATOM	863	CD1 PHE 123	3.538	8.494	31.064	1.00	12.96
	ATOM	864	CD2 PHE 123	3.028	10.457	32.328	1.00	13.35
	ATOM	865	CE1 PHE 123	4.067	7.910	32.217	1.00	12.87
	ATOM	866	CE2 PHE 123	3.552	9.879	33.484	1.00	9.69
5	ATOM	867	CZ PHE 123	4.072	8.609	33.432	1.00	9.56
	ATOM	868	C PHE 123	0.202	11.432	29.157	1.00	26.20
	ATOM	869	O PHE 123	-0.102	12.489	29.722	1.00	26.61
	ATOM	870	N ASP 124	-0.053	11.207	27.875	1.00	24.47
	ATOM	871	CA ASP 124	-0.750	12.210	27.090	1.00	23.14
10	ATOM	872	CB ASP 124	-1.228	11.614	25.785	1.00	24.52
	ATOM	873	CG ASP 124	-0.178	11.628	24.747	1.00	27.01
	ATOM	874	OD1 ASP 124	-0.376	10.955	23.715	1.00	26.39
	ATOM	875	OD2 ASP 124	0.839	12.325	24.968	1.00	29.23
	ATOM	876	C ASP 124	-1.967	12.650	27.875	1.00	21.89
15	ATOM	877	O ASP 124	-2.361	13.815	27.841	1.00	20.01
	ATOM	878	N TYR 125	-2.562	11.688	28.574	1.00	20.84
	ATOM	879	CA TYR 125	-3.749	11.943	29.371	1.00	20.51
	ATOM	880	CB TYR 125	-4.414	10.619	29.792	1.00	20.43
	ATOM	881	CG TYR 125	-5.796	10.794	30.394	1.00	22.84
20	ATOM	882	CD1 TYR 125	-6.083	10.358	31.692	1.00	23.51
	ATOM	883	CE1 TYR 125	-7.345	10.584	32.268	1.00	31.08
	ATOM	884	CD2 TYR 125	-6.803	11.451	29.678	1.00	26.43
	ATOM	885	CE2 TYR 125	-8.064	11.685	30.232	1.00	31.61
	ATOM	886	CZ TYR 125	-8.336	11.255	31.528	1.00	34.64
25	ATOM	887	OH TYR 125	-9.585	11.520	32.073	1.00	38.10
	ATOM	888	C TYR 125	-3.382	12.752	30.605	1.00	19.11
	ATOM	889	O TYR 125	-3.904	13.848	30.824	1.00	16.08
	ATOM	890	N ILE 126	-2.465	12.212	31.399	1.00	17.91
	ATOM	891	CA ILE 126	-2.049	12.879	32.615	1.00	17.82

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	ATOM	892	CB	ILE 126	-0.819	12.236	33.203	1.00	19.82
	ATOM	893	CG2	ILE 126	-0.489	12.905	34.538	1.00	18.77
	ATOM	894	CG1	ILE 126	-1.055	10.732	33.331	1.00	21.27
	ATOM	895	CD1	ILE 126	0.045	9.984	34.062	1.00	23.92
5	ATOM	896	C	ILE 126	-1.717	14.313	32.325	1.00	18.09
	ATOM	897	O	ILE 126	-1.991	15.205	33.123	1.00	16.68
	ATOM	898	N	SER 127	-1.108	14.532	31.172	1.00	19.12
	ATOM	899	CA	SER 127	-0.747	15.877	30.789	1.00	20.96
	ATOM	900	CB	SER 127	-0.057	15.857	29.432	1.00	19.89
10	ATOM	901	OG	SER 127	0.569	17.100	29.190	1.00	22.20
	ATOM	902	C	SER 127	-2.011	16.742	30.746	1.00	21.92
	ATOM	903	O	SER 127	-2.177	17.658	31.551	1.00	20.25
	ATOM	904	N	GLU 128	-2.902	16.431	29.813	1.00	23.87
	ATOM	905	CA	GLU 128	-4.152	17.161	29.670	1.00	26.98
15	ATOM	906	CB	GLU 128	-5.111	16.353	28.802	1.00	33.10
	ATOM	907	CG	GLU 128	-6.471	16.990	28.544	1.00	39.51
	ATOM	908	CD	GLU 128	-7.280	16.175	27.544	1.00	44.52
	ATOM	909	OE1	GLU 128	-7.211	16.481	26.327	1.00	46.11
	ATOM	910	OE2	GLU 128	-7.963	15.218	27.980	1.00	43.93
20	ATOM	911	C	GLU 128	-4.797	17.431	31.020	1.00	26.55
	ATOM	912	O	GLU 128	-5.177	18.561	31.334	1.00	26.16
	ATOM	913	N	CYS 129	-4.929	16.384	31.820	1.00	26.36
	ATOM	914	CA	CYS 129	-5.532	16.535	33.130	1.00	26.47
	ATOM	915	CB	CYS 129	-5.452	15.219	33.893	1.00	28.39
25	ATOM	916	SG	CYS 129	-6.450	13.922	33.126	1.00	37.58
	ATOM	917	C	CYS 129	-4.853	17.636	33.914	1.00	25.00
	ATOM	918	O	CYS 129	-5.515	18.561	34.372	1.00	24.97
	ATOM	919	N	ILE 130	-3.532	17.536	34.059	1.00	24.74
	ATOM	920	CA	ILE 130	-2.763	18.536	34.793	1.00	21.55

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	ATOM	921	CB	ILE	130	-1.245	18.255	34.709	1.00	17.55
	ATOM	922	CG2	ILE	130	-0.458	19.404	35.304	1.00	15.00
	ATOM	923	CG1	ILE	130	-0.915	16.984	35.490	1.00	16.42
	ATOM	924	CD1	ILE	130	0.574	16.713	35.623	1.00	18.34
5	ATOM	925	C	ILE	130	-3.070	19.910	34.219	1.00	23.54
	ATOM	926	O	ILE	130	-3.572	20.780	34.926	1.00	21.27
	ATOM	927	N	SER	131	-2.785	20.091	32.933	1.00	26.25
	ATOM	928	CA	SER	131	-3.048	21.353	32.270	1.00	28.50
	ATOM	929	CB	SER	131	-3.011	21.186	30.764	1.00	28.76
10	ATOM	930	OG	SER	131	-3.856	22.154	30.164	1.00	32.87
	ATOM	931	C	SER	131	-4.417	21.851	32.661	1.00	31.48
	ATOM	932	O	SER	131	-4.586	23.002	33.057	1.00	33.67
	ATOM	933	N	ASP	132	-5.411	20.986	32.546	1.00	34.56
	ATOM	934	CA	ASP	132	-6.753	21.397	32.908	1.00	39.04
15	ATOM	935	CB	ASP	132	-7.735	20.248	32.694	1.00	44.84
	ATOM	936	CG	ASP	132	-9.165	20.650	32.987	1.00	50.51
	ATOM	937	OD1	ASP	132	-9.764	21.347	32.131	1.00	53.56
	ATOM	938	OD2	ASP	132	-9.674	20.283	34.078	1.00	52.37
	ATOM	939	C	ASP	132	-6.790	21.843	34.376	1.00	38.23
20	ATOM	940	O	ASP	132	-7.160	22.982	34.677	1.00	36.81
	ATOM	941	N	PHE	133	-6.394	20.932	35.270	1.00	36.88
	ATOM	942	CA	PHE	133	-6.372	21.170	36.713	1.00	34.85
	ATOM	943	CB	PHE	133	-5.604	20.060	37.433	1.00	33.59
	ATOM	944	CG	PHE	133	-5.343	20.362	38.878	1.00	34.77
25	ATOM	945	CD1	PHE	133	-6.396	20.547	39.760	1.00	35.58
	ATOM	946	CD2	PHE	133	-4.043	20.523	39.348	1.00	37.81
	ATOM	947	CE1	PHE	133	-6.159	20.896	41.091	1.00	37.66
	ATOM	948	CE2	PHE	133	-3.792	20.872	40.678	1.00	38.00
	ATOM	949	CZ	PHE	133	-4.850	21.059	41.548	1.00	38.85

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	ATOM	950	C	PHE 133	-5.755	22.503	37.094	1.00	34.28
	ATOM	951	O	PHE 133	-6.274	23.226	37.947	1.00	33.97
	ATOM	952	N	LEU 134	-4.622	22.813	36.482	1.00	33.97
	ATOM	953	CA	LEU 134	-3.958	24.070	36.766	1.00	31.79
5	ATOM	954	CB	LEU 134	-2.590	24.109	36.089	1.00	24.12
	ATOM	955	CG	LEU 134	-1.618	23.026	36.545	1.00	16.64
	ATOM	956	CD1	LEU 134	-0.368	23.101	35.705	1.00	15.98
	ATOM	957	CD2	LEU 134	-1.305	23.184	38.014	1.00	10.77
	ATOM	958	C	LEU 134	-4.855	25.176	36.234	1.00	34.44
10	ATOM	959	O	LEU 134	-5.111	26.163	36.920	1.00	34.41
	ATOM	960	N	ASP 135	-5.365	24.999	35.022	1.00	37.26
	ATOM	961	CA	ASP 135	-6.230	26.014	34.454	1.00	42.65
	ATOM	962	CB	ASP 135	-6.815	25.565	33.121	1.00	46.76
	ATOM	963	CG	ASP 135	-7.707	26.629	32.509	1.00	52.18
15	ATOM	964	OD1	ASP 135	-8.659	26.271	31.772	1.00	53.75
	ATOM	965	OD2	ASP 135	-7.443	27.829	32.772	1.00	52.70
	ATOM	966	C	ASP 135	-7.386	26.381	35.383	1.00	43.96
	ATOM	967	O	ASP 135	-7.643	27.563	35.619	1.00	44.98
	ATOM	968	N	LYS 136	-8.084	25.368	35.894	1.00	44.30
20	ATOM	969	CA	LYS 136	-9.225	25.578	36.780	1.00	44.56
	ATOM	970	CB	LYS 136	-9.889	24.237	37.124	1.00	46.76
	ATOM	971	CG	LYS 136	-11.195	24.350	37.941	1.00	52.67
	ATOM	972	CD	LYS 136	-11.910	22.981	38.128	1.00	55.98
	ATOM	973	CE	LYS 136	-13.367	23.120	38.628	1.00	55.25
25	ATOM	974	NZ	LYS 136	-14.106	21.817	38.719	1.00	51.28
	ATOM	975	C	LYS 136	-8.862	26.306	38.069	1.00	44.85
	ATOM	976	O	LYS 136	-9.730	26.894	38.717	1.00	45.87
	ATOM	977	N	HIS 137	-7.586	26.273	38.444	1.00	44.25
	ATOM	978	CA	HIS 137	-7.149	26.937	39.670	1.00	43.21

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	ATOM	979	CB	HIS	137	-6.434	25.937	40.585	1.00	44.13
	ATOM	980	CG	HIS	137	-7.344	24.915	41.199	1.00	45.24
	ATOM	981	CD2	HIS	137	-7.676	24.680	42.492	1.00	45.35
	ATOM	982	ND1	HIS	137	-8.042	23.991	40.452	1.00	45.45
5	ATOM	983	CE1	HIS	137	-8.764	23.231	41.257	1.00	45.40
	ATOM	984	NE2	HIS	137	-8.560	23.629	42.500	1.00	44.34
	ATOM	985	C	HIS	137	-6.242	28.132	39.400	1.00	41.96
	ATOM	986	O	HIS	137	-5.592	28.649	40.307	1.00	40.24
	ATOM	987	N	GLN	138	-6.217	28.577	38.151	1.00	42.87
10	ATOM	988	CA	GLN	138	-5.390	29.706	37.766	1.00	44.93
	ATOM	989	CB	GLN	138	-5.949	30.993	38.373	1.00	47.58
	ATOM	990	CG	GLN	138	-7.258	31.448	37.749	1.00	51.96
	ATOM	991	CD	GLN	138	-7.416	32.966	37.766	1.00	55.20
	ATOM	992	OE1	GLN	138	-6.680	33.698	37.088	1.00	56.05
15	ATOM	993	NE2	GLN	138	-8.375	33.445	38.546	1.00	55.44
	ATOM	994	C	GLN	138	-3.921	29.537	38.162	1.00	44.67
	ATOM	995	O	GLN	138	-3.316	30.437	38.747	1.00	45.78
	ATOM	996	N	MET	139	-3.350	28.383	37.836	1.00	41.86
	ATOM	997	CA	MET	139	-1.951	28.109	38.138	1.00	38.60
20	ATOM	998	CB	MET	139	-1.846	27.062	39.236	1.00	39.19
	ATOM	999	CG	MET	139	-2.048	27.660	40.604	1.00	41.24
	ATOM	1000	SD	MET	139	-0.859	28.992	40.852	1.00	47.65
	ATOM	1001	CE	MET	139	0.308	28.217	42.007	1.00	44.32
	ATOM	1002	C	MET	139	-1.232	27.653	36.881	1.00	36.60
25	ATOM	1003	O	MET	139	-0.316	26.823	36.910	1.00	35.29
	ATOM	1004	N	LYS	140	-1.659	28.237	35.771	1.00	34.23
	ATOM	1005	CA	LYS	140	-1.101	27.921	34.477	1.00	32.15
	ATOM	1006	CB	LYS	140	-2.198	28.062	33.417	1.00	31.04
	ATOM	1007	CG	LYS	140	-1.970	27.293	32.116	1.00	31.48

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	ATOM	1008	CD	LYS 140	-2.184	25.780	32.275	1.00	32.43
	ATOM	1009	CE	LYS 140	-2.112	25.015	30.925	1.00	30.89
	ATOM	1010	NZ	LYS 140	-0.811	25.130	30.168	1.00	29.56
	ATOM	1011	C	LYS 140	0.085	28.834	34.161	1.00	31.02
5	ATOM	1012	O	LYS 140	0.047	30.045	34.412	1.00	29.99
	ATOM	1013	N	HIS 141	1.143	28.228	33.627	1.00	31.35
	ATOM	1014	CA	HIS 141	2.353	28.940	33.244	1.00	30.03
	ATOM	1015	CB	HIS 141	1.989	30.145	32.385	1.00	30.05
	ATOM	1016	CG	HIS 141	1.001	29.836	31.305	1.00	31.15
10	ATOM	1017	CD2	HIS 141	-0.132	30.473	30.927	1.00	30.91
	ATOM	1018	ND1	HIS 141	1.148	28.769	30.448	1.00	33.49
	ATOM	1019	CE1	HIS 141	0.147	28.763	29.584	1.00	35.03
	ATOM	1020	NE2	HIS 141	-0.643	29.787	29.853	1.00	32.67
	ATOM	1021	C	HIS 141	3.138	29.396	34.460	1.00	29.17
15	ATOM	1022	O	HIS 141	4.211	29.983	34.341	1.00	28.17
	ATOM	1023	N	LYS 142	2.601	29.108	35.635	1.00	28.81
	ATOM	1024	CA	LYS 142	3.248	29.505	36.869	1.00	29.17
	ATOM	1025	CB	LYS 142	2.317	29.240	38.065	1.00	33.65
	ATOM	1026	CG	LYS 142	0.986	30.042	38.072	1.00	39.35
20	ATOM	1027	CD	LYS 142	1.194	31.561	38.214	1.00	42.74
	ATOM	1028	CE	LYS 142	-0.122	32.360	38.170	1.00	45.49
	ATOM	1029	NZ	LYS 142	0.110	33.844	38.325	1.00	46.19
	ATOM	1030	C	LYS 142	4.575	28.785	37.075	1.00	26.49
	ATOM	1031	O	LYS 142	5.340	29.138	37.966	1.00	26.10
25	ATOM	1032	N	LYS 143	4.862	27.784	36.254	1.00	24.58
	ATOM	1033	CA	LYS 143	6.106	27.042	36.416	1.00	22.67
	ATOM	1034	CB	LYS 143	7.258	27.847	35.836	1.00	21.51
	ATOM	1035	CG	LYS 143	8.533	27.071	35.737	1.00	22.59
	ATOM	1036	CD	LYS 143	9.319	27.510	34.516	1.00	25.81



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	ATOM	1037	CE	LYS 143	10.455	26.542	34.240	1.00	28.01
	ATOM	1038	NZ	LYS 143	11.140	26.828	32.959	1.00	27.25
	ATOM	1039	C	LYS 143	6.383	26.732	37.896	1.00	22.14
	ATOM	1040	O	LYS 143	7.133	27.459	38.556	1.00	21.99
5	ATOM	1041	N	LEU 144	5.766	25.655	38.401	1.00	20.81
	ATOM	1042	CA	LEU 144	5.910	25.214	39.797	1.00	16.90
	ATOM	1043	CB	LEU 144	4.577	25.351	40.567	1.00	16.78
	ATOM	1044	CG	LEU 144	3.208	24.956	39.983	1.00	18.43
	ATOM	1045	CD1	LEU 144	2.148	24.915	41.074	1.00	17.60
10	ATOM	1046	CD2	LEU 144	2.795	25.960	38.929	1.00	19.20
	ATOM	1047	C	LEU 144	6.432	23.781	39.933	1.00	15.80
	ATOM	1048	O	LEU 144	6.265	22.958	39.032	1.00	12.24
	ATOM	1049	N	PRO 145	7.078	23.478	41.076	1.00	16.26
	ATOM	1050	CD	PRO 145	7.227	24.446	42.172	1.00	15.64
15	ATOM	1051	CA	PRO 145	7.678	22.196	41.467	1.00	14.17
	ATOM	1052	CB	PRO 145	8.079	22.427	42.923	1.00	18.10
	ATOM	1053	CG	PRO 145	8.378	23.860	42.963	1.00	17.14
	ATOM	1054	C	PRO 145	6.707	21.050	41.357	1.00	12.75
	ATOM	1055	O	PRO 145	5.580	21.141	41.852	1.00	12.27
20	ATOM	1056	N	LEU 146	7.160	19.957	40.758	1.00	10.29
	ATOM	1057	CA	LEU 146	6.290	18.804	40.560	1.00	11.21
	ATOM	1058	CB	LEU 146	6.156	18.539	39.075	1.00	7.24
	ATOM	1059	CG	LEU 146	5.160	17.439	38.824	1.00	3.01
	ATOM	1060	CD1	LEU 146	3.817	17.832	39.389	1.00	1.00
25	ATOM	1061	CD2	LEU 146	5.083	17.215	37.342	1.00	3.06
	ATOM	1062	C	LEU 146	6.696	17.502	41.233	1.00	12.36
	ATOM	1063	O	LEU 146	7.629	16.851	40.790	1.00	15.11
	ATOM	1064	N	GLY 147	5.972	17.086	42.262	1.00	14.72
	ATOM	1065	CA	GLY 147	6.333	15.851	42.937	1.00	17.81

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	ATOM	1066	C	GLY 147	5.716	14.586	42.371	1.00	18.51
	ATOM	1067	O	GLY 147	4.689	14.644	41.704	1.00	20.85
	ATOM	1068	N	PHE 148	6.342	13.440	42.631	1.00	19.28
	ATOM	1069	CA	PHE 148	5.825	12.167	42.142	1.00	20.55
5	ATOM	1070	CB	PHE 148	6.707	11.635	41.023	1.00	16.36
	ATOM	1071	CG	PHE 148	6.593	12.409	39.759	1.00	17.72
	ATOM	1072	CD1	PHE 148	6.792	13.779	39.753	1.00	17.99
	ATOM	1073	CD2	PHE 148	6.298	11.769	38.560	1.00	21.10
	ATOM	1074	CE1	PHE 148	6.695	14.509	38.570	1.00	22.37
10	ATOM	1075	CE2	PHE 148	6.198	12.494	37.362	1.00	22.82
	ATOM	1076	CZ	PHE 148	6.398	13.864	37.366	1.00	21.67
	ATOM	1077	C	PHE 148	5.712	11.104	43.222	1.00	22.75
	ATOM	1078	O	PHE 148	6.691	10.783	43.885	1.00	24.66
	ATOM	1079	N	THR 149	4.513	10.562	43.403	1.00	24.45
15	ATOM	1080	CA	THR 149	4.312	9.514	44.387	1.00	24.75
	ATOM	1081	CB	THR 149	3.365	9.917	45.497	1.00	23.76
	ATOM	1082	OG1	THR 149	2.757	11.175	45.192	1.00	25.51
	ATOM	1083	CG2	THR 149	4.107	9.989	46.786	1.00	22.63
	ATOM	1084	C	THR 149	3.705	8.306	43.715	1.00	27.38
20	ATOM	1085	O	THR 149	3.093	8.405	42.647	1.00	24.58
	ATOM	1086	N	PHE 150	3.857	7.160	44.361	1.00	30.07
	ATOM	1087	CA	PHE 150	3.327	5.936	43.811	1.00	32.54
	ATOM	1088	CB	PHE 150	4.455	5.120	43.215	1.00	29.97
	ATOM	1089	CG	PHE 150	5.172	5.820	42.119	1.00	27.55
25	ATOM	1090	CD1	PHE 150	6.134	6.770	42.397	1.00	27.41
	ATOM	1091	CD2	PHE 150	4.850	5.561	40.798	1.00	27.56
	ATOM	1092	CE1	PHE 150	6.770	7.447	41.366	1.00	28.61
	ATOM	1093	CE2	PHE 150	5.481	6.231	39.762	1.00	26.86
	ATOM	1094	CZ	PHE 150	6.437	7.177	40.045	1.00	27.37

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	ATOM	1095	C	PHE 150	2.561	5.093	44.808	1.00	35.78
	ATOM	1096	O	PHE 150	3.095	4.695	45.845	1.00	36.93
	ATOM	1097	N	SER 151	1.305	4.813	44.467	1.00	38.60
	ATOM	1098	CA	SER 151	0.420	4.006	45.295	1.00	40.51
5	ATOM	1099	CB	SER 151	-0.830	4.802	45.641	1.00	41.51
	ATOM	1100	OG	SER 151	-1.507	5.159	44.453	1.00	47.40
	ATOM	1101	C	SER 151	0.038	2.736	44.533	1.00	41.75
	ATOM	1102	O	SER 151	0.069	2.696	43.301	1.00	40.78
	ATOM	1103	N	PHE 152	-0.336	1.704	45.278	1.00	43.86
10	ATOM	1104	CA	PHE 152	-0.684	0.421	44.687	1.00	45.76
	ATOM	1105	CB	PHE 152	0.465	-0.557	44.965	1.00	51.67
	ATOM	1106	CG	PHE 152	0.429	-1.808	44.133	1.00	57.82
	ATOM	1107	CD1	PHE 152	0.597	-1.749	42.751	1.00	59.39
	ATOM	1108	CD2	PHE 152	0.256	-3.056	44.739	1.00	60.37
15	ATOM	1109	CE1	PHE 152	0.598	-2.915	41.979	1.00	61.23
	ATOM	1110	CE2	PHE 152	0.254	-4.232	43.978	1.00	61.76
	ATOM	1111	CZ	PHE 152	0.426	-4.161	42.593	1.00	61.46
	ATOM	1112	C	PHE 152	-2.007	-0.134	45.238	1.00	43.74
	ATOM	1113	O	PHE 152	-2.137	-0.382	46.437	1.00	43.01
20	ATOM	1114	N	PRO 153	-3.005	-0.322	44.359	1.00	40.65
	ATOM	1115	CD	PRO 153	-2.993	0.179	42.979	1.00	39.35
	ATOM	1116	CA	PRO 153	-4.330	-0.844	44.685	1.00	38.88
	ATOM	1117	CB	PRO 153	-5.045	-0.803	43.352	1.00	36.16
	ATOM	1118	CG	PRO 153	-4.454	0.359	42.711	1.00	37.38
25	ATOM	1119	C	PRO 153	-4.235	-2.255	45.192	1.00	41.30
	ATOM	1120	O	PRO 153	-3.481	-3.057	44.657	1.00	42.17
	ATOM	1121	N	VAL 154	-5.013	-2.565	46.215	1.00	45.30
	ATOM	1122	CA	VAL 154	-5.016	-3.905	46.767	1.00	49.50
	ATOM	1123	CB	VAL 154	-4.124	-3.989	47.990	1.00	45.75

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	ATOM	1124	CG1	VAL	154	-4.297	-5.331	48.638	1.00	45.79
	ATOM	1125	CG2	VAL	154	-2.684	-3.772	47.594	1.00	44.88
	ATOM	1126	C	VAL	154	-6.432	-4.268	47.181	1.00	55.51
	ATOM	1127	O	VAL	154	-6.963	-3.683	48.119	1.00	58.30
5	ATOM	1128	N	ARG	155	-7.042	-5.232	46.495	1.00	61.06
	ATOM	1129	CA	ARG	155	-8.413	-5.643	46.812	1.00	67.71
	ATOM	1130	CB	ARG	155	-8.812	-6.847	45.956	1.00	71.43
	ATOM	1131	CG	ARG	155	-9.033	-6.501	44.501	1.00	76.11
	ATOM	1132	CD	ARG	155	-9.094	-7.736	43.621	1.00	78.73
10	ATOM	1133	NE	ARG	155	-9.292	-7.352	42.226	1.00	81.59
	ATOM	1134	CZ	ARG	155	-9.138	-8.168	41.190	1.00	82.83
	ATOM	1135	NH1	ARG	155	-8.778	-9.432	41.386	1.00	83.55
	ATOM	1136	NH2	ARG	155	-9.340	-7.717	39.956	1.00	82.01
	ATOM	1137	C	ARG	155	-8.639	-5.965	48.291	1.00	70.15
15	ATOM	1138	O	ARG	155	-7.689	-6.255	49.022	1.00	71.24
	ATOM	1139	N	HIS	156	-9.903	-5.923	48.720	1.00	71.23
	ATOM	1140	CA	HIS	156	-10.265	-6.184	50.117	1.00	72.30
	ATOM	1141	CB	HIS	156	-11.724	-5.769	50.365	1.00	73.82
	ATOM	1142	CG	HIS	156	-12.049	-5.506	51.808	1.00	76.32
20	ATOM	1143	CD2	HIS	156	-11.335	-5.722	52.941	1.00	76.70
	ATOM	1144	ND1	HIS	156	-13.243	-4.944	52.211	1.00	76.54
	ATOM	1145	CE1	HIS	156	-13.251	-4.823	53.527	1.00	76.16
	ATOM	1146	NE2	HIS	156	-12.106	-5.288	53.994	1.00	77.55
	ATOM	1147	C	HIS	156	-10.063	-7.645	50.522	1.00	72.42
25	ATOM	1148	O	HIS	156	-9.196	-7.957	51.345	1.00	71.15
	ATOM	1149	N	ASN	180	11.816	6.551	32.482	1.00	43.22
	ATOM	1150	CA	ASN	180	11.492	7.278	33.706	1.00	42.73
	ATOM	1151	CB	ASN	180	12.677	8.168	34.155	1.00	46.67
	ATOM	1152	CG	ASN	180	13.189	9.094	33.052	1.00	50.13

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	ATOM	1153	OD1	ASN	180	14.152	8.777	32.336	1.00	51.24
	ATOM	1154	ND2	ASN	180	12.547	10.250	32.915	1.00	51.73
	ATOM	1155	C	ASN	180	10.228	8.110	33.523	1.00	38.44
	ATOM	1156	O	ASN	180	9.941	8.600	32.431	1.00	36.40
5	ATOM	1157	N	VAL	181	9.473	8.257	34.603	1.00	34.02
	ATOM	1158	CA	VAL	181	8.218	8.995	34.577	1.00	31.37
	ATOM	1159	CB	VAL	181	7.498	8.874	35.957	1.00	34.84
	ATOM	1160	CG1	VAL	181	6.091	9.484	35.909	1.00	32.59
	ATOM	1161	CG2	VAL	181	7.414	7.405	36.353	1.00	38.00
10	ATOM	1162	C	VAL	181	8.426	10.458	34.221	1.00	26.36
	ATOM	1163	O	VAL	181	7.882	10.964	33.237	1.00	23.28
	ATOM	1164	N	VAL	182	9.228	11.131	35.030	1.00	23.56
	ATOM	1165	CA	VAL	182	9.518	12.538	34.826	1.00	18.23
	ATOM	1166	CB	VAL	182	10.702	12.958	35.716	1.00	14.26
15	ATOM	1167	CG1	VAL	182	11.905	12.084	35.426	1.00	14.73
	ATOM	1168	CG2	VAL	182	11.001	14.403	35.508	1.00	11.08
	ATOM	1169	C	VAL	182	9.773	12.882	33.352	1.00	15.36
	ATOM	1170	O	VAL	182	9.330	13.924	32.875	1.00	15.32
	ATOM	1171	N	GLY	183	10.467	12.009	32.632	1.00	13.34
20	ATOM	1172	CA	GLY	183	10.713	12.267	31.228	1.00	12.56
	ATOM	1173	C	GLY	183	9.458	12.098	30.382	1.00	13.06
	ATOM	1174	O	GLY	183	9.104	12.978	29.601	1.00	12.05
	ATOM	1175	N	LEU	184	8.772	10.971	30.540	1.00	15.78
	ATOM	1176	CA	LEU	184	7.549	10.708	29.777	1.00	15.21
25	ATOM	1177	CB	LEU	184	6.858	9.435	30.295	1.00	16.78
	ATOM	1178	CG	LEU	184	7.613	8.108	30.075	1.00	15.45
	ATOM	1179	CD1	LEU	184	7.037	7.023	30.951	1.00	10.71
	ATOM	1180	CD2	LEU	184	7.548	7.708	28.608	1.00	16.62
	ATOM	1181	C	LEU	184	6.601	11.894	29.863	1.00	13.07

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	ATOM	1182	O	LEU 184	6.041	12.311	28.855	1.00	13.90
	ATOM	1183	N	LEU 185	6.430	12.436	31.064	1.00	11.99
	ATOM	1184	CA	LEU 185	5.571	13.600	31.250	1.00	12.43
	ATOM	1185	CB	LEU 185	5.524	13.997	32.729	1.00	13.27
5	ATOM	1186	CG	LEU 185	4.630	15.191	33.080	1.00	11.52
	ATOM	1187	CD1	LEU 185	3.256	14.936	32.515	1.00	10.60
	ATOM	1188	CD2	LEU 185	4.553	15.395	34.600	1.00	12.16
	ATOM	1189	C	LEU 185	6.077	14.788	30.419	1.00	12.48
	ATOM	1190	O	LEU 185	5.289	15.488	29.784	1.00	9.22
10	ATOM	1191	N	ARG 186	7.388	15.020	30.428	1.00	13.24
	ATOM	1192	CA	ARG 186	7.946	16.123	29.661	1.00	14.83
	ATOM	1193	CB	ARG 186	9.478	16.135	29.727	1.00	14.69
	ATOM	1194	CG	ARG 186	10.112	17.274	30.526	1.00	18.47
	ATOM	1195	CD	ARG 186	11.633	17.063	30.663	1.00	25.71
15	ATOM	1196	NE	ARG 186	12.325	18.069	31.484	1.00	37.62
	ATOM	1197	CZ	ARG 186	12.048	18.357	32.764	1.00	42.54
	ATOM	1198	NH1	ARG 186	11.070	17.721	33.407	1.00	43.86
	ATOM	1199	NH2	ARG 186	12.762	19.277	33.414	1.00	39.97
	ATOM	1200	C	ARG 186	7.510	15.968	28.220	1.00	16.38
20	ATOM	1201	O	ARG 186	6.857	16.851	27.673	1.00	17.00
	ATOM	1202	N	ASP 187	7.850	14.832	27.616	1.00	19.34
	ATOM	1203	CA	ASP 187	7.519	14.579	26.214	1.00	24.04
	ATOM	1204	CB	ASP 187	7.799	13.123	25.822	1.00	30.35
	ATOM	1205	CG	ASP 187	9.226	12.696	26.123	1.00	37.33
25	ATOM	1206	OD1	ASP 187	9.479	12.216	27.251	1.00	40.99
	ATOM	1207	OD2	ASP 187	10.096	12.845	25.234	1.00	40.65
	ATOM	1208	C	ASP 187	6.069	14.889	25.912	1.00	23.78
	ATOM	1209	O	ASP 187	5.756	15.541	24.909	1.00	25.37
	ATOM	1210	N	ALA 188	5.185	14.413	26.780	1.00	20.98

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	ATOM	1211	CA	ALA 188	3.761	14.634	26.603	1.00	17.11
	ATOM	1212	CB	ALA 188	2.996	13.943	27.722	1.00	19.70
	ATOM	1213	C	ALA 188	3.475	16.130	26.600	1.00	14.48
	ATOM	1214	O	ALA 188	2.911	16.660	25.646	1.00	11.69
5	ATOM	1215	N	ILE 189	3.873	16.801	27.677	1.00	13.32
	ATOM	1216	CA	ILE 189	3.682	18.239	27.817	1.00	13.84
	ATOM	1217	CB	ILE 189	4.422	18.754	29.056	1.00	12.34
	ATOM	1218	CG2	ILE 189	4.368	20.266	29.118	1.00	13.98
	ATOM	1219	CG1	ILE 189	3.776	18.153	30.302	1.00	14.10
10	ATOM	1220	CD1	ILE 189	4.455	18.530	31.595	1.00	14.04
	ATOM	1221	C	ILE 189	4.223	18.928	26.575	1.00	15.60
	ATOM	1222	O	ILE 189	3.634	19.888	26.058	1.00	14.87
	ATOM	1223	N	LYS 190	5.351	18.408	26.103	1.00	16.13
	ATOM	1224	CA	LYS 190	6.010	18.913	24.918	1.00	16.34
15	ATOM	1225	CB	LYS 190	7.361	18.211	24.737	1.00	18.43
	ATOM	1226	CG	LYS 190	8.503	19.081	24.175	1.00	24.32
	ATOM	1227	CD	LYS 190	8.539	19.154	22.631	1.00	28.76
	ATOM	1228	CE	LYS 190	9.830	19.841	22.125	1.00	30.07
	ATOM	1229	NZ	LYS 190	10.060	19.788	20.642	1.00	27.01
20	ATOM	1230	C	LYS 190	5.101	18.652	23.718	1.00	16.41
	ATOM	1231	O	LYS 190	4.786	19.575	22.981	1.00	17.80
	ATOM	1232	N	ARG 191	4.656	17.413	23.529	1.00	14.92
	ATOM	1233	CA	ARG 191	3.798	17.107	22.386	1.00	15.62
	ATOM	1234	CB	ARG 191	3.241	15.684	22.491	1.00	19.10
25	ATOM	1235	CG	ARG 191	4.071	14.622	21.775	1.00	20.57
	ATOM	1236	CD	ARG 191	3.634	13.221	22.156	1.00	19.26
	ATOM	1237	NE	ARG 191	3.950	12.925	23.547	1.00	23.45
	ATOM	1238	CZ	ARG 191	3.732	11.747	24.119	1.00	28.59
	ATOM	1239	NH1	ARG 191	3.194	10.767	23.406	1.00	32.19

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	ATOM	1240	NH2	ARG	191	4.062	11.537	25.391	1.00	29.84
	ATOM	1241	C	ARG	191	2.652	18.086	22.207	1.00	15.44
	ATOM	1242	O	ARG	191	2.383	18.513	21.098	1.00	15.17
	ATOM	1243	N	ARG	192	1.980	18.441	23.295	1.00	17.09
5	ATOM	1244	CA	ARG	192	0.853	19.372	23.253	1.00	19.02
	ATOM	1245	CB	ARG	192	0.588	19.885	24.647	1.00	17.94
	ATOM	1246	CG	ARG	192	0.579	18.785	25.635	1.00	20.35
	ATOM	1247	CD	ARG	192	-0.812	18.328	25.855	1.00	22.03
	ATOM	1248	NE	ARG	192	-1.565	19.332	26.586	1.00	27.30
10	ATOM	1249	CZ	ARG	192	-2.824	19.164	26.954	1.00	32.13
	ATOM	1250	NH1	ARG	192	-3.437	18.028	26.639	1.00	34.51
	ATOM	1251	NH2	ARG	192	-3.465	20.115	27.631	1.00	33.64
	ATOM	1252	C	ARG	192	1.010	20.572	22.321	1.00	22.21
	ATOM	1253	O	ARG	192	0.017	21.184	21.937	1.00	24.03
15	ATOM	1254	N	GLY	193	2.245	20.923	21.975	1.00	24.28
	ATOM	1255	CA	GLY	193	2.472	22.052	21.088	1.00	25.59
	ATOM	1256	C	GLY	193	2.351	23.417	21.750	1.00	27.55
	ATOM	1257	O	GLY	193	2.734	24.437	21.163	1.00	26.53
	ATOM	1258	N	ASP	194	1.836	23.434	22.981	1.00	28.09
20	ATOM	1259	CA	ASP	194	1.634	24.678	23.725	1.00	28.74
	ATOM	1260	CB	ASP	194	0.349	24.597	24.548	1.00	32.11
	ATOM	1261	CG	ASP	194	-0.873	24.329	23.692	1.00	36.60
	ATOM	1262	OD1	ASP	194	-1.053	25.025	22.668	1.00	38.48
	ATOM	1263	OD2	ASP	194	-1.659	23.424	24.046	1.00	40.23
25	ATOM	1264	C	ASP	194	2.774	25.089	24.641	1.00	27.04
	ATOM	1265	O	ASP	194	3.815	24.439	24.689	1.00	26.55
	ATOM	1266	N	PHE	195	2.565	26.181	25.370	1.00	25.47
	ATOM	1267	CA	PHE	195	3.582	26.691	26.274	1.00	25.41
	ATOM	1268	CB	PHE	195	3.083	27.932	27.016	1.00	27.05



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	ATOM	1269	CG	PHE	195	3.156	29.192	26.201	1.00	28.43
	ATOM	1270	CD1	PHE	195	2.032	29.686	25.550	1.00	31.56
	ATOM	1271	CD2	PHE	195	4.353	29.880	26.067	1.00	29.11
	ATOM	1272	CE1	PHE	195	2.097	30.852	24.771	1.00	30.45
5	ATOM	1273	CE2	PHE	195	4.426	31.046	25.290	1.00	30.62
	ATOM	1274	CZ	PHE	195	3.294	31.528	24.644	1.00	29.47
	ATOM	1275	C	PHE	195	4.024	25.642	27.267	1.00	24.15
	ATOM	1276	O	PHE	195	3.214	25.083	28.000	1.00	25.61
	ATOM	1277	N	GLU	196	5.324	25.385	27.280	1.00	22.49
10	ATOM	1278	CA	GLU	196	5.897	24.394	28.166	1.00	23.12
	ATOM	1279	CB	GLU	196	7.117	23.754	27.499	1.00	21.72
	ATOM	1280	CG	GLU	196	6.942	23.418	26.020	1.00	22.22
	ATOM	1281	CD	GLU	196	8.121	22.629	25.477	1.00	24.60
	ATOM	1282	OE1	GLU	196	8.336	22.601	24.241	1.00	23.54
15	ATOM	1283	OE2	GLU	196	8.839	22.026	26.301	1.00	26.49
	ATOM	1284	C	GLU	196	6.314	25.066	29.466	1.00	24.25
	ATOM	1285	O	GLU	196	7.467	24.966	29.882	1.00	26.05
	ATOM	1286	N	MET	197	5.376	25.729	30.126	1.00	25.12
	ATOM	1287	CA	MET	197	5.711	26.444	31.352	1.00	27.52
20	ATOM	1288	CB	MET	197	5.546	27.942	31.096	1.00	29.51
	ATOM	1289	CG	MET	197	6.758	28.782	31.466	1.00	33.61
	ATOM	1290	SD	MET	197	7.208	29.992	30.181	1.00	35.72
	ATOM	1291	CE	MET	197	5.967	31.256	30.466	1.00	37.45
	ATOM	1292	C	MET	197	4.906	26.045	32.583	1.00	27.47
25	ATOM	1293	O	MET	197	4.921	26.749	33.597	1.00	25.63
	ATOM	1294	N	ASP	198	4.230	24.903	32.502	1.00	27.57
	ATOM	1295	CA	ASP	198	3.384	24.430	33.598	1.00	26.12
	ATOM	1296	CB	ASP	198	2.462	23.298	33.110	1.00	29.89
	ATOM	1297	CG	ASP	198	1.326	23.796	32.232	1.00	31.76

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	ATOM	1298	OD1	ASP	198	0.736	24.840	32.590	1.00	30.59
	ATOM	1299	OD2	ASP	198	1.023	23.135	31.203	1.00	32.71
	ATOM	1300	C	ASP	198	4.110	23.959	34.853	1.00	22.26
	ATOM	1301	O	ASP	198	3.960	24.551	35.923	1.00	18.00
5	ATOM	1302	N	VAL	199	4.873	22.878	34.717	1.00	19.81
	ATOM	1303	CA	VAL	199	5.605	22.301	35.841	1.00	18.78
	ATOM	1304	CB	VAL	199	5.133	20.852	36.115	1.00	16.48
	ATOM	1305	CG1	VAL	199	3.736	20.859	36.696	1.00	19.07
	ATOM	1306	CG2	VAL	199	5.150	20.042	34.823	1.00	10.86
10	ATOM	1307	C	VAL	199	7.121	22.267	35.648	1.00	20.19
	ATOM	1308	O	VAL	199	7.665	22.752	34.655	1.00	21.16
	ATOM	1309	N	VAL	200	7.798	21.695	36.629	1.00	20.40
	ATOM	1310	CA	VAL	200	9.237	21.547	36.594	1.00	22.39
	ATOM	1311	CB	VAL	200	9.975	22.834	37.007	1.00	24.84
15	ATOM	1312	CG1	VAL	200	9.331	23.406	38.255	1.00	31.58
	ATOM	1313	CG2	VAL	200	11.465	22.539	37.266	1.00	21.54
	ATOM	1314	C	VAL	200	9.502	20.457	37.598	1.00	23.06
	ATOM	1315	O	VAL	200	9.039	20.501	38.755	1.00	22.26
	ATOM	1316	N	ALA	201	10.229	19.460	37.120	1.00	23.03
20	ATOM	1317	CA	ALA	201	10.569	18.300	37.907	1.00	22.74
	ATOM	1318	CB	ALA	201	11.460	17.418	37.112	1.00	23.66
	ATOM	1319	C	ALA	201	11.236	18.646	39.209	1.00	24.47
	ATOM	1320	O	ALA	201	12.045	19.564	39.285	1.00	27.55
	ATOM	1321	N	MET	202	10.872	17.914	40.244	1.00	25.96
25	ATOM	1322	CA	MET	202	11.479	18.106	41.547	1.00	27.52
	ATOM	1323	CB	MET	202	10.720	19.124	42.386	1.00	27.45
	ATOM	1324	CG	MET	202	11.516	19.580	43.597	1.00	27.56
	ATOM	1325	SD	MET	202	11.967	18.244	44.740	1.00	28.85
	ATOM	1326	CE	MET	202	10.732	18.486	46.045	1.00	23.74

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	ATOM	1327	C	MET 202	11.436	16.752	42.219	1.00	28.79
	ATOM	1328	O	MET 202	10.377	16.290	42.653	1.00	25.51
	ATOM	1329	N	VAL 203	12.600	16.118	42.293	1.00	29.76
	ATOM	1330	CA	VAL 203	12.695	14.802	42.883	1.00	28.97
5	ATOM	1331	CB	VAL 203	12.943	13.727	41.813	1.00	25.86
	ATOM	1332	CG1	VAL 203	11.936	13.870	40.681	1.00	22.02
	ATOM	1333	CG2	VAL 203	14.361	13.831	41.310	1.00	23.30
	ATOM	1334	C	VAL 203	13.815	14.713	43.890	1.00	31.36
	ATOM	1335	O	VAL 203	13.934	13.713	44.585	1.00	34.93
10	ATOM	1336	N	ASN 204	14.638	15.745	43.987	1.00	32.12
	ATOM	1337	CA	ASN 204	15.741	15.674	44.929	1.00	33.37
	ATOM	1338	CB	ASN 204	16.667	16.867	44.736	1.00	36.19
	ATOM	1339	CG	ASN 204	18.052	16.601	45.260	1.00	39.20
	ATOM	1340	OD1	ASN 204	18.847	15.905	44.621	1.00	41.71
15	ATOM	1341	ND2	ASN 204	18.349	17.133	46.440	1.00	39.72
	ATOM	1342	C	ASN 204	15.220	15.625	46.363	1.00	32.02
	ATOM	1343	O	ASN 204	14.382	16.439	46.751	1.00	28.87
	ATOM	1344	N	ASP 205	15.705	14.665	47.149	1.00	31.97
	ATOM	1345	CA	ASP 205	15.245	14.538	48.541	1.00	33.94
20	ATOM	1346	CB	ASP 205	15.792	13.266	49.197	1.00	32.38
	ATOM	1347	CG	ASP 205	15.163	12.017	48.642	1.00	31.18
	ATOM	1348	OD1	ASP 205	15.386	10.935	49.217	1.00	31.15
	ATOM	1349	OD2	ASP 205	14.450	12.118	47.625	1.00	28.42
	ATOM	1350	C	ASP 205	15.626	15.722	49.414	1.00	33.64
25	ATOM	1351	O	ASP 205	14.909	16.080	50.356	1.00	33.83
	ATOM	1352	N	THR 206	16.770	16.313	49.092	1.00	31.15
	ATOM	1353	CA	THR 206	17.290	17.449	49.826	1.00	25.09
	ATOM	1354	CB	THR 206	18.646	17.825	49.278	1.00	25.45
	ATOM	1355	OG1	THR 206	19.423	16.630	49.123	1.00	24.81

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	ATOM	1356	CG2	THR	206	19.350	18.769	50.232	1.00	26.26
	ATOM	1357	C	THR	206	16.347	18.634	49.734	1.00	20.16
	ATOM	1358	O	THR	206	15.923	19.184	50.755	1.00	17.86
	ATOM	1359	N	VAL	207	16.009	19.016	48.510	1.00	12.86
5	ATOM	1360	CA	VAL	207	15.106	20.133	48.308	1.00	9.27
	ATOM	1361	CB	VAL	207	14.582	20.164	46.867	1.00	5.21
	ATOM	1362	CG1	VAL	207	13.555	21.243	46.720	1.00	1.26
	ATOM	1363	CG2	VAL	207	15.714	20.397	45.910	1.00	4.57
	ATOM	1364	C	VAL	207	13.917	19.992	49.255	1.00	11.72
10	ATOM	1365	O	VAL	207	13.584	20.909	50.016	1.00	9.00
	ATOM	1366	N	ALA	208	13.291	18.819	49.212	1.00	14.04
	ATOM	1367	CA	ALA	208	12.122	18.523	50.041	1.00	14.67
	ATOM	1368	CB	ALA	208	11.598	17.148	49.702	1.00	14.60
	ATOM	1369	C	ALA	208	12.422	18.615	51.537	1.00	15.41
15	ATOM	1370	O	ALA	208	11.514	18.770	52.362	1.00	14.28
	ATOM	1371	N	THR	209	13.699	18.498	51.879	1.00	13.94
	ATOM	1372	CA	THR	209	14.123	18.591	53.261	1.00	13.05
	ATOM	1373	CB	THR	209	15.567	18.237	53.423	1.00	11.66
	ATOM	1374	OG1	THR	209	15.887	17.177	52.525	1.00	12.70
20	ATOM	1375	CG2	THR	209	15.833	17.807	54.846	1.00	7.92
	ATOM	1376	C	THR	209	14.007	20.041	53.626	1.00	14.97
	ATOM	1377	O	THR	209	13.554	20.401	54.714	1.00	14.80
	ATOM	1378	N	MET	210	14.447	20.885	52.707	1.00	15.34
	ATOM	1379	CA	MET	210	14.363	22.298	52.965	1.00	16.36
25	ATOM	1380	CB	MET	210	15.043	23.091	51.845	1.00	19.89
	ATOM	1381	CG	MET	210	15.119	24.592	52.103	1.00	23.82
	ATOM	1382	SD	MET	210	15.258	25.542	50.561	1.00	29.33
	ATOM	1383	CE	MET	210	13.547	25.995	50.325	1.00	27.80
	ATOM	1384	C	MET	210	12.864	22.592	53.031	1.00	14.33

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	ATOM	1385	O	MET	210	12.332	22.896	54.102	1.00	15.04
	ATOM	1386	N	ILE	211	12.180	22.452	51.898	1.00	11.15
	ATOM	1387	CA	ILE	211	10.743	22.708	51.831	1.00	9.09
	ATOM	1388	CB	ILE	211	10.157	22.122	50.566	1.00	5.39
5	ATOM	1389	CG2	ILE	211	8.748	22.693	50.337	1.00	3.22
	ATOM	1390	CG1	ILE	211	11.111	22.412	49.412	1.00	2.02
	ATOM	1391	CD1	ILE	211	10.580	22.065	48.067	1.00	1.00
	ATOM	1392	C	ILE	211	9.987	22.129	53.022	1.00	10.92
	ATOM	1393	O	ILE	211	9.117	22.781	53.605	1.00	7.92
10	ATOM	1394	N	SER	212	10.319	20.891	53.364	1.00	12.74
	ATOM	1395	CA	SER	212	9.701	20.254	54.489	1.00	15.18
	ATOM	1396	CB	SER	212	10.300	18.880	54.704	1.00	12.84
	ATOM	1397	OG	SER	212	10.216	18.533	56.078	1.00	19.56
	ATOM	1398	C	SER	212	9.918	21.101	55.736	1.00	19.90
15	ATOM	1399	O	SER	212	8.969	21.432	56.435	1.00	21.30
	ATOM	1400	N	CYS	213	11.161	21.476	56.016	1.00	24.22
	ATOM	1401	CA	CYS	213	11.432	22.259	57.219	1.00	28.52
	ATOM	1402	CB	CYS	213	12.934	22.367	57.464	1.00	30.65
	ATOM	1403	SG	CYS	213	13.713	20.766	57.805	1.00	39.09
20	ATOM	1404	C	CYS	213	10.822	23.637	57.168	1.00	29.40
	ATOM	1405	O	CYS	213	10.366	24.150	58.186	1.00	30.64
	ATOM	1406	N	TYR	214	10.816	24.229	55.981	1.00	29.50
	ATOM	1407	CA	TYR	214	10.243	25.548	55.788	1.00	29.27
	ATOM	1408	CB	TYR	214	10.168	25.846	54.292	1.00	31.33
25	ATOM	1409	CG	TYR	214	9.637	27.212	53.985	1.00	33.15
	ATOM	1410	CD1	TYR	214	10.182	28.328	54.594	1.00	36.28
	ATOM	1411	CE1	TYR	214	9.694	29.592	54.341	1.00	39.73
	ATOM	1412	CD2	TYR	214	8.582	27.390	53.100	1.00	35.23
	ATOM	1413	CE2	TYR	214	8.080	28.656	52.833	1.00	39.38

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	ATOM	1414	CZ	TYR 214	8.644	29.758	53.463	1.00	41.11
	ATOM	1415	OH	TYR 214	8.168	31.034	53.241	1.00	43.33
	ATOM	1416	C	TYR 214	8.848	25.649	56.429	1.00	28.57
	ATOM	1417	O	TYR 214	8.561	26.578	57.185	1.00	27.99
5	ATOM	1418	N	TYR 215	7.986	24.685	56.136	1.00	27.91
	ATOM	1419	CA	TYR 215	6.642	24.685	56.691	1.00	27.12
	ATOM	1420	CB	TYR 215	5.922	23.403	56.309	1.00	21.95
	ATOM	1421	CG	TYR 215	5.723	23.235	54.829	1.00	18.06
	ATOM	1422	CD1	TYR 215	6.064	22.048	54.197	1.00	17.25
10	ATOM	1423	CE1	TYR 215	5.835	21.867	52.841	1.00	17.47
	ATOM	1424	CD2	TYR 215	5.152	24.246	54.065	1.00	16.51
	ATOM	1425	CE2	TYR 215	4.917	24.075	52.711	1.00	15.51
	ATOM	1426	CZ	TYR 215	5.257	22.882	52.109	1.00	17.82
	ATOM	1427	OH	TYR 215	4.979	22.681	50.785	1.00	20.98
15	ATOM	1428	C	TYR 215	6.658	24.810	58.201	1.00	30.19
	ATOM	1429	O	TYR 215	5.780	25.438	58.778	1.00	31.10
	ATOM	1430	N	GLU 216	7.640	24.197	58.850	1.00	35.15
	ATOM	1431	CA	GLU 216	7.725	24.278	60.306	1.00	41.19
	ATOM	1432	CB	GLU 216	8.560	23.132	60.876	1.00	44.10
20	ATOM	1433	CG	GLU 216	7.877	21.767	60.887	1.00	52.19
	ATOM	1434	CD	GLU 216	6.579	21.749	61.685	1.00	54.93
	ATOM	1435	OE1	GLU 216	6.491	22.481	62.702	1.00	55.44
	ATOM	1436	OE2	GLU 216	5.658	20.988	61.296	1.00	56.26
	ATOM	1437	C	GLU 216	8.369	25.591	60.707	1.00	43.33
25	ATOM	1438	O	GLU 216	7.787	26.385	61.449	1.00	44.64
	ATOM	1439	N	ASP 217	9.583	25.802	60.209	1.00	44.35
	ATOM	1440	CA	ASP 217	10.357	27.007	60.489	1.00	44.65
	ATOM	1441	CB	ASP 217	11.734	26.623	61.033	1.00	47.71
	ATOM	1442	CG	ASP 217	12.667	27.806	61.136	1.00	50.46

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	ATOM	1443	OD1	ASP	217	13.252	28.205	60.106	1.00	51.95
	ATOM	1444	OD2	ASP	217	12.804	28.346	62.252	1.00	54.06
	ATOM	1445	C	ASP	217	10.514	27.820	59.215	1.00	43.04
	ATOM	1446	O	ASP	217	11.372	27.527	58.385	1.00	44.60
5	ATOM	1447	N	HIS	218	9.691	28.848	59.059	1.00	41.00
	ATOM	1448	CA	HIS	218	9.750	29.671	57.862	1.00	39.42
	ATOM	1449	CB	HIS	218	8.569	30.630	57.826	1.00	40.46
	ATOM	1450	CG	HIS	218	7.261	29.960	58.083	1.00	44.54
	ATOM	1451	CD2	HIS	218	6.652	28.930	57.450	1.00	45.30
10	ATOM	1452	ND1	HIS	218	6.449	30.290	59.147	1.00	47.09
	ATOM	1453	CE1	HIS	218	5.397	29.492	59.161	1.00	45.61
	ATOM	1454	NE2	HIS	218	5.497	28.657	58.142	1.00	46.44
	ATOM	1455	C	HIS	218	11.036	30.452	57.759	1.00	37.69
	ATOM	1456	O	HIS	218	11.120	31.381	56.974	1.00	37.21
15	ATOM	1457	N	GLN	219	12.041	30.076	58.537	1.00	37.38
	ATOM	1458	CA	GLN	219	13.312	30.779	58.494	1.00	38.18
	ATOM	1459	CB	GLN	219	13.727	31.186	59.910	1.00	41.72
	ATOM	1460	CG	GLN	219	14.577	32.451	60.011	1.00	48.69
	ATOM	1461	CD	GLN	219	13.836	33.718	59.546	1.00	55.14
20	ATOM	1462	OE1	GLN	219	12.665	33.945	59.908	1.00	55.89
	ATOM	1463	NE2	GLN	219	14.523	34.555	58.751	1.00	55.41
	ATOM	1464	C	GLN	219	14.348	29.846	57.886	1.00	36.85
	ATOM	1465	O	GLN	219	15.508	30.200	57.735	1.00	37.28
	ATOM	1466	N	CYS	220	13.912	28.647	57.535	1.00	36.02
25	ATOM	1467	CA	CYS	220	14.790	27.646	56.950	1.00	37.10
	ATOM	1468	CB	CYS	220	14.103	26.286	57.043	1.00	38.40
	ATOM	1469	SG	CYS	220	15.067	24.916	56.396	1.00	44.24
	ATOM	1470	C	CYS	220	15.106	27.970	55.486	1.00	37.48
	ATOM	1471	O	CYS	220	14.193	28.081	54.672	1.00	40.52

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	ATOM	1472	N	GLU	221	16.382	28.123	55.137	1.00	36.17
	ATOM	1473	CA	GLU	221	16.742	28.428	53.746	1.00	35.58
	ATOM	1474	CB	GLU	221	17.116	29.911	53.591	1.00	38.60
	ATOM	1475	CG	GLU	221	15.921	30.878	53.645	1.00	42.48
5	ATOM	1476	CD	GLU	221	16.325	32.347	53.760	1.00	42.62
	ATOM	1477	OE1	GLU	221	17.120	32.815	52.909	1.00	42.89
	ATOM	1478	OE2	GLU	221	15.835	33.024	54.700	1.00	40.36
	ATOM	1479	C	GLU	221	17.896	27.566	53.260	1.00	33.89
	ATOM	1480	O	GLU	221	18.498	27.826	52.217	1.00	32.29
10	ATOM	1481	N	VAL	222	18.199	26.525	54.018	1.00	32.57
	ATOM	1482	CA	VAL	222	19.286	25.654	53.645	1.00	31.01
	ATOM	1483	CB	VAL	222	20.548	26.041	54.376	1.00	29.59
	ATOM	1484	CG1	VAL	222	21.673	25.102	53.995	1.00	29.07
	ATOM	1485	CG2	VAL	222	20.895	27.465	54.043	1.00	30.00
15	ATOM	1486	C	VAL	222	18.983	24.214	53.966	1.00	31.75
	ATOM	1487	O	VAL	222	18.872	23.846	55.132	1.00	33.50
	ATOM	1488	N	GLY	223	18.858	23.400	52.925	1.00	31.02
	ATOM	1489	CA	GLY	223	18.575	21.994	53.119	1.00	28.49
	ATOM	1490	C	GLY	223	19.847	21.184	53.026	1.00	26.21
20	ATOM	1491	O	GLY	223	20.757	21.528	52.267	1.00	25.39
	ATOM	1492	N	MET	224	19.911	20.098	53.786	1.00	24.93
	ATOM	1493	CA	MET	224	21.101	19.267	53.774	1.00	24.66
	ATOM	1494	CB	MET	224	22.164	19.958	54.623	1.00	26.07
	ATOM	1495	CG	MET	224	23.584	19.535	54.358	1.00	26.25
25	ATOM	1496	SD	MET	224	24.664	20.375	55.525	1.00	28.76
	ATOM	1497	CE	MET	224	24.493	19.328	56.939	1.00	27.46
	ATOM	1498	C	MET	224	20.867	17.819	54.253	1.00	23.62
	ATOM	1499	O	MET	224	20.243	17.581	55.294	1.00	21.62
	ATOM	1500	N	ILE	225	21.389	16.867	53.478	1.00	21.96



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	ATOM	1501	CA	ILE	225	21.265	15.434	53.764	1.00	21.80
	ATOM	1502	CB	ILE	225	20.514	14.706	52.662	1.00	23.26
	ATOM	1503	CG2	ILE	225	20.389	13.242	53.026	1.00	22.57
	ATOM	1504	CG1	ILE	225	19.142	15.332	52.463	1.00	26.22
5	ATOM	1505	CD1	ILE	225	18.270	15.229	53.688	1.00	30.06
	ATOM	1506	C	ILE	225	22.595	14.702	53.904	1.00	21.76
	ATOM	1507	O	ILE	225	23.204	14.299	52.909	1.00	20.84
	ATOM	1508	N	VAL	226	23.008	14.492	55.146	1.00	22.14
	ATOM	1509	CA	VAL	226	24.263	13.824	55.454	1.00	22.07
10	ATOM	1510	CB	VAL	226	25.031	14.613	56.514	1.00	22.20
	ATOM	1511	CG1	VAL	226	26.321	13.905	56.872	1.00	20.57
	ATOM	1512	CG2	VAL	226	25.283	16.016	56.005	1.00	22.66
	ATOM	1513	C	VAL	226	24.060	12.411	55.972	1.00	22.96
	ATOM	1514	O	VAL	226	24.032	12.172	57.183	1.00	23.79
15	ATOM	1515	N	GLY	227	23.924	11.470	55.054	1.00	23.08
	ATOM	1516	CA	GLY	227	23.738	10.094	55.459	1.00	25.20
	ATOM	1517	C	GLY	227	24.623	9.207	54.621	1.00	25.79
	ATOM	1518	O	GLY	227	25.820	9.447	54.501	1.00	26.18
	ATOM	1519	N	THR	228	24.039	8.181	54.026	1.00	27.28
20	ATOM	1520	CA	THR	228	24.822	7.291	53.200	1.00	29.44
	ATOM	1521	CB	THR	228	23.900	6.356	52.413	1.00	28.91
	ATOM	1522	OG1	THR	228	24.691	5.441	51.650	1.00	27.54
	ATOM	1523	CG2	THR	228	22.983	7.159	51.496	1.00	30.69
	ATOM	1524	C	THR	228	25.705	8.139	52.267	1.00	30.87
25	ATOM	1525	O	THR	228	26.878	7.834	52.072	1.00	32.00
	ATOM	1526	N	GLY	229	25.140	9.216	51.723	1.00	31.23
	ATOM	1527	CA	GLY	229	25.888	10.111	50.855	1.00	30.25
	ATOM	1528	C	GLY	229	25.716	11.501	51.434	1.00	32.12
	ATOM	1529	O	GLY	229	25.139	11.632	52.518	1.00	33.23

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	ATOM	1530	N	CYS 230	26.208	12.535	50.749	1.00	31.95
	ATOM	1531	CA	CYS 230	26.057	13.909	51.247	1.00	31.05
	ATOM	1532	CB	CYS 230	27.344	14.417	51.891	1.00	31.11
	ATOM	1533	SG	CYS 230	27.145	16.090	52.562	1.00	40.64
5	ATOM	1534	C	CYS 230	25.650	14.909	50.183	1.00	29.04
	ATOM	1535	O	CYS 230	26.202	14.913	49.087	1.00	30.85
	ATOM	1536	N	ASN 231	24.701	15.775	50.513	1.00	26.12
	ATOM	1537	CA	ASN 231	24.267	16.773	49.554	1.00	26.17
	ATOM	1538	CB	ASN 231	23.380	16.130	48.505	1.00	24.13
10	ATOM	1539	CG	ASN 231	23.146	17.030	47.341	1.00	24.98
	ATOM	1540	OD1	ASN 231	22.505	18.064	47.463	1.00	24.73
	ATOM	1541	ND2	ASN 231	23.684	16.656	46.196	1.00	29.51
	ATOM	1542	C	ASN 231	23.529	17.927	50.213	1.00	27.77
	ATOM	1543	O	ASN 231	22.929	17.757	51.275	1.00	28.70
15	ATOM	1544	N	ALA 232	23.569	19.103	49.587	1.00	27.44
	ATOM	1545	CA	ALA 232	22.890	20.258	50.158	1.00	26.70
	ATOM	1546	CB	ALA 232	23.806	20.963	51.113	1.00	26.89
	ATOM	1547	C	ALA 232	22.366	21.245	49.144	1.00	26.61
	ATOM	1548	O	ALA 232	22.693	21.184	47.963	1.00	26.44
20	ATOM	1549	N	CYS 233	21.537	22.161	49.617	1.00	27.04
	ATOM	1550	CA	CYS 233	20.976	23.172	48.743	1.00	31.21
	ATOM	1551	CB	CYS 233	19.676	22.666	48.127	1.00	31.60
	ATOM	1552	SG	CYS 233	18.376	22.446	49.348	1.00	35.31
	ATOM	1553	C	CYS 233	20.708	24.408	49.589	1.00	31.98
25	ATOM	1554	O	CYS 233	20.596	24.303	50.809	1.00	32.62
	ATOM	1555	N	TYR 234	20.621	25.572	48.949	1.00	30.70
	ATOM	1556	CA	TYR 234	20.366	26.822	49.660	1.00	30.60
	ATOM	1557	CB	TYR 234	21.684	27.524	50.026	1.00	29.53
	ATOM	1558	CG	TYR 234	22.464	28.011	48.829	1.00	27.41

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	ATOM	1559	CD1	TYR	234	22.363	29.327	48.393	1.00	25.56
	ATOM	1560	CE1	TYR	234	22.981	29.739	47.217	1.00	25.47
	ATOM	1561	CD2	TYR	234	23.218	27.121	48.061	1.00	28.10
	ATOM	1562	CE2	TYR	234	23.838	27.524	46.882	1.00	26.39
5	ATOM	1563	CZ	TYR	234	23.707	28.830	46.462	1.00	25.77
	ATOM	1564	OH	TYR	234	24.240	29.201	45.253	1.00	27.36
	ATOM	1565	C	TYR	234	19.531	27.742	48.797	1.00	32.10
	ATOM	1566	O	TYR	234	19.211	27.411	47.657	1.00	32.79
	ATOM	1567	N	MET	235	19.184	28.897	49.357	1.00	34.08
10	ATOM	1568	CA	MET	235	18.380	29.908	48.679	1.00	34.57
	ATOM	1569	CB	MET	235	17.492	30.617	49.697	1.00	34.74
	ATOM	1570	CG	MET	235	16.489	29.699	50.305	1.00	34.74
	ATOM	1571	SD	MET	235	15.575	28.985	48.959	1.00	35.81
	ATOM	1572	CE	MET	235	14.171	30.092	48.917	1.00	34.50
15	ATOM	1573	C	MET	235	19.270	30.933	48.009	1.00	35.41
	ATOM	1574	O	MET	235	19.631	31.930	48.625	1.00	37.55
	ATOM	1575	N	GLU	236	19.626	30.702	46.753	1.00	35.58
	ATOM	1576	CA	GLU	236	20.487	31.643	46.049	1.00	36.59
	ATOM	1577	CB	GLU	236	21.168	30.949	44.869	1.00	38.16
20	ATOM	1578	CG	GLU	236	22.051	31.861	44.051	1.00	39.44
	ATOM	1579	CD	GLU	236	23.107	32.542	44.890	1.00	41.44
	ATOM	1580	OE1	GLU	236	24.116	31.891	45.240	1.00	40.65
	ATOM	1581	OE2	GLU	236	22.918	33.735	45.208	1.00	42.03
	ATOM	1582	C	GLU	236	19.679	32.838	45.564	1.00	37.02
25	ATOM	1583	O	GLU	236	18.452	32.810	45.580	1.00	38.00
	ATOM	1584	N	GLU	237	20.354	33.898	45.149	1.00	38.75
	ATOM	1585	CA	GLU	237	19.634	35.062	44.668	1.00	41.18
	ATOM	1586	CB	GLU	237	20.482	36.317	44.830	1.00	39.63
	ATOM	1587	CG	GLU	237	20.912	36.579	46.258	1.00	36.10

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	ATOM	1588	CD	GLU 237	19.764	37.022	47.131	1.00	35.20
	ATOM	1589	OE1	GLU 237	19.056	37.971	46.726	1.00	34.49
	ATOM	1590	OE2	GLU 237	19.574	36.434	48.221	1.00	33.72
	ATOM	1591	C	GLU 237	19.307	34.836	43.206	1.00	43.71
5	ATOM	1592	O	GLU 237	20.143	34.351	42.437	1.00	43.65
	ATOM	1593	N	MET 238	18.078	35.172	42.832	1.00	45.47
	ATOM	1594	CA	MET 238	17.625	35.013	41.457	1.00	47.13
	ATOM	1595	CB	MET 238	16.275	35.705	41.275	1.00	47.10
	ATOM	1596	CG	MET 238	15.094	34.875	41.721	1.00	46.82
10	ATOM	1597	SD	MET 238	14.773	33.548	40.554	1.00	45.37
	ATOM	1598	CE	MET 238	13.564	34.332	39.412	1.00	46.47
	ATOM	1599	C	MET 238	18.629	35.589	40.466	1.00	48.34
	ATOM	1600	O	MET 238	18.814	35.061	39.371	1.00	49.97
	ATOM	1601	N	GLN 239	19.280	36.672	40.868	1.00	48.44
15	ATOM	1602	CA	GLN 239	20.252	37.344	40.026	1.00	49.76
	ATOM	1603	CB	GLN 239	20.398	38.794	40.491	1.00	54.00
	ATOM	1604	CG	GLN 239	20.375	38.963	42.007	1.00	58.66
	ATOM	1605	CD	GLN 239	20.056	40.394	42.447	1.00	63.23
	ATOM	1606	OE1	GLN 239	19.660	40.624	43.593	1.00	65.75
20	ATOM	1607	NE2	GLN 239	20.233	41.359	41.540	1.00	63.23
	ATOM	1608	C	GLN 239	21.612	36.665	40.011	1.00	48.87
	ATOM	1609	O	GLN 239	22.611	37.295	39.687	1.00	49.50
	ATOM	1610	N	ASN 240	21.656	35.384	40.354	1.00	47.67
	ATOM	1611	CA	ASN 240	22.926	34.660	40.379	1.00	47.01
25	ATOM	1612	CB	ASN 240	23.301	34.278	41.809	1.00	47.66
	ATOM	1613	CG	ASN 240	24.101	35.347	42.518	1.00	45.71
	ATOM	1614	OD1	ASN 240	23.553	36.328	43.021	1.00	43.88
	ATOM	1615	ND2	ASN 240	25.414	35.159	42.561	1.00	46.64
	ATOM	1616	C	ASN 240	22.861	33.393	39.550	1.00	46.58

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	ATOM	1617	O	ASN 240	23.888	32.840	39.137	1.00	46.44
	ATOM	1618	N	VAL 241	21.643	32.919	39.340	1.00	44.69
	ATOM	1619	CA	VAL 241	21.426	31.717	38.564	1.00	43.22
	ATOM	1620	CB	VAL 241	20.103	31.056	38.948	1.00	43.93
5	ATOM	1621	CG1	VAL 241	20.071	29.643	38.412	1.00	44.87
	ATOM	1622	CG2	VAL 241	19.922	31.091	40.456	1.00	40.98
	ATOM	1623	C	VAL 241	21.358	32.182	37.126	1.00	41.83
	ATOM	1624	O	VAL 241	20.351	32.739	36.685	1.00	42.56
	ATOM	1625	N	GLU 242	22.433	31.974	36.386	1.00	39.79
10	ATOM	1626	CA	GLU 242	22.426	32.440	35.017	1.00	38.35
	ATOM	1627	CB	GLU 242	23.841	32.438	34.435	1.00	41.38
	ATOM	1628	CG	GLU 242	24.874	33.080	35.345	1.00	43.21
	ATOM	1629	CD	GLU 242	26.062	33.639	34.588	1.00	46.65
	ATOM	1630	OE1	GLU 242	26.489	33.026	33.581	1.00	46.29
15	ATOM	1631	OE2	GLU 242	26.581	34.694	35.014	1.00	49.23
	ATOM	1632	C	GLU 242	21.495	31.626	34.144	1.00	34.71
	ATOM	1633	O	GLU 242	21.135	32.057	33.054	1.00	33.08
	ATOM	1634	N	LEU 243	21.085	30.456	34.612	1.00	31.90
	ATOM	1635	CA	LEU 243	20.194	29.652	33.794	1.00	30.72
20	ATOM	1636	CB	LEU 243	20.125	28.214	34.285	1.00	29.40
	ATOM	1637	CG	LEU 243	21.244	27.279	33.833	1.00	28.38
	ATOM	1638	CD1	LEU 243	21.264	27.192	32.321	1.00	23.84
	ATOM	1639	CD2	LEU 243	22.570	27.786	34.381	1.00	31.28
	ATOM	1640	C	LEU 243	18.799	30.222	33.763	1.00	31.18
25	ATOM	1641	O	LEU 243	18.143	30.153	32.729	1.00	32.86
	ATOM	1642	N	VAL 244	18.350	30.779	34.887	1.00	30.11
	ATOM	1643	CA	VAL 244	17.011	31.361	34.979	1.00	30.23
	ATOM	1644	CB	VAL 244	16.549	31.527	36.432	1.00	31.77
	ATOM	1645	CG1	VAL 244	15.085	31.981	36.444	1.00	31.84

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	ATOM	1646	CG2	VAL	244	16.748	30.234	37.213	1.00	31.59
	ATOM	1647	C	VAL	244	16.955	32.746	34.361	1.00	30.94
	ATOM	1648	O	VAL	244	17.919	33.499	34.458	1.00	31.77
	ATOM	1649	N	GLU	245	15.819	33.083	33.753	1.00	32.44
5	ATOM	1650	CA	GLU	245	15.625	34.389	33.125	1.00	36.05
	ATOM	1651	CB	GLU	245	14.384	34.384	32.237	1.00	35.98
	ATOM	1652	CG	GLU	245	14.542	35.203	30.981	1.00	38.72
	ATOM	1653	CD	GLU	245	15.357	34.449	29.959	1.00	41.52
	ATOM	1654	OE1	GLU	245	15.957	33.428	30.356	1.00	40.02
10	ATOM	1655	OE2	GLU	245	15.402	34.859	28.776	1.00	43.26
	ATOM	1656	C	GLU	245	15.453	35.511	34.149	1.00	39.49
	ATOM	1657	O	GLU	245	15.995	36.603	33.978	1.00	39.69
	ATOM	1658	N	GLY	246	14.676	35.239	35.197	1.00	42.62
	ATOM	1659	CA	GLY	246	14.417	36.228	36.233	1.00	44.14
15	ATOM	1660	C	GLY	246	15.642	36.762	36.953	1.00	44.54
	ATOM	1661	O	GLY	246	16.720	36.163	36.906	1.00	43.59
	ATOM	1662	N	ASP	247	15.476	37.896	37.627	1.00	44.51
	ATOM	1663	CA	ASP	247	16.582	38.500	38.345	1.00	45.26
	ATOM	1664	CB	ASP	247	17.179	39.654	37.540	1.00	48.06
20	ATOM	1665	CG	ASP	247	18.102	39.173	36.436	1.00	52.60
	ATOM	1666	OD1	ASP	247	19.016	38.376	36.744	1.00	54.76
	ATOM	1667	OD2	ASP	247	17.923	39.584	35.265	1.00	54.15
	ATOM	1668	C	ASP	247	16.213	38.993	39.720	1.00	44.83
	ATOM	1669	O	ASP	247	17.087	39.306	40.518	1.00	45.80
25	ATOM	1670	N	GLU	248	14.930	39.064	40.022	1.00	44.56
	ATOM	1671	CA	GLU	248	14.561	39.546	41.336	1.00	45.70
	ATOM	1672	CB	GLU	248	13.610	40.727	41.206	1.00	50.66
	ATOM	1673	CG	GLU	248	12.441	40.458	40.298	1.00	60.84
	ATOM	1674	CD	GLU	248	11.394	41.556	40.355	1.00	67.29

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	ATOM	1675	OE1	GLU	248	10.742	41.702	41.414	1.00	69.90
	ATOM	1676	OE2	GLU	248	11.223	42.273	39.340	1.00	71.41
	ATOM	1677	C	GLU	248	13.952	38.482	42.224	1.00	43.15
	ATOM	1678	O	GLU	248	12.986	37.827	41.855	1.00	42.29
5	ATOM	1679	N	GLY	249	14.530	38.315	43.404	1.00	42.35
	ATOM	1680	CA	GLY	249	14.023	37.327	44.330	1.00	42.91
	ATOM	1681	C	GLY	249	15.044	36.247	44.625	1.00	43.93
	ATOM	1682	O	GLY	249	16.177	36.294	44.145	1.00	43.62
	ATOM	1683	N	ARG	250	14.644	35.267	45.427	1.00	43.38
10	ATOM	1684	CA	ARG	250	15.526	34.160	45.781	1.00	41.04
	ATOM	1685	CB	ARG	250	15.819	34.207	47.293	1.00	42.27
	ATOM	1686	CG	ARG	250	14.745	34.934	48.114	1.00	46.82
	ATOM	1687	CD	ARG	250	15.139	35.142	49.584	1.00	51.21
	ATOM	1688	NE	ARG	250	16.425	35.828	49.730	1.00	55.52
15	ATOM	1689	CZ	ARG	250	16.864	36.394	50.855	1.00	55.63
	ATOM	1690	NH1	ARG	250	16.121	36.375	51.956	1.00	55.05
	ATOM	1691	NH2	ARG	250	18.063	36.962	50.885	1.00	54.32
	ATOM	1692	C	ARG	250	14.905	32.812	45.359	1.00	38.25
	ATOM	1693	O	ARG	250	13.681	32.640	45.394	1.00	37.44
20	ATOM	1694	N	MET	251	15.760	31.880	44.932	1.00	33.58
	ATOM	1695	CA	MET	251	15.352	30.543	44.492	1.00	29.34
	ATOM	1696	CB	MET	251	15.326	30.471	42.966	1.00	24.54
	ATOM	1697	CG	MET	251	15.180	29.069	42.379	1.00	17.89
	ATOM	1698	SD	MET	251	14.994	29.090	40.552	1.00	18.23
25	ATOM	1699	CE	MET	251	16.329	28.087	40.075	1.00	12.48
	ATOM	1700	C	MET	251	16.316	29.481	45.004	1.00	30.48
	ATOM	1701	O	MET	251	17.529	29.640	44.895	1.00	31.49
	ATOM	1702	N	CYS	252	15.775	28.392	45.546	1.00	29.56
	ATOM	1703	CA	CYS	252	16.599	27.298	46.059	1.00	26.54

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	ATOM	1704	CB	CYS 252	15.710	26.185	46.612	1.00	27.29
	ATOM	1705	SG	CYS 252	16.613	24.659	46.927	1.00	29.14
	ATOM	1706	C	CYS 252	17.492	26.704	44.975	1.00	23.38
	ATOM	1707	O	CYS 252	17.104	26.639	43.816	1.00	22.79
5	ATOM	1708	N	VAL 253	18.688	26.268	45.349	1.00	20.80
	ATOM	1709	CA	VAL 253	19.584	25.660	44.377	1.00	20.25
	ATOM	1710	CB	VAL 253	20.740	26.583	43.969	1.00	19.02
	ATOM	1711	CG1	VAL 253	21.623	25.881	42.936	1.00	15.42
	ATOM	1712	CG2	VAL 253	20.198	27.866	43.411	1.00	19.77
10	ATOM	1713	C	VAL 253	20.191	24.374	44.900	1.00	22.35
	ATOM	1714	O	VAL 253	20.705	24.305	46.023	1.00	22.21
	ATOM	1715	N	ASN 254	20.127	23.352	44.060	1.00	24.23
	ATOM	1716	CA	ASN 254	20.661	22.045	44.390	1.00	22.10
	ATOM	1717	CB	ASN 254	19.860	20.975	43.647	1.00	21.49
15	ATOM	1718	CG	ASN 254	20.479	19.604	43.747	1.00	22.93
	ATOM	1719	OD1	ASN 254	21.074	19.232	44.764	1.00	20.03
	ATOM	1720	ND2	ASN 254	20.325	18.827	42.687	1.00	26.40
	ATOM	1721	C	ASN 254	22.124	22.046	43.975	1.00	19.26
	ATOM	1722	O	ASN 254	22.454	22.155	42.795	1.00	15.88
20	ATOM	1723	N	THR 255	23.001	21.949	44.961	1.00	15.23
	ATOM	1724	CA	THR 255	24.428	21.962	44.691	1.00	15.03
	ATOM	1725	CB	THR 255	25.193	22.217	45.944	1.00	13.56
	ATOM	1726	OG1	THR 255	25.035	21.087	46.808	1.00	14.56
	ATOM	1727	CG2	THR 255	24.670	23.458	46.617	1.00	14.18
25	ATOM	1728	C	THR 255	24.957	20.665	44.127	1.00	15.21
	ATOM	1729	O	THR 255	25.675	20.647	43.126	1.00	12.07
	ATOM	1730	N	GLU 256	24.594	19.570	44.777	1.00	18.83
	ATOM	1731	CA	GLU 256	25.076	18.268	44.355	1.00	22.28
	ATOM	1732	CB	GLU 256	24.795	18.025	42.876	1.00	25.93



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	ATOM	1733	CG	GLU 256	23.377	18.345	42.454	1.00	31.90
	ATOM	1734	CD	GLU 256	22.500	17.121	42.336	1.00	34.74
	ATOM	1735	OE1	GLU 256	22.191	16.510	43.386	1.00	36.97
	ATOM	1736	OE2	GLU 256	22.122	16.777	41.188	1.00	35.26
5	ATOM	1737	C	GLU 256	26.562	18.402	44.559	1.00	21.32
	ATOM	1738	O	GLU 256	27.359	18.032	43.701	1.00	23.09
	ATOM	1739	N	TRP 257	26.931	18.966	45.699	1.00	17.36
	ATOM	1740	CA	TRP 257	28.327	19.141	45.985	1.00	14.83
	ATOM	1741	CB	TRP 257	28.514	20.074	47.176	1.00	11.59
10	ATOM	1742	CG	TRP 257	28.038	19.561	48.478	1.00	8.69
	ATOM	1743	CD2	TRP 257	27.830	20.332	49.676	1.00	9.05
	ATOM	1744	CE2	TRP 257	27.562	19.410	50.715	1.00	7.00
	ATOM	1745	CE3	TRP 257	27.845	21.703	49.964	1.00	7.18
	ATOM	1746	CD1	TRP 257	27.881	18.265	48.827	1.00	7.58
15	ATOM	1747	NE1	TRP 257	27.602	18.163	50.172	1.00	7.99
	ATOM	1748	CZ2	TRP 257	27.325	19.818	52.038	1.00	4.73
	ATOM	1749	CZ3	TRP 257	27.605	22.108	51.280	1.00	7.12
	ATOM	1750	CH2	TRP 257	27.346	21.164	52.300	1.00	5.47
	ATOM	1751	C	TRP 257	29.033	17.813	46.224	1.00	17.81
20	ATOM	1752	O	TRP 257	30.221	17.776	46.523	1.00	19.44
	ATOM	1753	N	GLY 258	28.318	16.708	46.099	1.00	21.88
	ATOM	1754	CA	GLY 258	28.991	15.444	46.303	1.00	23.25
	ATOM	1755	C	GLY 258	30.137	15.303	45.316	1.00	23.01
	ATOM	1756	O	GLY 258	31.133	14.629	45.600	1.00	21.92
25	ATOM	1757	N	ALA 259	29.997	15.943	44.156	1.00	23.11
	ATOM	1758	CA	ALA 259	31.015	15.863	43.113	1.00	27.74
	ATOM	1759	CB	ALA 259	30.400	16.139	41.766	1.00	27.03
	ATOM	1760	C	ALA 259	32.176	16.806	43.335	1.00	30.23
	ATOM	1761	O	ALA 259	33.178	16.748	42.622	1.00	32.12

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	ATOM	1762	N	PHE 260	32.041	17.680	44.320	1.00	32.43
	ATOM	1763	CA	PHE 260	33.093	18.627	44.611	1.00	36.43
	ATOM	1764	CB	PHE 260	32.804	19.343	45.924	1.00	39.42
	ATOM	1765	CG	PHE 260	33.932	20.206	46.411	1.00	43.92
5	ATOM	1766	CD1	PHE 260	34.660	21.003	45.534	1.00	46.49
	ATOM	1767	CD2	PHE 260	34.232	20.263	47.765	1.00	45.64
	ATOM	1768	CE1	PHE 260	35.672	21.835	46.002	1.00	47.73
	ATOM	1769	CE2	PHE 260	35.242	21.093	48.242	1.00	46.62
	ATOM	1770	CZ	PHE 260	35.958	21.882	47.360	1.00	47.27
10	ATOM	1771	C	PHE 260	34.412	17.897	44.695	1.00	39.39
	ATOM	1772	O	PHE 260	34.495	16.800	45.243	1.00	40.20
	ATOM	1773	N	GLY 261	35.441	18.511	44.127	1.00	41.71
	ATOM	1774	CA	GLY 261	36.753	17.911	44.152	1.00	43.62
	ATOM	1775	C	GLY 261	36.967	16.857	43.090	1.00	44.99
15	ATOM	1776	O	GLY 261	38.049	16.282	43.015	1.00	47.22
	ATOM	1777	N	ASP 262	35.961	16.578	42.270	1.00	46.06
	ATOM	1778	CA	ASP 262	36.143	15.574	41.229	1.00	47.68
	ATOM	1779	CB	ASP 262	34.800	15.197	40.602	1.00	50.82
	ATOM	1780	CG	ASP 262	34.024	14.187	41.445	1.00	53.64
20	ATOM	1781	OD1	ASP 262	32.815	13.996	41.191	1.00	54.63
	ATOM	1782	OD2	ASP 262	34.624	13.578	42.356	1.00	54.71
	ATOM	1783	C	ASP 262	37.089	16.129	40.177	1.00	47.19
	ATOM	1784	O	ASP 262	37.539	15.400	39.292	1.00	47.09
	ATOM	1785	N	SER 263	37.380	17.427	40.298	1.00	46.38
25	ATOM	1786	CA	SER 263	38.289	18.147	39.401	1.00	44.53
	ATOM	1787	CB	SER 263	37.651	19.445	38.903	1.00	43.57
	ATOM	1788	OG	SER 263	36.341	19.246	38.415	1.00	43.79
	ATOM	1789	C	SER 263	39.552	18.513	40.174	1.00	43.93
	ATOM	1790	O	SER 263	40.061	19.632	40.059	1.00	44.40

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	ATOM	1791	N	GLY 264	40.039	17.577	40.979	1.00	43.71
	ATOM	1792	CA	GLY 264	41.235	17.825	41.762	1.00	42.64
	ATOM	1793	C	GLY 264	41.133	18.889	42.845	1.00	40.75
	ATOM	1794	O	GLY 264	42.052	19.012	43.648	1.00	42.90
5	ATOM	1795	N	GLU 265	40.040	19.647	42.887	1.00	38.43
	ATOM	1796	CA	GLU 265	39.881	20.700	43.893	1.00	37.42
	ATOM	1797	CB	GLU 265	38.437	21.227	43.907	1.00	39.11
	ATOM	1798	CG	GLU 265	37.986	21.928	42.632	1.00	40.76
	ATOM	1799	CD	GLU 265	37.198	21.023	41.701	1.00	43.56
10	ATOM	1800	OE1	GLU 265	36.904	21.461	40.565	1.00	45.26
	ATOM	1801	OE2	GLU 265	36.863	19.883	42.099	1.00	42.42
	ATOM	1802	C	GLU 265	40.266	20.299	45.321	1.00	36.38
	ATOM	1803	O	GLU 265	40.410	21.160	46.185	1.00	33.59
	ATOM	1804	N	LEU 266	40.425	19.004	45.573	1.00	37.71
15	ATOM	1805	CA	LEU 266	40.783	18.534	46.912	1.00	40.56
	ATOM	1806	CB	LEU 266	39.597	17.831	47.567	1.00	40.03
	ATOM	1807	CG	LEU 266	38.371	18.631	48.001	1.00	40.79
	ATOM	1808	CD1	LEU 266	37.234	17.673	48.259	1.00	40.27
	ATOM	1809	CD2	LEU 266	38.677	19.432	49.253	1.00	41.81
20	ATOM	1810	C	LEU 266	41.949	17.563	46.880	1.00	43.51
	ATOM	1811	O	LEU 266	42.363	17.045	47.919	1.00	43.63
	ATOM	1812	N	ASP 267	42.475	17.324	45.682	1.00	47.00
	ATOM	1813	CA	ASP 267	43.584	16.393	45.480	1.00	48.18
	ATOM	1814	CB	ASP 267	44.222	16.622	44.097	1.00	50.89
25	ATOM	1815	CG	ASP 267	44.982	15.391	43.584	1.00	54.98
	ATOM	1816	OD1	ASP 267	45.239	15.317	42.360	1.00	56.65
	ATOM	1817	OD2	ASP 267	45.328	14.499	44.398	1.00	55.43
	ATOM	1818	C	ASP 267	44.659	16.440	46.571	1.00	46.46
	ATOM	1819	O	ASP 267	45.205	15.397	46.960	1.00	45.37

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	ATOM	1820	N	GLU 268	44.957	17.630	47.084	1.00	44.63
	ATOM	1821	CA	GLU 268	45.990	17.721	48.109	1.00	44.67
	ATOM	1822	CB	GLU 268	46.805	19.024	47.956	1.00	44.68
	ATOM	1823	CG	GLU 268	46.508	20.163	48.934	1.00	43.60
5	ATOM	1824	CD	GLU 268	45.234	20.915	48.613	1.00	43.53
	ATOM	1825	OE1	GLU 268	45.020	21.258	47.423	1.00	42.43
	ATOM	1826	OE2	GLU 268	44.461	21.174	49.561	1.00	40.84
	ATOM	1827	C	GLU 268	45.457	17.569	49.528	1.00	43.45
	ATOM	1828	O	GLU 268	46.102	17.961	50.499	1.00	46.29
10	ATOM	1829	N	PHE 269	44.286	16.971	49.656	1.00	38.78
	ATOM	1830	CA	PHE 269	43.729	16.785	50.974	1.00	33.75
	ATOM	1831	CB	PHE 269	42.480	17.614	51.135	1.00	33.69
	ATOM	1832	CG	PHE 269	42.733	18.990	51.639	1.00	34.75
	ATOM	1833	CD1	PHE 269	43.435	19.193	52.822	1.00	36.51
15	ATOM	1834	CD2	PHE 269	42.161	20.079	51.001	1.00	34.78
	ATOM	1835	CE1	PHE 269	43.548	20.469	53.365	1.00	37.39
	ATOM	1836	CE2	PHE 269	42.266	21.354	51.532	1.00	35.15
	ATOM	1837	CZ	PHE 269	42.955	21.551	52.717	1.00	37.68
	ATOM	1838	C	PHE 269	43.405	15.343	51.225	1.00	32.83
20	ATOM	1839	O	PHE 269	43.206	14.952	52.365	1.00	31.85
	ATOM	1840	N	LEU 270	43.355	14.555	50.157	1.00	33.85
	ATOM	1841	CA	LEU 270	43.046	13.130	50.259	1.00	34.53
	ATOM	1842	CB	LEU 270	42.712	12.553	48.884	1.00	35.63
	ATOM	1843	CG	LEU 270	41.326	12.857	48.321	1.00	37.61
25	ATOM	1844	CD1	LEU 270	41.323	14.293	47.842	1.00	35.85
	ATOM	1845	CD2	LEU 270	40.966	11.878	47.177	1.00	37.50
	ATOM	1846	C	LEU 270	44.172	12.298	50.845	1.00	33.68
	ATOM	1847	O	LEU 270	45.334	12.640	50.695	1.00	35.64
	ATOM	1848	N	LEU 271	43.829	11.200	51.507	1.00	33.66

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	ATOM	1849	CA	LEU 271	44.850	10.324	52.059	1.00	34.55
	ATOM	1850	CB	LEU 271	44.610	10.032	53.519	1.00	30.63
	ATOM	1851	CG	LEU 271	44.870	11.238	54.383	1.00	29.49
	ATOM	1852	CD1	LEU 271	43.855	12.324	54.075	1.00	27.82
5	ATOM	1853	CD2	LEU 271	44.783	10.798	55.824	1.00	31.04
	ATOM	1854	C	LEU 271	44.884	9.010	51.324	1.00	37.04
	ATOM	1855	O	LEU 271	44.009	8.715	50.513	1.00	36.79
	ATOM	1856	N	GLU 272	45.890	8.209	51.638	1.00	40.66
	ATOM	1857	CA	GLU 272	46.052	6.927	50.989	1.00	44.99
10	ATOM	1858	CB	GLU 272	47.256	6.182	51.590	1.00	51.18
	ATOM	1859	CG	GLU 272	47.124	5.781	53.075	1.00	58.46
	ATOM	1860	CD	GLU 272	48.371	5.077	53.641	1.00	62.56
	ATOM	1861	OE1	GLU 272	49.393	5.772	53.876	1.00	64.96
	ATOM	1862	OE2	GLU 272	48.325	3.835	53.849	1.00	61.73
15	ATOM	1863	C	GLU 272	44.789	6.080	51.092	1.00	44.62
	ATOM	1864	O	GLU 272	44.377	5.452	50.116	1.00	44.50
	ATOM	1865	N	TYR 273	44.163	6.079	52.266	1.00	43.42
	ATOM	1866	CA	TYR 273	42.955	5.284	52.486	1.00	40.23
	ATOM	1867	CB	TYR 273	42.537	5.377	53.958	1.00	38.82
20	ATOM	1868	CG	TYR 273	43.709	5.401	54.923	1.00	36.38
	ATOM	1869	CD1	TYR 273	44.126	6.602	55.505	1.00	35.57
	ATOM	1870	CE1	TYR 273	45.210	6.647	56.380	1.00	34.95
	ATOM	1871	CD2	TYR 273	44.413	4.231	55.243	1.00	35.34
	ATOM	1872	CE2	TYR 273	45.509	4.264	56.122	1.00	34.05
25	ATOM	1873	CZ	TYR 273	45.897	5.481	56.685	1.00	34.66
	ATOM	1874	OH	TYR 273	46.966	5.556	57.550	1.00	33.77
	ATOM	1875	C	TYR 273	41.826	5.749	51.567	1.00	38.50
	ATOM	1876	O	TYR 273	41.264	4.967	50.804	1.00	35.21
	ATOM	1877	N	ASP 274	41.507	7.030	51.638	1.00	38.17

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	ATOM	1878	CA	ASP 274	40.473	7.579	50.796	1.00	40.03
	ATOM	1879	CB	ASP 274	40.470	9.083	50.929	1.00	41.17
	ATOM	1880	CG	ASP 274	40.252	9.512	52.341	1.00	43.77
	ATOM	1881	OD1	ASP 274	39.123	9.327	52.839	1.00	46.59
5	ATOM	1882	OD2	ASP 274	41.212	10.010	52.958	1.00	44.41
	ATOM	1883	C	ASP 274	40.740	7.200	49.359	1.00	40.92
	ATOM	1884	O	ASP 274	39.819	6.937	48.595	1.00	41.41
	ATOM	1885	N	ARG 275	42.007	7.160	48.984	1.00	42.93
	ATOM	1886	CA	ARG 275	42.333	6.819	47.613	1.00	45.81
10	ATOM	1887	CB	ARG 275	43.831	6.993	47.365	1.00	49.53
	ATOM	1888	CG	ARG 275	44.191	7.563	45.995	1.00	53.24
	ATOM	1889	CD	ARG 275	45.702	7.772	45.886	1.00	58.85
	ATOM	1890	NE	ARG 275	46.213	8.663	46.933	1.00	62.67
	ATOM	1891	CZ	ARG 275	47.088	8.308	47.876	1.00	62.82
15	ATOM	1892	NH1	ARG 275	47.571	7.068	47.922	1.00	61.28
	ATOM	1893	NH2	ARG 275	47.476	9.201	48.777	1.00	61.64
	ATOM	1894	C	ARG 275	41.901	5.390	47.316	1.00	46.01
	ATOM	1895	O	ARG 275	41.134	5.160	46.382	1.00	45.19
	ATOM	1896	N	LEU 276	42.382	4.437	48.113	1.00	47.51
20	ATOM	1897	CA	LEU 276	42.026	3.030	47.922	1.00	48.68
	ATOM	1898	CB	LEU 276	42.460	2.197	49.134	1.00	45.63
	ATOM	1899	CG	LEU 276	43.971	1.999	49.287	1.00	43.28
	ATOM	1900	CD1	LEU 276	44.418	2.379	50.686	1.00	42.53
	ATOM	1901	CD2	LEU 276	44.321	0.557	48.994	1.00	42.97
25	ATOM	1902	C	LEU 276	40.520	2.915	47.718	1.00	51.24
	ATOM	1903	O	LEU 276	40.050	2.133	46.891	1.00	52.38
	ATOM	1904	N	VAL 277	39.772	3.710	48.475	1.00	53.11
	ATOM	1905	CA	VAL 277	38.321	3.722	48.372	1.00	54.05
	ATOM	1906	CB	VAL 277	37.703	4.640	49.423	1.00	52.84

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	ATOM	1907	CG1	VAL 277	36.210	4.682	49.249	1.00	52.71
	ATOM	1908	CG2	VAL 277	38.069	4.156	50.804	1.00	54.87
	ATOM	1909	C	VAL 277	37.906	4.231	46.999	1.00	55.80
	ATOM	1910	O	VAL 277	37.381	3.474	46.185	1.00	57.15
5	ATOM	1911	N	ASP 278	38.146	5.518	46.754	1.00	56.71
	ATOM	1912	CA	ASP 278	37.804	6.146	45.481	1.00	57.65
	ATOM	1913	CB	ASP 278	38.479	7.514	45.353	1.00	59.73
	ATOM	1914	CG	ASP 278	38.243	8.163	43.989	1.00	61.93
	ATOM	1915	OD1	ASP 278	38.990	9.110	43.642	1.00	61.47
10	ATOM	1916	OD2	ASP 278	37.308	7.733	43.273	1.00	62.11
	ATOM	1917	C	ASP 278	38.263	5.281	44.328	1.00	58.14
	ATOM	1918	O	ASP 278	37.645	5.271	43.266	1.00	58.75
	ATOM	1919	N	GLU 279	39.358	4.563	44.538	1.00	58.33
	ATOM	1920	CA	GLU 279	39.900	3.710	43.498	1.00	59.14
15	ATOM	1921	CB	GLU 279	41.437	3.808	43.477	1.00	60.99
	ATOM	1922	CG	GLU 279	41.978	5.219	43.178	1.00	61.92
	ATOM	1923	CD	GLU 279	43.497	5.276	43.014	1.00	60.92
	ATOM	1924	OE1	GLU 279	44.219	4.874	43.953	1.00	60.85
	ATOM	1925	OE2	GLU 279	43.965	5.733	41.946	1.00	58.99
20	ATOM	1926	C	GLU 279	39.467	2.261	43.664	1.00	58.04
	ATOM	1927	O	GLU 279	40.196	1.346	43.298	1.00	59.38
	ATOM	1928	N	SER 280	38.283	2.044	44.219	1.00	57.21
	ATOM	1929	CA	SER 280	37.798	0.679	44.390	1.00	56.55
	ATOM	1930	CB	SER 280	38.283	0.091	45.719	1.00	56.66
25	ATOM	1931	OG	SER 280	38.015	-1.298	45.774	1.00	54.41
	ATOM	1932	C	SER 280	36.282	0.671	44.334	1.00	55.29
	ATOM	1933	O	SER 280	35.640	-0.371	44.472	1.00	53.68
	ATOM	1934	N	SER 281	35.725	1.854	44.113	1.00	54.58
	ATOM	1935	CA	SER 281	34.288	2.038	44.020	1.00	55.36

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	ATOM	1936	CB	SER 281	33.919	3.451	44.464	1.00	56.89
	ATOM	1937	OG	SER 281	34.565	4.415	43.649	1.00	56.89
	ATOM	1938	C	SER 281	33.843	1.832	42.584	1.00	54.80
	ATOM	1939	O	SER 281	34.652	1.905	41.664	1.00	55.85
5	ATOM	1940	N	ALA 282	32.553	1.587	42.389	1.00	53.75
	ATOM	1941	CA	ALA 282	32.025	1.379	41.050	1.00	52.42
	ATOM	1942	CB	ALA 282	30.626	0.809	41.133	1.00	52.26
	ATOM	1943	C	ALA 282	32.012	2.679	40.250	1.00	51.83
	ATOM	1944	O	ALA 282	31.632	2.685	39.081	1.00	52.27
10	ATOM	1945	N	ASN 283	32.441	3.772	40.879	1.00	50.19
	ATOM	1946	CA	ASN 283	32.465	5.089	40.239	1.00	47.37
	ATOM	1947	CB	ASN 283	31.338	5.945	40.790	1.00	47.04
	ATOM	1948	CG	ASN 283	31.482	6.191	42.276	1.00	47.38
	ATOM	1949	OD1	ASN 283	31.584	5.255	43.068	1.00	46.86
15	ATOM	1950	ND2	ASN 283	31.497	7.455	42.662	1.00	49.96
	ATOM	1951	C	ASN 283	33.777	5.806	40.513	1.00	46.64
	ATOM	1952	O	ASN 283	33.783	6.894	41.081	1.00	48.74
	ATOM	1953	N	PRO 284	34.905	5.214	40.110	1.00	45.15
	ATOM	1954	CD	PRO 284	35.028	3.896	39.462	1.00	44.41
20	ATOM	1955	CA	PRO 284	36.227	5.814	40.327	1.00	43.24
	ATOM	1956	CB	PRO 284	37.151	4.855	39.583	1.00	44.66
	ATOM	1957	CG	PRO 284	36.459	3.532	39.756	1.00	44.93
	ATOM	1958	C	PRO 284	36.389	7.267	39.856	1.00	41.14
	ATOM	1959	O	PRO 284	35.978	7.624	38.755	1.00	40.17
25	ATOM	1960	N	GLY 285	36.994	8.099	40.695	1.00	39.45
	ATOM	1961	CA	GLY 285	37.208	9.484	40.321	1.00	40.34
	ATOM	1962	C	GLY 285	35.964	10.343	40.401	1.00	42.06
	ATOM	1963	O	GLY 285	36.035	11.576	40.367	1.00	43.11
	ATOM	1964	N	GLN 286	34.811	9.699	40.510	1.00	42.34



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	ATOM	1965	CA	GLN 286	33.555	10.427	40.601	1.00	41.88
	ATOM	1966	CB	GLN 286	32.490	9.717	39.758	1.00	44.97
	ATOM	1967	CG	GLN 286	31.973	10.544	38.588	1.00	49.89
	ATOM	1968	CD	GLN 286	31.043	11.668	39.043	1.00	54.72
5	ATOM	1969	OE1	GLN 286	29.911	11.419	39.483	1.00	56.09
	ATOM	1970	NE2	GLN 286	31.519	12.911	38.950	1.00	54.20
	ATOM	1971	C	GLN 286	33.113	10.541	42.063	1.00	40.59
	ATOM	1972	O	GLN 286	33.396	9.660	42.879	1.00	39.39
	ATOM	1973	N	GLN 287	32.445	11.648	42.389	1.00	39.59
10	ATOM	1974	CA	GLN 287	31.939	11.913	43.741	1.00	38.06
	ATOM	1975	CB	GLN 287	30.770	10.969	44.053	1.00	37.29
	ATOM	1976	CG	GLN 287	29.732	10.837	42.939	1.00	35.04
	ATOM	1977	CD	GLN 287	28.912	12.100	42.736	1.00	33.74
	ATOM	1978	OE1	GLN 287	28.906	12.692	41.647	1.00	28.89
15	ATOM	1979	NE2	GLN 287	28.204	12.514	43.786	1.00	31.49
	ATOM	1980	C	GLN 287	33.015	11.744	44.820	1.00	37.30
	ATOM	1981	O	GLN 287	32.958	10.813	45.624	1.00	37.53
	ATOM	1982	N	LEU 288	33.990	12.643	44.856	1.00	34.03
	ATOM	1983	CA	LEU 288	35.051	12.516	45.844	1.00	29.84
20	ATOM	1984	CB	LEU 288	36.351	13.071	45.293	1.00	30.50
	ATOM	1985	CG	LEU 288	37.285	11.960	44.819	1.00	32.69
	ATOM	1986	CD1	LEU 288	36.645	11.102	43.728	1.00	31.90
	ATOM	1987	CD2	LEU 288	38.546	12.611	44.323	1.00	36.00
	ATOM	1988	C	LEU 288	34.729	13.180	47.156	1.00	26.53
25	ATOM	1989	O	LEU 288	34.991	12.627	48.218	1.00	26.76
	ATOM	1990	N	TYR 289	34.172	14.374	47.086	1.00	23.58
	ATOM	1991	CA	TYR 289	33.809	15.074	48.292	1.00	22.36
	ATOM	1992	CB	TYR 289	33.086	16.365	47.939	1.00	20.16
	ATOM	1993	CG	TYR 289	32.716	17.186	49.136	1.00	18.61

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	ATOM	1994	CD1	TYR	289	33.660	17.486	50.105	1.00	18.65
	ATOM	1995	CE1	TYR	289	33.347	18.269	51.195	1.00	18.34
	ATOM	1996	CD2	TYR	289	31.433	17.693	49.288	1.00	18.91
	ATOM	1997	CE2	TYR	289	31.105	18.484	50.378	1.00	18.97
5	ATOM	1998	CZ	TYR	289	32.073	18.768	51.327	1.00	20.15
	ATOM	1999	OH	TYR	289	31.788	19.565	52.408	1.00	22.93
	ATOM	2000	C	TYR	289	32.894	14.165	49.105	1.00	25.30
	ATOM	2001	O	TYR	289	32.991	14.106	50.337	1.00	24.21
	ATOM	2002	N	GLU	290	32.005	13.448	48.411	1.00	27.35
10	ATOM	2003	CA	GLU	290	31.071	12.532	49.084	1.00	26.68
	ATOM	2004	CB	GLU	290	30.081	11.904	48.090	1.00	26.17
	ATOM	2005	CG	GLU	290	28.614	12.216	48.413	1.00	25.68
	ATOM	2006	CD	GLU	290	27.617	11.404	47.591	1.00	26.93
	ATOM	2007	OE1	GLU	290	27.735	11.363	46.337	1.00	22.27
15	ATOM	2008	OE2	GLU	290	26.702	10.815	48.215	1.00	27.37
	ATOM	2009	C	GLU	290	31.838	11.425	49.781	1.00	25.75
	ATOM	2010	O	GLU	290	31.649	11.193	50.974	1.00	26.23
	ATOM	2011	N	LYS	291	32.706	10.756	49.024	1.00	24.16
	ATOM	2012	CA	LYS	291	33.526	9.666	49.538	1.00	24.45
20	ATOM	2013	CB	LYS	291	34.342	9.063	48.408	1.00	24.19
	ATOM	2014	CG	LYS	291	33.506	8.383	47.354	1.00	28.37
	ATOM	2015	CD	LYS	291	34.322	8.162	46.094	1.00	31.52
	ATOM	2016	CE	LYS	291	33.533	7.434	45.030	1.00	31.16
	ATOM	2017	NZ	LYS	291	34.367	7.299	43.813	1.00	33.55
25	ATOM	2018	C	LYS	291	34.460	10.143	50.636	1.00	24.99
	ATOM	2019	O	LYS	291	35.488	9.522	50.918	1.00	25.78
	ATOM	2020	N	LEU	292	34.095	11.254	51.255	1.00	24.20
	ATOM	2021	CA	LEU	292	34.894	11.809	52.318	1.00	25.20
	ATOM	2022	CB	LEU	292	35.544	13.106	51.843	1.00	25.62

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	ATOM	2023	CG	LEU	292	36.904	13.450	52.464	1.00	26.59
	ATOM	2024	CD1	LEU	292	37.935	12.396	52.035	1.00	26.37
	ATOM	2025	CD2	LEU	292	37.343	14.853	52.025	1.00	24.08
	ATOM	2026	C	LEU	292	33.999	12.063	53.528	1.00	26.58
5	ATOM	2027	O	LEU	292	34.431	11.924	54.671	1.00	27.91
	ATOM	2028	N	ILE	293	32.744	12.421	53.272	1.00	27.03
	ATOM	2029	CA	ILE	293	31.783	12.689	54.342	1.00	26.01
	ATOM	2030	CB	ILE	293	30.948	13.956	54.019	1.00	26.42
	ATOM	2031	CG2	ILE	293	30.184	14.431	55.247	1.00	25.08
10	ATOM	2032	CG1	ILE	293	31.866	15.085	53.573	1.00	24.53
	ATOM	2033	CD1	ILE	293	31.131	16.366	53.336	1.00	23.77
	ATOM	2034	C	ILE	293	30.827	11.503	54.489	1.00	24.65
	ATOM	2035	O	ILE	293	30.681	10.919	55.565	1.00	23.84
	ATOM	2036	N	GLY	294	30.197	11.159	53.374	1.00	24.02
15	ATOM	2037	CA	GLY	294	29.237	10.073	53.325	1.00	25.49
	ATOM	2038	C	GLY	294	29.454	8.815	54.142	1.00	24.75
	ATOM	2039	O	GLY	294	30.427	8.079	53.953	1.00	26.25
	ATOM	2040	N	GLY	295	28.517	8.556	55.044	1.00	22.54
	ATOM	2041	CA	GLY	295	28.607	7.369	55.851	1.00	22.80
20	ATOM	2042	C	GLY	295	28.530	6.125	54.986	1.00	25.08
	ATOM	2043	O	GLY	295	28.252	5.047	55.497	1.00	27.80
	ATOM	2044	N	LYS	296	28.748	6.238	53.680	1.00	25.43
	ATOM	2045	CA	LYS	296	28.696	5.039	52.849	1.00	25.87
	ATOM	2046	CB	LYS	296	28.313	5.354	51.411	1.00	27.04
25	ATOM	2047	CG	LYS	296	28.036	4.096	50.587	1.00	30.40
	ATOM	2048	CD	LYS	296	29.249	3.562	49.842	1.00	30.20
	ATOM	2049	CE	LYS	296	28.954	2.204	49.176	1.00	32.59
	ATOM	2050	NZ	LYS	296	29.015	1.038	50.135	1.00	32.31
	ATOM	2051	C	LYS	296	30.044	4.364	52.828	1.00	28.34

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	ATOM	2052	O	LYS 296	30.158	3.185	52.507	1.00	29.08
	ATOM	2053	N	TYR 297	31.075	5.122	53.163	1.00	29.56
	ATOM	2054	CA	TYR 297	32.414	4.582	53.147	1.00	29.25
	ATOM	2055	CB	TYR 297	33.208	5.230	52.022	1.00	30.07
5	ATOM	2056	CG	TYR 297	32.620	5.025	50.650	1.00	30.84
	ATOM	2057	CD1	TYR 297	32.023	6.082	49.960	1.00	32.45
	ATOM	2058	CE1	TYR 297	31.544	5.915	48.665	1.00	35.21
	ATOM	2059	CD2	TYR 297	32.715	3.789	50.015	1.00	30.51
	ATOM	2060	CE2	TYR 297	32.244	3.604	48.724	1.00	34.82
10	ATOM	2061	CZ	TYR 297	31.661	4.673	48.049	1.00	37.82
	ATOM	2062	OH	TYR 297	31.219	4.504	46.753	1.00	41.74
	ATOM	2063	C	TYR 297	33.097	4.842	54.465	1.00	27.53
	ATOM	2064	O	TYR 297	34.174	4.312	54.731	1.00	28.35
	ATOM	2065	N	MET 298	32.464	5.665	55.288	1.00	24.45
15	ATOM	2066	CA	MET 298	33.025	6.000	56.580	1.00	23.96
	ATOM	2067	CB	MET 298	31.959	6.652	57.454	1.00	21.69
	ATOM	2068	CG	MET 298	32.436	6.992	58.850	1.00	20.73
	ATOM	2069	SD	MET 298	31.288	8.100	59.701	1.00	20.68
	ATOM	2070	CE	MET 298	31.435	9.523	58.620	1.00	18.32
20	ATOM	2071	C	MET 298	33.579	4.750	57.254	1.00	24.25
	ATOM	2072	O	MET 298	34.776	4.656	57.529	1.00	24.74
	ATOM	2073	N	GLY 299	32.707	3.779	57.494	1.00	26.72
	ATOM	2074	CA	GLY 299	33.135	2.552	58.135	1.00	25.77
	ATOM	2075	C	GLY 299	34.301	1.906	57.424	1.00	25.50
25	ATOM	2076	O	GLY 299	35.162	1.331	58.076	1.00	26.16
	ATOM	2077	N	GLU 300	34.325	2.004	56.095	1.00	25.37
	ATOM	2078	CA	GLU 300	35.389	1.418	55.282	1.00	24.57
	ATOM	2079	CB	GLU 300	35.057	1.551	53.800	1.00	24.05
	ATOM	2080	CG	GLU 300	36.066	0.859	52.905	1.00	24.66

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	ATOM	2081	CD	GLU 300	36.018	-0.662	53.004	1.00	24.52
	ATOM	2082	OE1	GLU 300	35.581	-1.195	54.054	1.00	24.02
	ATOM	2083	OE2	GLU 300	36.438	-1.319	52.026	1.00	22.70
	ATOM	2084	C	GLU 300	36.734	2.082	55.550	1.00	25.31
5	ATOM	2085	O	GLU 300	37.769	1.408	55.663	1.00	22.71
	ATOM	2086	N	LEU 301	36.712	3.409	55.622	1.00	26.47
	ATOM	2087	CA	LEU 301	37.919	4.174	55.900	1.00	26.65
	ATOM	2088	CB	LEU 301	37.600	5.676	55.992	1.00	26.57
	ATOM	2089	CG	LEU 301	37.165	6.395	54.701	1.00	26.02
10	ATOM	2090	CD1	LEU 301	36.684	7.784	55.047	1.00	27.06
	ATOM	2091	CD2	LEU 301	38.312	6.474	53.701	1.00	25.38
	ATOM	2092	C	LEU 301	38.452	3.648	57.226	1.00	26.23
	ATOM	2093	O	LEU 301	39.594	3.209	57.313	1.00	26.97
	ATOM	2094	N	VAL 302	37.623	3.670	58.259	1.00	26.05
15	ATOM	2095	CA	VAL 302	38.068	3.154	59.542	1.00	27.56
	ATOM	2096	CB	VAL 302	36.911	3.034	60.524	1.00	28.13
	ATOM	2097	CG1	VAL 302	37.354	2.285	61.777	1.00	26.62
	ATOM	2098	CG2	VAL 302	36.433	4.424	60.882	1.00	30.95
	ATOM	2099	C	VAL 302	38.723	1.786	59.386	1.00	27.42
20	ATOM	2100	O	VAL 302	39.765	1.529	59.977	1.00	29.00
	ATOM	2101	N	ARG 303	38.127	0.906	58.593	1.00	25.04
	ATOM	2102	CA	ARG 303	38.723	-0.395	58.417	1.00	25.12
	ATOM	2103	CB	ARG 303	37.906	-1.254	57.475	1.00	26.51
	ATOM	2104	CG	ARG 303	38.587	-2.558	57.126	1.00	28.11
25	ATOM	2105	CD	ARG 303	37.609	-3.520	56.490	1.00	31.77
	ATOM	2106	NE	ARG 303	38.260	-4.456	55.583	1.00	32.46
	ATOM	2107	CZ	ARG 303	38.483	-4.215	54.296	1.00	34.64
	ATOM	2108	NH1	ARG 303	38.103	-3.059	53.759	1.00	33.51
	ATOM	2109	NH2	ARG 303	39.082	-5.136	53.546	1.00	35.80

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	ATOM	2110	C	ARG 303	40.111	-0.242	57.854	1.00	27.77
	ATOM	2111	O	ARG 303	41.073	-0.788	58.401	1.00	30.47
	ATOM	2112	N	LEU 304	40.236	0.495	56.754	1.00	27.67
	ATOM	2113	CA	LEU 304	41.562	0.674	56.147	1.00	24.93
5	ATOM	2114	CB	LEU 304	41.464	1.526	54.865	1.00	22.51
	ATOM	2115	CG	LEU 304	40.640	0.902	53.718	1.00	19.14
	ATOM	2116	CD1	LEU 304	40.386	1.957	52.675	1.00	19.15
	ATOM	2117	CD2	LEU 304	41.352	-0.295	53.105	1.00	14.45
	ATOM	2118	C	LEU 304	42.523	1.290	57.168	1.00	21.35
10	ATOM	2119	O	LEU 304	43.584	0.736	57.432	1.00	20.90
	ATOM	2120	N	VAL 305	42.142	2.406	57.770	1.00	17.52
	ATOM	2121	CA	VAL 305	43.003	3.011	58.758	1.00	17.43
	ATOM	2122	CB	VAL 305	42.316	4.162	59.423	1.00	14.40
	ATOM	2123	CG1	VAL 305	43.154	4.673	60.583	1.00	14.53
15	ATOM	2124	CG2	VAL 305	42.095	5.240	58.408	1.00	14.33
	ATOM	2125	C	VAL 305	43.400	2.010	59.829	1.00	20.92
	ATOM	2126	O	VAL 305	44.497	2.071	60.387	1.00	22.69
	ATOM	2127	N	LEU 306	42.502	1.085	60.126	1.00	24.02
	ATOM	2128	CA	LEU 306	42.783	0.081	61.144	1.00	26.64
20	ATOM	2129	CB	LEU 306	41.481	-0.585	61.594	1.00	27.02
	ATOM	2130	CG	LEU 306	41.154	-0.563	63.087	1.00	27.64
	ATOM	2131	CD1	LEU 306	41.094	0.873	63.592	1.00	27.51
	ATOM	2132	CD2	LEU 306	39.826	-1.267	63.311	1.00	28.07
	ATOM	2133	C	LEU 306	43.721	-0.965	60.566	1.00	27.73
25	ATOM	2134	O	LEU 306	44.745	-1.303	61.157	1.00	26.86
	ATOM	2135	N	LEU 307	43.360	-1.467	59.394	1.00	28.77
	ATOM	2136	CA	LEU 307	44.156	-2.478	58.733	1.00	32.47
	ATOM	2137	CB	LEU 307	43.465	-2.893	57.437	1.00	29.90
	ATOM	2138	CG	LEU 307	43.477	-4.392	57.130	1.00	29.19

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	ATOM	2139	CD1	LEU 307	43.104	-5.210	58.361	1.00	28.38
	ATOM	2140	CD2	LEU 307	42.495	-4.648	56.015	1.00	29.88
	ATOM	2141	C	LEU 307	45.553	-1.916	58.466	1.00	35.49
	ATOM	2142	O	LEU 307	46.542	-2.645	58.394	1.00	36.50
5	ATOM	2143	N	ARG 308	45.622	-0.602	58.332	1.00	38.03
	ATOM	2144	CA	ARG 308	46.882	0.080	58.101	1.00	41.29
	ATOM	2145	CB	ARG 308	46.603	1.580	57.936	1.00	47.88
	ATOM	2146	CG	ARG 308	47.706	2.544	58.368	1.00	54.88
	ATOM	2147	CD	ARG 308	48.819	2.693	57.338	1.00	60.14
10	ATOM	2148	NE	ARG 308	49.524	3.958	57.540	1.00	65.47
	ATOM	2149	CZ	ARG 308	50.523	4.401	56.784	1.00	67.54
	ATOM	2150	NH1	ARG 308	50.954	3.673	55.757	1.00	68.57
	ATOM	2151	NH2	ARG 308	51.074	5.584	57.046	1.00	66.83
	ATOM	2152	C	ARG 308	47.783	-0.182	59.301	1.00	40.42
15	ATOM	2153	O	ARG 308	48.889	-0.694	59.159	1.00	40.04
	ATOM	2154	N	LEU 309	47.287	0.152	60.487	1.00	39.27
	ATOM	2155	CA	LEU 309	48.043	-0.027	61.717	1.00	38.92
	ATOM	2156	CB	LEU 309	47.224	0.484	62.895	1.00	33.74
	ATOM	2157	CG	LEU 309	46.852	1.958	62.854	1.00	30.26
20	ATOM	2158	CD1	LEU 309	45.453	2.121	63.368	1.00	30.84
	ATOM	2159	CD2	LEU 309	47.819	2.766	63.683	1.00	27.57
	ATOM	2160	C	LEU 309	48.461	-1.473	61.984	1.00	41.92
	ATOM	2161	O	LEU 309	49.600	-1.741	62.364	1.00	42.73
	ATOM	2162	N	VAL 310	47.541	-2.406	61.788	1.00	44.59
25	ATOM	2163	CA	VAL 310	47.829	-3.811	62.039	1.00	46.67
	ATOM	2164	CB	VAL 310	46.606	-4.651	61.798	1.00	46.95
	ATOM	2165	CG1	VAL 310	45.419	-4.006	62.479	1.00	49.54
	ATOM	2166	CG2	VAL 310	46.368	-4.779	60.312	1.00	47.77
	ATOM	2167	C	VAL 310	48.929	-4.321	61.139	1.00	47.55

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	ATOM	2168	O	VAL 310	49.488	-5.392	61.374	1.00	48.66
	ATOM	2169	N	ASP 311	49.217	-3.559	60.093	1.00	48.93
	ATOM	2170	CA	ASP 311	50.262	-3.927	59.160	1.00	52.04
	ATOM	2171	CB	ASP 311	49.993	-3.298	57.793	1.00	57.14
5	ATOM	2172	CG	ASP 311	48.752	-3.869	57.135	1.00	61.79
	ATOM	2173	OD1	ASP 311	48.348	-3.377	56.054	1.00	63.59
	ATOM	2174	OD2	ASP 311	48.180	-4.819	57.713	1.00	63.98
	ATOM	2175	C	ASP 311	51.618	-3.490	59.698	1.00	51.94
	ATOM	2176	O	ASP 311	52.580	-4.256	59.653	1.00	53.89
10	ATOM	2177	N	GLU 312	51.702	-2.267	60.212	1.00	49.51
	ATOM	2178	CA	GLU 312	52.961	-1.785	60.762	1.00	47.68
	ATOM	2179	CB	GLU 312	53.071	-0.272	60.632	1.00	48.44
	ATOM	2180	CG	GLU 312	52.900	0.221	59.216	1.00	51.79
	ATOM	2181	CD	GLU 312	53.122	1.713	59.084	1.00	53.56
15	ATOM	2182	OE1	GLU 312	52.698	2.280	58.047	1.00	49.90
	ATOM	2183	OE2	GLU 312	53.725	2.309	60.013	1.00	56.82
	ATOM	2184	C	GLU 312	53.075	-2.172	62.222	1.00	46.11
	ATOM	2185	O	GLU 312	53.514	-1.377	63.049	1.00	46.75
	ATOM	2186	N	ASN 313	52.666	-3.397	62.527	1.00	45.02
20	ATOM	2187	CA	ASN 313	52.720	-3.938	63.879	1.00	44.64
	ATOM	2188	CB	ASN 313	54.100	-4.550	64.119	1.00	43.84
	ATOM	2189	CG	ASN 313	54.028	-5.860	64.863	1.00	45.16
	ATOM	2190	OD1	ASN 313	53.377	-5.965	65.906	1.00	43.79
	ATOM	2191	ND2	ASN 313	54.701	-6.875	64.333	1.00	46.05
25	ATOM	2192	C	ASN 313	52.408	-2.921	64.991	1.00	44.49
	ATOM	2193	O	ASN 313	53.303	-2.509	65.728	1.00	45.19
	ATOM	2194	N	LEU 314	51.142	-2.530	65.126	1.00	43.02
	ATOM	2195	CA	LEU 314	50.743	-1.563	66.159	1.00	40.80
	ATOM	2196	CB	LEU 314	50.639	-0.167	65.549	1.00	34.97



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	ATOM	2197	CG	LEU 314	51.940	0.499	65.127	1.00	29.58
	ATOM	2198	CD1	LEU 314	51.698	1.453	63.981	1.00	28.94
	ATOM	2199	CD2	LEU 314	52.516	1.212	66.311	1.00	28.16
	ATOM	2200	C	LEU 314	49.396	-1.924	66.777	1.00	42.38
5	ATOM	2201	O	LEU 314	49.026	-1.422	67.848	1.00	39.73
	ATOM	2202	N	LEU 315	48.689	-2.812	66.078	1.00	44.49
	ATOM	2203	CA	LEU 315	47.352	-3.268	66.439	1.00	45.22
	ATOM	2204	CB	LEU 315	46.354	-2.695	65.445	1.00	43.49
	ATOM	2205	CG	LEU 315	45.121	-2.063	66.045	1.00	43.28
10	ATOM	2206	CD1	LEU 315	44.055	-1.976	64.972	1.00	43.01
	ATOM	2207	CD2	LEU 315	44.643	-2.907	67.209	1.00	46.13
	ATOM	2208	C	LEU 315	47.214	-4.781	66.407	1.00	46.34
	ATOM	2209	O	LEU 315	47.828	-5.439	65.577	1.00	47.74
	ATOM	2210	N	PHE 316	46.380	-5.318	67.292	1.00	48.50
15	ATOM	2211	CA	PHE 316	46.125	-6.760	67.369	1.00	50.80
	ATOM	2212	CB	PHE 316	45.054	-7.186	66.347	1.00	48.89
	ATOM	2213	CG	PHE 316	43.829	-6.312	66.331	1.00	46.47
	ATOM	2214	CD1	PHE 316	43.163	-5.999	67.508	1.00	45.93
	ATOM	2215	CD2	PHE 316	43.350	-5.791	65.134	1.00	44.48
20	ATOM	2216	CE1	PHE 316	42.043	-5.183	67.491	1.00	44.57
	ATOM	2217	CE2	PHE 316	42.229	-4.974	65.109	1.00	43.59
	ATOM	2218	CZ	PHE 316	41.577	-4.669	66.290	1.00	44.05
	ATOM	2219	C	PHE 316	47.371	-7.605	67.124	1.00	53.06
	ATOM	2220	O	PHE 316	47.342	-8.521	66.299	1.00	54.62
25	ATOM	2221	N	HIS 317	48.456	-7.304	67.835	1.00	54.60
	ATOM	2222	CA	HIS 317	49.710	-8.046	67.691	1.00	55.95
	ATOM	2223	CB	HIS 317	49.676	-9.301	68.569	1.00	54.90
	ATOM	2224	CG	HIS 317	49.708	-9.004	70.034	1.00	55.21
	ATOM	2225	CD2	HIS 317	49.686	-9.823	71.113	1.00	55.22

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	ATOM	2226	ND1	HIS	317	49.778	-7.718	70.528	1.00	54.55
	ATOM	2227	CE1	HIS	317	49.798	-7.756	71.848	1.00	55.21
	ATOM	2228	NE2	HIS	317	49.744	-9.020	72.229	1.00	56.90
	ATOM	2229	C	HIS	317	50.004	-8.426	66.240	1.00	58.27
5	ATOM	2230	O	HIS	317	50.521	-9.514	65.950	1.00	58.90
	ATOM	2231	N	GLY	318	49.665	-7.513	65.335	1.00	59.86
	ATOM	2232	CA	GLY	318	49.881	-7.734	63.921	1.00	60.72
	ATOM	2233	C	GLY	318	49.290	-9.022	63.379	1.00	62.25
	ATOM	2234	O	GLY	318	50.031	-9.956	63.080	1.00	63.75
10	ATOM	2235	N	GLU	319	47.962	-9.087	63.277	1.00	62.86
	ATOM	2236	CA	GLU	319	47.277	-10.257	62.716	1.00	62.72
	ATOM	2237	CB	GLU	319	47.663	-11.545	63.439	1.00	66.93
	ATOM	2238	CG	GLU	319	47.437	-12.784	62.575	1.00	73.23
	ATOM	2239	CD	GLU	319	47.862	-14.068	63.262	1.00	78.58
15	ATOM	2240	OE1	GLU	319	49.020	-14.129	63.745	1.00	80.57
	ATOM	2241	OE2	GLU	319	47.043	-15.019	63.310	1.00	81.49
	ATOM	2242	C	GLU	319	45.765	-10.097	62.739	1.00	59.42
	ATOM	2243	O	GLU	319	45.098	-10.387	63.735	1.00	57.03
	ATOM	2244	N	ALA	320	45.246	-9.643	61.604	1.00	55.74
20	ATOM	2245	CA	ALA	320	43.828	-9.394	61.414	1.00	54.02
	ATOM	2246	CB	ALA	320	43.657	-8.357	60.338	1.00	52.55
	ATOM	2247	C	ALA	320	43.052	-10.650	61.043	1.00	54.49
	ATOM	2248	O	ALA	320	43.620	-11.565	60.457	1.00	55.61
	ATOM	2249	N	SER	321	41.762	-10.698	61.388	1.00	55.01
25	ATOM	2250	CA	SER	321	40.924	-11.856	61.050	1.00	55.90
	ATOM	2251	CB	SER	321	39.649	-11.911	61.895	1.00	56.08
	ATOM	2252	OG	SER	321	38.814	-12.975	61.445	1.00	53.96
	ATOM	2253	C	SER	321	40.513	-11.780	59.589	1.00	55.49
	ATOM	2254	O	SER	321	40.367	-10.689	59.041	1.00	54.92

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	ATOM	2255	N	GLU 322	40.292	-12.933	58.967	1.00	54.84
	ATOM	2256	CA	GLU 322	39.917	-12.951	57.563	1.00	56.14
	ATOM	2257	CB	GLU 322	39.646	-14.382	57.092	1.00	58.38
	ATOM	2258	CG	GLU 322	40.173	-14.697	55.681	1.00	63.26
5	ATOM	2259	CD	GLU 322	41.712	-14.670	55.574	1.00	66.36
	ATOM	2260	OE1	GLU 322	42.296	-13.571	55.432	1.00	66.15
	ATOM	2261	OE2	GLU 322	42.339	-15.754	55.637	1.00	66.78
	ATOM	2262	C	GLU 322	38.685	-12.085	57.354	1.00	55.71
	ATOM	2263	O	GLU 322	38.343	-11.727	56.227	1.00	54.93
10	ATOM	2264	N	GLN 323	38.027	-11.740	58.454	1.00	55.82
	ATOM	2265	CA	GLN 323	36.838	-10.904	58.393	1.00	55.20
	ATOM	2266	CB	GLN 323	35.995	-11.101	59.659	1.00	57.22
	ATOM	2267	CG	GLN 323	35.737	-12.571	59.983	1.00	60.42
	ATOM	2268	CD	GLN 323	34.801	-12.778	61.164	1.00	62.11
15	ATOM	2269	OE1	GLN 323	34.596	-13.909	61.612	1.00	63.58
	ATOM	2270	NE2	GLN 323	34.223	-11.690	61.668	1.00	61.37
	ATOM	2271	C	GLN 323	37.259	-9.445	58.249	1.00	53.59
	ATOM	2272	O	GLN 323	36.963	-8.800	57.242	1.00	53.27
	ATOM	2273	N	LEU 324	37.973	-8.936	59.248	1.00	50.98
20	ATOM	2274	CA	LEU 324	38.430	-7.553	59.224	1.00	48.40
	ATOM	2275	CB	LEU 324	39.396	-7.294	60.378	1.00	46.63
	ATOM	2276	CG	LEU 324	39.956	-5.876	60.498	1.00	44.87
	ATOM	2277	CD1	LEU 324	38.846	-4.837	60.390	1.00	44.21
	ATOM	2278	CD2	LEU 324	40.671	-5.758	61.827	1.00	43.22
25	ATOM	2279	C	LEU 324	39.115	-7.224	57.911	1.00	47.25
	ATOM	2280	O	LEU 324	39.181	-6.065	57.505	1.00	44.86
	ATOM	2281	N	ARG 325	39.627	-8.253	57.252	1.00	48.35
	ATOM	2282	CA	ARG 325	40.309	-8.057	55.988	1.00	50.22
	ATOM	2283	CB	ARG 325	41.473	-9.055	55.839	1.00	53.47

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	ATOM	2284	CG	ARG 325	42.580	-8.896	56.894	1.00	57.97
	ATOM	2285	CD	ARG 325	43.660	-9.986	56.808	1.00	61.92
	ATOM	2286	NE	ARG 325	44.564	-9.957	57.966	1.00	67.95
	ATOM	2287	CZ	ARG 325	45.535	-10.844	58.206	1.00	70.27
5	ATOM	2288	NH1	ARG 325	45.753	-11.854	57.371	1.00	69.69
	ATOM	2289	NH2	ARG 325	46.290	-10.725	59.293	1.00	70.39
	ATOM	2290	C	ARG 325	39.320	-8.224	54.850	1.00	48.80
	ATOM	2291	O	ARG 325	39.617	-8.859	53.847	1.00	50.46
	ATOM	2292	N	THR 326	38.131	-7.663	54.999	1.00	46.54
10	ATOM	2293	CA	THR 326	37.162	-7.783	53.929	1.00	45.13
	ATOM	2294	CB	THR 326	36.108	-8.810	54.264	1.00	44.85
	ATOM	2295	OG1	THR 326	36.749	-10.061	54.546	1.00	44.98
	ATOM	2296	CG2	THR 326	35.160	-8.973	53.092	1.00	43.46
	ATOM	2297	C	THR 326	36.500	-6.453	53.687	1.00	44.79
15	ATOM	2298	O	THR 326	36.256	-5.705	54.626	1.00	45.01
	ATOM	2299	N	ARG 327	36.216	-6.143	52.430	1.00	45.02
	ATOM	2300	CA	ARG 327	35.590	-4.866	52.136	1.00	45.97
	ATOM	2301	CB	ARG 327	35.476	-4.655	50.623	1.00	48.63
	ATOM	2302	CG	ARG 327	34.961	-3.283	50.229	1.00	53.97
20	ATOM	2303	CD	ARG 327	34.975	-3.072	48.722	1.00	58.44
	ATOM	2304	NE	ARG 327	33.747	-2.410	48.282	1.00	66.14
	ATOM	2305	CZ	ARG 327	33.387	-1.178	48.648	1.00	69.53
	ATOM	2306	NH1	ARG 327	34.167	-0.471	49.458	1.00	69.84
	ATOM	2307	NH2	ARG 327	32.242	-0.652	48.220	1.00	68.29
25	ATOM	2308	C	ARG 327	34.217	-4.790	52.794	1.00	44.69
	ATOM	2309	O	ARG 327	33.486	-5.784	52.861	1.00	44.55
	ATOM	2310	N	GLY 328	33.888	-3.605	53.302	1.00	42.14
	ATOM	2311	CA	GLY 328	32.606	-3.394	53.952	1.00	37.48
	ATOM	2312	C	GLY 328	32.480	-4.007	55.334	1.00	33.00

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	ATOM	2313	O	GLY 328	31.693	-3.532	56.148	1.00	32.88
	ATOM	2314	N	ALA 329	33.258	-5.049	55.601	1.00	29.02
	ATOM	2315	CA	ALA 329	33.227	-5.743	56.885	1.00	26.22
	ATOM	2316	CB	ALA 329	34.452	-6.623	57.028	1.00	28.65
5	ATOM	2317	C	ALA 329	33.092	-4.861	58.115	1.00	24.38
	ATOM	2318	O	ALA 329	32.490	-5.276	59.097	1.00	26.43
	ATOM	2319	N	PHE 330	33.663	-3.663	58.091	1.00	21.81
	ATOM	2320	CA	PHE 330	33.547	-2.776	59.242	1.00	18.07
	ATOM	2321	CB	PHE 330	34.887	-2.137	59.558	1.00	13.90
10	ATOM	2322	CG	PHE 330	34.913	-1.404	60.862	1.00	12.45
	ATOM	2323	CD1	PHE 330	34.460	-0.096	60.961	1.00	12.64
	ATOM	2324	CD2	PHE 330	35.436	-2.009	61.995	1.00	12.73
	ATOM	2325	CE1	PHE 330	34.535	0.605	62.188	1.00	12.83
	ATOM	2326	CE2	PHE 330	35.515	-1.315	63.221	1.00	11.49
15	ATOM	2327	CZ	PHE 330	35.066	-0.008	63.315	1.00	8.96
	ATOM	2328	C	PHE 330	32.528	-1.716	58.886	1.00	17.48
	ATOM	2329	O	PHE 330	32.855	-0.702	58.273	1.00	17.97
	ATOM	2330	N	GLU 331	31.288	-1.976	59.275	1.00	16.36
	ATOM	2331	CA	GLU 331	30.149	-1.105	58.998	1.00	18.14
20	ATOM	2332	CB	GLU 331	28.865	-1.889	59.308	1.00	22.08
	ATOM	2333	CG	GLU 331	28.790	-3.226	58.546	1.00	26.82
	ATOM	2334	CD	GLU 331	28.183	-4.382	59.346	1.00	28.86
	ATOM	2335	OE1	GLU 331	28.381	-5.552	58.931	1.00	28.12
	ATOM	2336	OE2	GLU 331	27.509	-4.129	60.371	1.00	30.16
25	ATOM	2337	C	GLU 331	30.126	0.248	59.719	1.00	16.36
	ATOM	2338	O	GLU 331	30.596	0.380	60.849	1.00	16.97
	ATOM	2339	N	THR 332	29.583	1.263	59.060	1.00	14.04
	ATOM	2340	CA	THR 332	29.494	2.568	59.695	1.00	14.47
	ATOM	2341	CB	THR 332	28.747	3.562	58.825	1.00	10.93

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	ATOM	2342	OG1	THR	332	29.473	3.751	57.611	1.00	6.57
	ATOM	2343	CG2	THR	332	28.597	4.890	59.550	1.00	6.34
	ATOM	2344	C	THR	332	28.725	2.382	60.994	1.00	18.42
	ATOM	2345	O	THR	332	29.125	2.872	62.052	1.00	17.70
5	ATOM	2346	N	ARG	333	27.609	1.671	60.892	1.00	21.79
	ATOM	2347	CA	ARG	333	26.783	1.346	62.040	1.00	24.44
	ATOM	2348	CB	ARG	333	26.095	0.001	61.764	1.00	28.62
	ATOM	2349	CG	ARG	333	25.291	-0.590	62.910	1.00	34.65
	ATOM	2350	CD	ARG	333	24.308	-1.664	62.401	1.00	39.87
10	ATOM	2351	NE	ARG	333	24.953	-2.887	61.910	1.00	43.42
	ATOM	2352	CZ	ARG	333	25.198	-3.969	62.653	1.00	46.01
	ATOM	2353	NH1	ARG	333	24.852	-3.992	63.940	1.00	45.10
	ATOM	2354	NH2	ARG	333	25.791	-5.030	62.104	1.00	43.75
	ATOM	2355	C	ARG	333	27.638	1.271	63.323	1.00	24.88
15	ATOM	2356	O	ARG	333	27.242	1.803	64.358	1.00	24.00
	ATOM	2357	N	PHE	334	28.818	0.635	63.232	1.00	23.97
	ATOM	2358	CA	PHE	334	29.740	0.458	64.371	1.00	19.64
	ATOM	2359	CB	PHE	334	30.877	-0.509	64.033	1.00	20.52
	ATOM	2360	CG	PHE	334	30.420	-1.813	63.468	1.00	24.74
20	ATOM	2361	CD1	PHE	334	29.469	-2.574	64.121	1.00	25.94
	ATOM	2362	CD2	PHE	334	30.938	-2.279	62.262	1.00	26.47
	ATOM	2363	CE1	PHE	334	29.039	-3.780	63.575	1.00	28.43
	ATOM	2364	CE2	PHE	334	30.514	-3.483	61.711	1.00	24.74
	ATOM	2365	CZ	PHE	334	29.565	-4.233	62.365	1.00	26.41
25	ATOM	2366	C	PHE	334	30.382	1.739	64.842	1.00	16.52
	ATOM	2367	O	PHE	334	30.434	2.020	66.039	1.00	16.16
	ATOM	2368	N	VAL	335	30.907	2.509	63.905	1.00	13.20
	ATOM	2369	CA	VAL	335	31.546	3.752	64.284	1.00	11.36
	ATOM	2370	CB	VAL	335	31.877	4.565	63.033	1.00	8.08

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	ATOM	2371	CG1	VAL 335	32.113	6.003	63.402	1.00	8.71
	ATOM	2372	CG2	VAL 335	33.082	3.979	62.358	1.00	1.00
	ATOM	2373	C	VAL 335	30.653	4.558	65.249	1.00	13.02
	ATOM	2374	O	VAL 335	31.126	5.066	66.264	1.00	10.40
5	ATOM	2375	N	SER 336	29.359	4.640	64.934	1.00	16.23
	ATOM	2376	CA	SER 336	28.365	5.372	65.740	1.00	18.55
	ATOM	2377	CB	SER 336	27.017	5.350	65.039	1.00	19.92
	ATOM	2378	OG	SER 336	26.611	3.999	64.866	1.00	25.40
	ATOM	2379	C	SER 336	28.162	4.766	67.118	1.00	17.99
10	ATOM	2380	O	SER 336	27.896	5.465	68.100	1.00	14.64
	ATOM	2381	N	GLN 337	28.239	3.445	67.159	1.00	19.48
	ATOM	2382	CA	GLN 337	28.061	2.719	68.394	1.00	21.39
	ATOM	2383	CB	GLN 337	27.995	1.223	68.123	1.00	21.42
	ATOM	2384	CG	GLN 337	26.829	0.800	67.264	1.00	23.07
15	ATOM	2385	CD	GLN 337	26.920	-0.654	66.895	1.00	24.96
	ATOM	2386	OE1	GLN 337	27.243	-1.496	67.735	1.00	28.83
	ATOM	2387	NE2	GLN 337	26.633	-0.966	65.638	1.00	24.29
	ATOM	2388	C	GLN 337	29.260	3.011	69.240	1.00	20.91
	ATOM	2389	O	GLN 337	29.205	2.963	70.464	1.00	23.32
20	ATOM	2390	N	VAL 338	30.362	3.317	68.584	1.00	20.52
	ATOM	2391	CA	VAL 338	31.559	3.589	69.337	1.00	21.67
	ATOM	2392	CB	VAL 338	32.812	3.470	68.443	1.00	20.93
	ATOM	2393	CG1	VAL 338	34.065	3.624	69.279	1.00	19.79
	ATOM	2394	CG2	VAL 338	32.811	2.126	67.739	1.00	16.69
25	ATOM	2395	C	VAL 338	31.480	4.973	69.977	1.00	23.61
	ATOM	2396	O	VAL 338	31.385	5.079	71.203	1.00	21.96
	ATOM	2397	N	GLU 339	31.486	6.020	69.146	1.00	25.05
	ATOM	2398	CA	GLU 339	31.455	7.406	69.620	1.00	26.21
	ATOM	2399	CB	GLU 339	31.460	8.402	68.440	1.00	26.37

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	ATOM	2400	CG	GLU 339	30.515	8.082	67.282	1.00	31.63
	ATOM	2401	CD	GLU 339	30.287	9.267	66.311	1.00	36.86
	ATOM	2402	OE1	GLU 339	29.542	10.219	66.663	1.00	37.19
	ATOM	2403	OE2	GLU 339	30.850	9.243	65.187	1.00	37.90
5	ATOM	2404	C	GLU 339	30.299	7.735	70.541	1.00	26.44
	ATOM	2405	O	GLU 339	30.423	8.613	71.396	1.00	27.55
	ATOM	2406	N	SER 340	29.189	7.017	70.380	1.00	26.30
	ATOM	2407	CA	SER 340	27.987	7.246	71.181	1.00	25.08
	ATOM	2408	CB	SER 340	26.861	6.322	70.717	1.00	23.68
10	ATOM	2409	OG	SER 340	27.191	4.970	70.957	1.00	23.58
	ATOM	2410	C	SER 340	28.211	7.065	72.676	1.00	26.02
	ATOM	2411	O	SER 340	27.415	7.539	73.488	1.00	26.83
	ATOM	2412	N	ASP 341	29.294	6.380	73.033	1.00	27.41
	ATOM	2413	CA	ASP 341	29.630	6.143	74.434	1.00	27.85
15	ATOM	2414	CB	ASP 341	28.939	4.885	74.953	1.00	27.41
	ATOM	2415	CG	ASP 341	29.253	4.621	76.410	1.00	26.49
	ATOM	2416	OD1	ASP 341	29.628	5.591	77.107	1.00	26.07
	ATOM	2417	OD2	ASP 341	29.117	3.463	76.862	1.00	25.64
	ATOM	2418	C	ASP 341	31.128	6.008	74.672	1.00	28.59
20	ATOM	2419	O	ASP 341	31.757	5.049	74.229	1.00	30.06
	ATOM	2420	N	THR 342	31.688	6.965	75.398	1.00	27.34
	ATOM	2421	CA	THR 342	33.105	6.953	75.694	1.00	26.74
	ATOM	2422	CB	THR 342	33.681	8.348	75.553	1.00	26.75
	ATOM	2423	OG1	THR 342	33.072	9.217	76.511	1.00	25.10
25	ATOM	2424	CG2	THR 342	33.387	8.881	74.171	1.00	29.29
	ATOM	2425	C	THR 342	33.292	6.477	77.114	1.00	27.84
	ATOM	2426	O	THR 342	34.365	6.625	77.692	1.00	27.29
	ATOM	2427	N	GLY 343	32.223	5.908	77.662	1.00	30.32
	ATOM	2428	CA	GLY 343	32.234	5.398	79.020	1.00	31.31



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	ATOM	2429	C	GLY 343	32.970	4.083	79.178	1.00	32.13
	ATOM	2430	O	GLY 343	33.765	3.944	80.105	1.00	34.00
	ATOM	2431	N	ASP 344	32.712	3.114	78.304	1.00	31.93
	ATOM	2432	CA	ASP 344	33.400	1.836	78.411	1.00	34.25
5	ATOM	2433	CB	ASP 344	32.592	0.857	79.267	1.00	38.13
	ATOM	2434	CG	ASP 344	31.205	0.646	78.744	1.00	43.49
	ATOM	2435	OD1	ASP 344	30.399	-0.029	79.426	1.00	47.59
	ATOM	2436	OD2	ASP 344	30.923	1.159	77.643	1.00	46.67
	ATOM	2437	C	ASP 344	33.744	1.196	77.075	1.00	33.85
10	ATOM	2438	O	ASP 344	33.354	1.681	76.015	1.00	32.12
	ATOM	2439	N	ARG 345	34.490	0.098	77.148	1.00	34.54
	ATOM	2440	CA	ARG 345	34.935	-0.626	75.968	1.00	35.60
	ATOM	2441	CB	ARG 345	36.297	-1.278	76.233	1.00	35.33
	ATOM	2442	CG	ARG 345	37.339	-0.370	76.864	1.00	35.88
15	ATOM	2443	CD	ARG 345	38.729	-1.006	76.879	1.00	35.19
	ATOM	2444	NE	ARG 345	39.507	-0.597	78.054	1.00	36.95
	ATOM	2445	CZ	ARG 345	39.984	0.629	78.275	1.00	36.97
	ATOM	2446	NH1	ARG 345	39.780	1.605	77.396	1.00	36.40
	ATOM	2447	NH2	ARG 345	40.654	0.885	79.394	1.00	36.46
20	ATOM	2448	C	ARG 345	33.961	-1.716	75.551	1.00	36.31
	ATOM	2449	O	ARG 345	34.080	-2.280	74.461	1.00	37.64
	ATOM	2450	N	LYS 346	33.004	-2.020	76.420	1.00	35.01
	ATOM	2451	CA	LYS 346	32.050	-3.081	76.134	1.00	33.81
	ATOM	2452	CB	LYS 346	30.824	-2.975	77.041	1.00	33.64
25	ATOM	2453	CG	LYS 346	29.942	-4.223	76.985	1.00	33.85
	ATOM	2454	CD	LYS 346	30.759	-5.505	77.186	1.00	31.48
	ATOM	2455	CE	LYS 346	30.061	-6.699	76.542	1.00	32.39
	ATOM	2456	NZ	LYS 346	30.855	-7.968	76.542	1.00	30.01
	ATOM	2457	C	LYS 346	31.613	-3.093	74.684	1.00	33.18

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	ATOM	2458	O	LYS 346	31.746	-4.101	73.995	1.00	31.98
	ATOM	2459	N	GLN 347	31.101	-1.967	74.214	1.00	33.36
	ATOM	2460	CA	GLN 347	30.662	-1.887	72.839	1.00	34.32
	ATOM	2461	CB	GLN 347	30.014	-0.530	72.589	1.00	37.17
5	ATOM	2462	CG	GLN 347	28.510	-0.578	72.703	1.00	39.97
	ATOM	2463	CD	GLN 347	27.905	-1.436	71.611	1.00	43.97
	ATOM	2464	OE1	GLN 347	28.219	-2.626	71.491	1.00	43.88
	ATOM	2465	NE2	GLN 347	27.039	-0.835	70.799	1.00	46.46
	ATOM	2466	C	GLN 347	31.799	-2.144	71.844	1.00	34.27
10	ATOM	2467	O	GLN 347	31.630	-2.922	70.902	1.00	35.29
	ATOM	2468	N	ILE 348	32.952	-1.502	72.054	1.00	31.49
	ATOM	2469	CA	ILE 348	34.109	-1.679	71.165	1.00	25.43
	ATOM	2470	CB	ILE 348	35.309	-0.826	71.614	1.00	21.01
	ATOM	2471	CG2	ILE 348	36.369	-0.826	70.540	1.00	15.50
15	ATOM	2472	CG1	ILE 348	34.852	0.606	71.875	1.00	22.27
	ATOM	2473	CD1	ILE 348	35.914	1.509	72.462	1.00	24.55
	ATOM	2474	C	ILE 348	34.524	-3.139	71.211	1.00	24.70
	ATOM	2475	O	ILE 348	34.793	-3.763	70.182	1.00	23.36
	ATOM	2476	N	TYR 349	34.560	-3.681	72.421	1.00	23.30
20	ATOM	2477	CA	TYR 349	34.933	-5.061	72.597	1.00	23.65
	ATOM	2478	CB	TYR 349	34.727	-5.491	74.047	1.00	25.21
	ATOM	2479	CG	TYR 349	34.779	-6.989	74.221	1.00	31.27
	ATOM	2480	CD1	TYR 349	35.990	-7.665	74.333	1.00	33.98
	ATOM	2481	CE1	TYR 349	36.028	-9.062	74.435	1.00	36.98
25	ATOM	2482	CD2	TYR 349	33.607	-7.740	74.216	1.00	34.38
	ATOM	2483	CE2	TYR 349	33.628	-9.125	74.312	1.00	36.69
	ATOM	2484	CZ	TYR 349	34.837	-9.786	74.421	1.00	37.89
	ATOM	2485	OH	TYR 349	34.834	-11.165	74.512	1.00	37.12
	ATOM	2486	C	TYR 349	34.105	-5.945	71.676	1.00	23.47

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	ATOM	2487	O	TYR 349	34.654	-6.602	70.794	1.00	21.02
	ATOM	2488	N	ASN 350	32.783	-5.934	71.872	1.00	25.29
	ATOM	2489	CA	ASN 350	31.850	-6.766	71.091	1.00	25.07
	ATOM	2490	CB	ASN 350	30.379	-6.500	71.482	1.00	23.90
5	ATOM	2491	CG	ASN 350	30.069	-6.844	72.941	1.00	25.09
	ATOM	2492	OD1	ASN 350	30.413	-7.924	73.440	1.00	22.84
	ATOM	2493	ND2	ASN 350	29.398	-5.923	73.626	1.00	25.65
	ATOM	2494	C	ASN 350	31.982	-6.620	69.580	1.00	25.25
	ATOM	2495	O	ASN 350	31.994	-7.619	68.859	1.00	25.84
10	ATOM	2496	N	ILE 351	32.068	-5.392	69.083	1.00	25.43
	ATOM	2497	CA	ILE 351	32.195	-5.227	67.642	1.00	25.64
	ATOM	2498	CB	ILE 351	32.388	-3.745	67.248	1.00	24.60
	ATOM	2499	CG2	ILE 351	32.282	-3.600	65.743	1.00	23.69
	ATOM	2500	CG1	ILE 351	31.305	-2.882	67.903	1.00	22.24
15	ATOM	2501	CD1	ILE 351	31.357	-1.431	67.509	1.00	19.88
	ATOM	2502	C	ILE 351	33.415	-6.047	67.224	1.00	26.73
	ATOM	2503	O	ILE 351	33.282	-7.047	66.517	1.00	25.71
	ATOM	2504	N	LEU 352	34.592	-5.629	67.695	1.00	27.08
	ATOM	2505	CA	LEU 352	35.847	-6.312	67.397	1.00	27.36
20	ATOM	2506	CB	LEU 352	36.994	-5.700	68.206	1.00	24.45
	ATOM	2507	CG	LEU 352	37.295	-4.208	68.090	1.00	23.84
	ATOM	2508	CD1	LEU 352	38.464	-3.838	68.995	1.00	21.54
	ATOM	2509	CD2	LEU 352	37.620	-3.872	66.660	1.00	23.96
	ATOM	2510	C	LEU 352	35.746	-7.798	67.737	1.00	29.42
25	ATOM	2511	O	LEU 352	36.045	-8.670	66.912	1.00	29.43
	ATOM	2512	N	SER 353	35.336	-8.087	68.965	1.00	30.73
	ATOM	2513	CA	SER 353	35.206	-9.468	69.398	1.00	32.72
	ATOM	2514	CB	SER 353	34.408	-9.531	70.711	1.00	32.86
	ATOM	2515	OG	SER 353	34.187	-10.870	71.126	1.00	35.10

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	ATOM	2516	C	SER 353	34.513	-10.277	68.295	1.00	33.76
	ATOM	2517	O	SER 353	35.123	-11.149	67.670	1.00	34.42
	ATOM	2518	N	THR 354	33.252	-9.941	68.035	1.00	34.17
	ATOM	2519	CA	THR 354	32.437	-10.621	67.031	1.00	32.96
5	ATOM	2520	CB	THR 354	30.999	-10.073	67.076	1.00	33.01
	ATOM	2521	OG1	THR 354	30.120	-10.980	66.408	1.00	32.52
	ATOM	2522	CG2	THR 354	30.922	-8.702	66.411	1.00	34.65
	ATOM	2523	C	THR 354	33.007	-10.503	65.608	1.00	32.28
	ATOM	2524	O	THR 354	32.444	-11.038	64.646	1.00	30.58
10	ATOM	2525	N	LEU 355	34.137	-9.807	65.497	1.00	31.47
	ATOM	2526	CA	LEU 355	34.832	-9.612	64.227	1.00	30.67
	ATOM	2527	CB	LEU 355	35.488	-8.239	64.187	1.00	28.42
	ATOM	2528	CG	LEU 355	34.780	-7.240	63.293	1.00	27.13
	ATOM	2529	CD1	LEU 355	35.387	-5.874	63.487	1.00	26.09
15	ATOM	2530	CD2	LEU 355	34.898	-7.698	61.859	1.00	27.39
	ATOM	2531	C	LEU 355	35.905	-10.668	64.061	1.00	31.14
	ATOM	2532	O	LEU 355	36.573	-10.735	63.033	1.00	30.59
	ATOM	2533	N	GLY 356	36.074	-11.484	65.091	1.00	32.64
	ATOM	2534	CA	GLY 356	37.068	-12.530	65.030	1.00	35.49
20	ATOM	2535	C	GLY 356	38.435	-12.074	65.493	1.00	37.44
	ATOM	2536	O	GLY 356	39.443	-12.492	64.930	1.00	37.31
	ATOM	2537	N	LEU 357	38.471	-11.222	66.516	1.00	39.40
	ATOM	2538	CA	LEU 357	39.729	-10.717	67.057	1.00	41.85
	ATOM	2539	CB	LEU 357	39.898	-9.239	66.705	1.00	41.35
25	ATOM	2540	CG	LEU 357	39.816	-8.876	65.218	1.00	43.17
	ATOM	2541	CD1	LEU 357	39.953	-7.375	65.064	1.00	42.98
	ATOM	2542	CD2	LEU 357	40.904	-9.585	64.428	1.00	43.93
	ATOM	2543	C	LEU 357	39.759	-10.888	68.571	1.00	44.59
	ATOM	2544	O	LEU 357	38.750	-11.247	69.176	1.00	45.94

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	ATOM	2545	N	ARG 358	40.919	-10.643	69.178	1.00	46.55
	ATOM	2546	CA	ARG 358	41.080	-10.752	70.632	1.00	48.12
	ATOM	2547	CB	ARG 358	42.113	-11.819	70.994	1.00	52.19
	ATOM	2548	CG	ARG 358	41.649	-13.258	70.839	1.00	61.21
5	ATOM	2549	CD	ARG 358	40.870	-13.768	72.064	1.00	68.48
	ATOM	2550	NE	ARG 358	39.519	-13.206	72.184	1.00	74.00
	ATOM	2551	CZ	ARG 358	38.629	-13.577	73.104	1.00	75.57
	ATOM	2552	NH1	ARG 358	38.935	-14.517	73.998	1.00	75.58
	ATOM	2553	NH2	ARG 358	37.431	-13.005	73.131	1.00	74.54
10	ATOM	2554	C	ARG 358	41.558	-9.418	71.174	1.00	46.76
	ATOM	2555	O	ARG 358	42.702	-9.284	71.580	1.00	49.52
	ATOM	2556	N	PRO 359	40.679	-8.412	71.197	1.00	45.33
	ATOM	2557	CD	PRO 359	39.271	-8.532	70.791	1.00	45.90
	ATOM	2558	CA	PRO 359	40.956	-7.056	71.677	1.00	44.06
15	ATOM	2559	CB	PRO 359	39.565	-6.449	71.784	1.00	45.14
	ATOM	2560	CG	PRO 359	38.865	-7.086	70.643	1.00	46.70
	ATOM	2561	C	PRO 359	41.725	-6.936	72.986	1.00	42.11
	ATOM	2562	O	PRO 359	41.662	-7.797	73.860	1.00	42.98
	ATOM	2563	N	SER 360	42.449	-5.840	73.118	1.00	38.55
20	ATOM	2564	CA	SER 360	43.209	-5.608	74.321	1.00	35.42
	ATOM	2565	CB	SER 360	44.701	-5.624	74.014	1.00	38.45
	ATOM	2566	OG	SER 360	45.100	-4.379	73.453	1.00	37.32
	ATOM	2567	C	SER 360	42.847	-4.234	74.818	1.00	33.26
	ATOM	2568	O	SER 360	42.530	-3.345	74.028	1.00	30.55
25	ATOM	2569	N	THR 361	42.907	-4.060	76.128	1.00	31.87
	ATOM	2570	CA	THR 361	42.625	-2.771	76.721	1.00	33.02
	ATOM	2571	CB	THR 361	43.285	-2.646	78.083	1.00	32.00
	ATOM	2572	OG1	THR 361	42.697	-3.593	78.981	1.00	31.30
	ATOM	2573	CG2	THR 361	43.135	-1.223	78.618	1.00	28.90

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	ATOM	2574	C	THR 361	43.162	-1.637	75.853	1.00	35.59
	ATOM	2575	O	THR 361	42.600	-0.545	75.837	1.00	37.16
	ATOM	2576	N	THR 362	44.253	-1.879	75.135	1.00	37.62
	ATOM	2577	CA	THR 362	44.812	-0.819	74.303	1.00	37.63
5	ATOM	2578	CB	THR 362	46.341	-0.949	74.156	1.00	38.04
	ATOM	2579	OG1	THR 362	46.950	-0.981	75.453	1.00	37.77
	ATOM	2580	CG2	THR 362	46.890	0.242	73.395	1.00	37.49
	ATOM	2581	C	THR 362	44.183	-0.839	72.928	1.00	36.67
	ATOM	2582	O	THR 362	43.758	0.194	72.416	1.00	34.48
10	ATOM	2583	N	ASP 363	44.132	-2.032	72.345	1.00	37.88
	ATOM	2584	CA	ASP 363	43.555	-2.246	71.024	1.00	40.18
	ATOM	2585	CB	ASP 363	43.238	-3.729	70.842	1.00	42.13
	ATOM	2586	CG	ASP 363	44.477	-4.557	70.666	1.00	45.73
	ATOM	2587	OD1	ASP 363	44.433	-5.779	70.932	1.00	49.54
15	ATOM	2588	OD2	ASP 363	45.500	-3.976	70.247	1.00	46.04
	ATOM	2589	C	ASP 363	42.289	-1.429	70.841	1.00	40.28
	ATOM	2590	O	ASP 363	42.070	-0.801	69.802	1.00	38.03
	ATOM	2591	N	CYS 364	41.455	-1.449	71.871	1.00	41.60
	ATOM	2592	CA	CYS 364	40.197	-0.724	71.849	1.00	41.33
20	ATOM	2593	CB	CYS 364	39.426	-1.036	73.131	1.00	41.81
	ATOM	2594	SG	CYS 364	39.078	-2.818	73.225	1.00	41.98
	ATOM	2595	C	CYS 364	40.447	0.766	71.685	1.00	39.78
	ATOM	2596	O	CYS 364	39.991	1.382	70.721	1.00	37.44
	ATOM	2597	N	ASP 365	41.194	1.333	72.622	1.00	38.65
25	ATOM	2598	CA	ASP 365	41.525	2.744	72.580	1.00	37.87
	ATOM	2599	CB	ASP 365	42.498	3.060	73.709	1.00	39.53
	ATOM	2600	CG	ASP 365	42.073	2.424	75.014	1.00	42.28
	ATOM	2601	OD1	ASP 365	40.887	2.000	75.096	1.00	43.06
	ATOM	2602	OD2	ASP 365	42.908	2.355	75.949	1.00	41.82

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	ATOM	2603	C	ASP 365	42.123	3.092	71.220	1.00	35.70
	ATOM	2604	O	ASP 365	41.887	4.173	70.682	1.00	35.49
	ATOM	2605	N	ILE 366	42.895	2.175	70.655	1.00	32.72
	ATOM	2606	CA	ILE 366	43.469	2.428	69.347	1.00	31.21
5	ATOM	2607	CB	ILE 366	44.345	1.241	68.891	1.00	30.98
	ATOM	2608	CG2	ILE 366	44.878	1.488	67.482	1.00	30.08
	ATOM	2609	CG1	ILE 366	45.472	1.010	69.907	1.00	30.05
	ATOM	2610	CD1	ILE 366	46.426	2.165	70.071	1.00	26.19
	ATOM	2611	C	ILE 366	42.292	2.622	68.384	1.00	30.65
10	ATOM	2612	O	ILE 366	42.140	3.686	67.790	1.00	29.65
	ATOM	2613	N	VAL 367	41.451	1.598	68.255	1.00	29.81
	ATOM	2614	CA	VAL 367	40.287	1.665	67.378	1.00	27.24
	ATOM	2615	CB	VAL 367	39.397	0.424	67.541	1.00	26.77
	ATOM	2616	CG1	VAL 367	38.193	0.520	66.630	1.00	25.16
15	ATOM	2617	CG2	VAL 367	40.190	-0.817	67.220	1.00	27.90
	ATOM	2618	C	VAL 367	39.453	2.910	67.657	1.00	26.82
	ATOM	2619	O	VAL 367	39.061	3.606	66.727	1.00	27.16
	ATOM	2620	N	ARG 368	39.171	3.191	68.927	1.00	25.49
	ATOM	2621	CA	ARG 368	38.398	4.380	69.266	1.00	24.26
20	ATOM	2622	CB	ARG 368	38.431	4.644	70.772	1.00	23.73
	ATOM	2623	CG	ARG 368	37.765	5.951	71.217	1.00	26.32
	ATOM	2624	CD	ARG 368	36.239	5.948	71.033	1.00	32.00
	ATOM	2625	NE	ARG 368	35.542	5.015	71.926	1.00	33.36
	ATOM	2626	CZ	ARG 368	35.558	5.096	73.253	1.00	33.30
25	ATOM	2627	NH1	ARG 368	36.237	6.069	73.843	1.00	36.87
	ATOM	2628	NH2	ARG 368	34.904	4.209	73.990	1.00	30.08
	ATOM	2629	C	ARG 368	39.034	5.545	68.539	1.00	25.24
	ATOM	2630	O	ARG 368	38.403	6.175	67.700	1.00	26.08
	ATOM	2631	N	ARG 369	40.299	5.808	68.844	1.00	26.69

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	ATOM	2632	CA	ARG 369	41.022	6.905	68.226	1.00	28.80
	ATOM	2633	CB	ARG 369	42.500	6.842	68.619	1.00	33.81
	ATOM	2634	CG	ARG 369	42.992	8.041	69.421	1.00	41.54
	ATOM	2635	CD	ARG 369	44.246	8.666	68.797	1.00	47.78
5	ATOM	2636	NE	ARG 369	44.827	9.709	69.642	1.00	53.83
	ATOM	2637	CZ	ARG 369	45.436	9.479	70.803	1.00	57.34
	ATOM	2638	NH1	ARG 369	45.547	8.234	71.256	1.00	57.39
	ATOM	2639	NH2	ARG 369	45.925	10.492	71.517	1.00	58.51
	ATOM	2640	C	ARG 369	40.888	6.941	66.704	1.00	27.66
10	ATOM	2641	O	ARG 369	40.898	8.017	66.116	1.00	27.35
	ATOM	2642	N	ALA 370	40.760	5.778	66.071	1.00	28.23
	ATOM	2643	CA	ALA 370	40.622	5.699	64.613	1.00	29.69
	ATOM	2644	CB	ALA 370	40.779	4.264	64.144	1.00	27.18
	ATOM	2645	C	ALA 370	39.266	6.218	64.184	1.00	32.49
15	ATOM	2646	O	ALA 370	39.155	7.084	63.313	1.00	33.37
	ATOM	2647	N	CYS 371	38.229	5.663	64.797	1.00	35.80
	ATOM	2648	CA	CYS 371	36.860	6.053	64.500	1.00	37.09
	ATOM	2649	CB	CYS 371	35.892	5.310	65.427	1.00	37.67
	ATOM	2650	SG	CYS 371	35.709	3.539	65.052	1.00	43.56
20	ATOM	2651	C	CYS 371	36.692	7.555	64.663	1.00	36.66
	ATOM	2652	O	CYS 371	36.237	8.231	63.746	1.00	36.14
	ATOM	2653	N	GLU 372	37.079	8.065	65.829	1.00	36.70
	ATOM	2654	CA	GLU 372	36.962	9.482	66.140	1.00	37.83
	ATOM	2655	CB	GLU 372	37.440	9.741	67.569	1.00	41.72
25	ATOM	2656	CG	GLU 372	37.405	11.202	67.993	1.00	50.44
	ATOM	2657	CD	GLU 372	38.615	11.981	67.504	1.00	56.78
	ATOM	2658	OE1	GLU 372	39.747	11.656	67.940	1.00	60.05
	ATOM	2659	OE2	GLU 372	38.437	12.914	66.685	1.00	59.31
	ATOM	2660	C	GLU 372	37.736	10.344	65.163	1.00	36.14



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	ATOM	2661	O	GLU 372	37.280	11.410	64.745	1.00	34.24
	ATOM	2662	N	SER 373	38.917	9.890	64.793	1.00	37.31
	ATOM	2663	CA	SER 373	39.703	10.662	63.856	1.00	39.48
	ATOM	2664	CB	SER 373	41.095	10.040	63.694	1.00	40.54
5	ATOM	2665	OG	SER 373	41.014	8.697	63.253	1.00	41.31
	ATOM	2666	C	SER 373	38.966	10.713	62.516	1.00	38.54
	ATOM	2667	O	SER 373	38.778	11.790	61.953	1.00	39.30
	ATOM	2668	N	VAL 374	38.528	9.552	62.029	1.00	35.74
	ATOM	2669	CA	VAL 374	37.817	9.462	60.755	1.00	34.53
10	ATOM	2670	CB	VAL 374	37.519	7.987	60.388	1.00	33.30
	ATOM	2671	CG1	VAL 374	36.688	7.897	59.119	1.00	30.40
	ATOM	2672	CG2	VAL 374	38.811	7.257	60.186	1.00	34.78
	ATOM	2673	C	VAL 374	36.512	10.250	60.736	1.00	35.17
	ATOM	2674	O	VAL 374	36.253	11.010	59.797	1.00	34.51
15	ATOM	2675	N	SER 375	35.700	10.080	61.775	1.00	35.24
	ATOM	2676	CA	SER 375	34.416	10.768	61.866	1.00	34.91
	ATOM	2677	CB	SER 375	33.641	10.312	63.103	1.00	35.91
	ATOM	2678	OG	SER 375	33.802	11.230	64.178	1.00	37.28
	ATOM	2679	C	SER 375	34.585	12.272	61.933	1.00	34.67
20	ATOM	2680	O	SER 375	33.865	13.010	61.266	1.00	35.17
	ATOM	2681	N	THR 376	35.534	12.725	62.743	1.00	34.00
	ATOM	2682	CA	THR 376	35.768	14.150	62.889	1.00	35.55
	ATOM	2683	CB	THR 376	36.827	14.421	63.954	1.00	38.06
	ATOM	2684	OG1	THR 376	36.461	13.739	65.158	1.00	40.51
25	ATOM	2685	CG2	THR 376	36.926	15.923	64.239	1.00	38.22
	ATOM	2686	C	THR 376	36.208	14.788	61.583	1.00	34.80
	ATOM	2687	O	THR 376	35.794	15.901	61.241	1.00	32.23
	ATOM	2688	N	ARG 377	37.049	14.078	60.848	1.00	36.51
	ATOM	2689	CA	ARG 377	37.523	14.601	59.581	1.00	38.20

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	ATOM	2690	CB	ARG 377	38.535	13.640	58.956	1.00	41.90
	ATOM	2691	CG	ARG 377	39.417	14.271	57.892	1.00	43.83
	ATOM	2692	CD	ARG 377	38.735	14.280	56.551	1.00	46.24
	ATOM	2693	NE	ARG 377	38.467	12.921	56.074	1.00	50.02
5	ATOM	2694	CZ	ARG 377	39.400	12.058	55.679	1.00	48.89
	ATOM	2695	NH1	ARG 377	40.681	12.405	55.700	1.00	47.77
	ATOM	2696	NH2	ARG 377	39.050	10.849	55.256	1.00	48.65
	ATOM	2697	C	ARG 377	36.311	14.759	58.688	1.00	37.15
	ATOM	2698	O	ARG 377	36.163	15.780	58.016	1.00	37.23
10	ATOM	2699	N	ALA 378	35.445	13.744	58.706	1.00	36.43
	ATOM	2700	CA	ALA 378	34.212	13.732	57.920	1.00	35.58
	ATOM	2701	CB	ALA 378	33.470	12.430	58.130	1.00	35.75
	ATOM	2702	C	ALA 378	33.314	14.897	58.304	1.00	34.75
	ATOM	2703	O	ALA 378	32.675	15.507	57.451	1.00	34.63
15	ATOM	2704	N	ALA 379	33.249	15.204	59.590	1.00	34.17
	ATOM	2705	CA	ALA 379	32.427	16.317	60.009	1.00	34.54
	ATOM	2706	CB	ALA 379	32.281	16.340	61.515	1.00	32.43
	ATOM	2707	C	ALA 379	33.073	17.607	59.519	1.00	35.95
	ATOM	2708	O	ALA 379	32.465	18.358	58.761	1.00	38.27
20	ATOM	2709	N	HIS 380	34.314	17.856	59.925	1.00	35.13
	ATOM	2710	CA	HIS 380	34.994	19.083	59.526	1.00	34.04
	ATOM	2711	CB	HIS 380	36.448	19.031	59.968	1.00	37.01
	ATOM	2712	CG	HIS 380	36.628	19.284	61.430	1.00	42.02
	ATOM	2713	CD2	HIS 380	35.734	19.637	62.385	1.00	43.27
25	ATOM	2714	ND1	HIS 380	37.852	19.206	62.058	1.00	44.66
	ATOM	2715	CE1	HIS 380	37.704	19.500	63.339	1.00	46.06
	ATOM	2716	NE2	HIS 380	36.429	19.766	63.562	1.00	44.63
	ATOM	2717	C	HIS 380	34.894	19.405	58.045	1.00	32.37
	ATOM	2718	O	HIS 380	34.581	20.536	57.671	1.00	29.98

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	ATOM	2719	N	MET 381	35.154	18.417	57.197	1.00	30.55
	ATOM	2720	CA	MET 381	35.055	18.640	55.764	1.00	30.35
	ATOM	2721	CB	MET 381	35.383	17.365	54.992	1.00	28.41
	ATOM	2722	CG	MET 381	36.852	17.181	54.767	1.00	28.31
5	ATOM	2723	SD	MET 381	37.505	18.684	54.017	1.00	31.73
	ATOM	2724	CE	MET 381	38.142	18.070	52.446	1.00	30.02
	ATOM	2725	C	MET 381	33.647	19.101	55.415	1.00	32.29
	ATOM	2726	O	MET 381	33.453	19.930	54.527	1.00	32.42
	ATOM	2727	N	CYS 382	32.660	18.566	56.124	1.00	33.02
10	ATOM	2728	CA	CYS 382	31.279	18.942	55.869	1.00	33.44
	ATOM	2729	CB	CYS 382	30.323	18.012	56.625	1.00	33.78
	ATOM	2730	SG	CYS 382	28.582	18.152	56.124	1.00	40.21
	ATOM	2731	C	CYS 382	31.087	20.387	56.316	1.00	33.02
	ATOM	2732	O	CYS 382	30.566	21.218	55.563	1.00	32.71
15	ATOM	2733	N	SER 383	31.528	20.686	57.537	1.00	33.57
	ATOM	2734	CA	SER 383	31.418	22.037	58.097	1.00	33.39
	ATOM	2735	CB	SER 383	32.232	22.159	59.392	1.00	32.88
	ATOM	2736	OG	SER 383	33.605	21.877	59.176	1.00	31.29
	ATOM	2737	C	SER 383	31.935	23.042	57.085	1.00	32.50
20	ATOM	2738	O	SER 383	31.314	24.073	56.832	1.00	32.64
	ATOM	2739	N	ALA 384	33.082	22.729	56.501	1.00	30.75
	ATOM	2740	CA	ALA 384	33.663	23.607	55.510	1.00	29.62
	ATOM	2741	CB	ALA 384	34.787	22.885	54.789	1.00	29.04
	ATOM	2742	C	ALA 384	32.604	24.095	54.509	1.00	29.94
25	ATOM	2743	O	ALA 384	32.211	25.259	54.544	1.00	28.35
	ATOM	2744	N	GLY 385	32.141	23.193	53.639	1.00	31.38
	ATOM	2745	CA	GLY 385	31.149	23.525	52.621	1.00	30.00
	ATOM	2746	C	GLY 385	29.870	24.198	53.090	1.00	30.54
	ATOM	2747	O	GLY 385	29.522	25.285	52.613	1.00	28.88

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	ATOM	2748	N	LEU 386	29.151	23.559	54.010	1.00	29.58
	ATOM	2749	CA	LEU 386	27.917	24.148	54.522	1.00	28.86
	ATOM	2750	CB	LEU 386	27.410	23.374	55.749	1.00	25.55
	ATOM	2751	CG	LEU 386	26.141	23.824	56.493	1.00	21.28
5	ATOM	2752	CD1	LEU 386	26.504	24.768	57.605	1.00	18.56
	ATOM	2753	CD2	LEU 386	25.157	24.456	55.533	1.00	17.77
	ATOM	2754	C	LEU 386	28.199	25.595	54.898	1.00	30.29
	ATOM	2755	O	LEU 386	27.344	26.458	54.728	1.00	30.86
	ATOM	2756	N	ALA 387	29.413	25.846	55.393	1.00	32.40
10	ATOM	2757	CA	ALA 387	29.851	27.184	55.799	1.00	32.84
	ATOM	2758	CB	ALA 387	31.181	27.101	56.536	1.00	31.99
	ATOM	2759	C	ALA 387	29.991	28.098	54.585	1.00	34.20
	ATOM	2760	O	ALA 387	29.509	29.235	54.588	1.00	34.34
	ATOM	2761	N	GLY 388	30.663	27.597	53.553	1.00	34.88
15	ATOM	2762	CA	GLY 388	30.831	28.378	52.344	1.00	35.13
	ATOM	2763	C	GLY 388	29.467	28.833	51.867	1.00	35.42
	ATOM	2764	O	GLY 388	29.257	30.005	51.545	1.00	36.39
	ATOM	2765	N	VAL 389	28.524	27.898	51.839	1.00	34.42
	ATOM	2766	CA	VAL 389	27.167	28.202	51.402	1.00	32.28
20	ATOM	2767	CB	VAL 389	26.266	26.949	51.487	1.00	31.56
	ATOM	2768	CG1	VAL 389	24.856	27.285	51.027	1.00	28.68
	ATOM	2769	CG2	VAL 389	26.853	25.836	50.638	1.00	28.05
	ATOM	2770	C	VAL 389	26.579	29.307	52.273	1.00	30.86
	ATOM	2771	O	VAL 389	26.072	30.304	51.762	1.00	26.91
25	ATOM	2772	N	ILE 390	26.665	29.115	53.586	1.00	31.06
	ATOM	2773	CA	ILE 390	26.146	30.073	54.548	1.00	34.83
	ATOM	2774	CB	ILE 390	26.262	29.538	56.001	1.00	32.76
	ATOM	2775	CG2	ILE 390	25.733	30.562	56.996	1.00	31.45
	ATOM	2776	CG1	ILE 390	25.425	28.274	56.154	1.00	32.06

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	ATOM	2777	CD1	ILE	390	25.311	27.804	57.572	1.00	31.73
	ATOM	2778	C	ILE	390	26.858	31.415	54.444	1.00	39.01
	ATOM	2779	O	ILE	390	26.209	32.465	54.370	1.00	42.11
	ATOM	2780	N	ASN	391	28.186	31.398	54.437	1.00	41.07
5	ATOM	2781	CA	ASN	391	28.921	32.652	54.326	1.00	42.97
	ATOM	2782	CB	ASN	391	30.430	32.386	54.290	1.00	47.00
	ATOM	2783	CG	ASN	391	31.061	32.452	55.678	1.00	51.32
	ATOM	2784	OD1	ASN	391	32.205	32.029	55.878	1.00	51.98
	ATOM	2785	ND2	ASN	391	30.312	32.996	56.646	1.00	51.87
10	ATOM	2786	C	ASN	391	28.459	33.377	53.070	1.00	42.59
	ATOM	2787	O	ASN	391	27.927	34.488	53.141	1.00	40.64
	ATOM	2788	N	ARG	392	28.638	32.723	51.928	1.00	43.30
	ATOM	2789	CA	ARG	392	28.237	33.277	50.644	1.00	45.75
	ATOM	2790	CB	ARG	392	28.328	32.182	49.571	1.00	48.20
15	ATOM	2791	CG	ARG	392	27.020	31.811	48.892	1.00	54.22
	ATOM	2792	CD	ARG	392	26.803	32.578	47.590	1.00	59.36
	ATOM	2793	NE	ARG	392	27.491	31.984	46.437	1.00	66.46
	ATOM	2794	CZ	ARG	392	28.794	32.098	46.156	1.00	69.91
	ATOM	2795	NH1	ARG	392	29.613	32.793	46.941	1.00	69.61
20	ATOM	2796	NH2	ARG	392	29.279	31.524	45.063	1.00	70.50
	ATOM	2797	C	ARG	392	26.822	33.854	50.711	1.00	45.30
	ATOM	2798	O	ARG	392	26.474	34.777	49.973	1.00	44.35
	ATOM	2799	N	MET	393	26.009	33.316	51.607	1.00	47.21
	ATOM	2800	CA	MET	393	24.640	33.785	51.739	1.00	50.87
25	ATOM	2801	CB	MET	393	23.761	32.687	52.346	1.00	49.84
	ATOM	2802	CG	MET	393	23.427	31.551	51.389	1.00	45.97
	ATOM	2803	SD	MET	393	22.244	30.416	52.096	1.00	42.67
	ATOM	2804	CE	MET	393	20.761	31.465	52.244	1.00	42.67
	ATOM	2805	C	MET	393	24.559	35.046	52.581	1.00	54.43

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	ATOM	2806	O	MET 393	23.631	35.851	52.443	1.00	53.85
	ATOM	2807	N	ARG 394	25.528	35.208	53.469	1.00	59.09
	ATOM	2808	CA	ARG 394	25.568	36.386	54.314	1.00	64.57
	ATOM	2809	CB	ARG 394	26.624	36.224	55.404	1.00	65.91
5	ATOM	2810	CG	ARG 394	26.830	37.477	56.228	1.00	67.95
	ATOM	2811	CD	ARG 394	28.048	37.364	57.130	1.00	69.02
	ATOM	2812	NE	ARG 394	28.499	38.673	57.600	1.00	68.97
	ATOM	2813	CZ	ARG 394	27.776	39.494	58.357	1.00	69.21
	ATOM	2814	NH1	ARG 394	26.553	39.151	58.743	1.00	70.35
10	ATOM	2815	NH2	ARG 394	28.281	40.662	58.732	1.00	68.24
	ATOM	2816	C	ARG 394	25.952	37.537	53.404	1.00	67.94
	ATOM	2817	O	ARG 394	25.306	38.588	53.391	1.00	67.14
	ATOM	2818	N	GLU 395	27.012	37.313	52.633	1.00	72.08
	ATOM	2819	CA	GLU 395	27.513	38.314	51.707	1.00	77.04
15	ATOM	2820	CB	GLU 395	28.578	37.691	50.784	1.00	78.09
	ATOM	2821	CG	GLU 395	29.425	38.685	49.955	1.00	81.99
	ATOM	2822	CD	GLU 395	30.402	39.533	50.789	1.00	84.19
	ATOM	2823	OE1	GLU 395	29.949	40.442	51.526	1.00	83.64
	ATOM	2824	OE2	GLU 395	31.631	39.290	50.702	1.00	84.22
20	ATOM	2825	C	GLU 395	26.340	38.873	50.898	1.00	79.30
	ATOM	2826	O	GLU 395	26.250	40.078	50.683	1.00	81.15
	ATOM	2827	N	SER 396	25.423	38.007	50.481	1.00	81.59
	ATOM	2828	CA	SER 396	24.276	38.451	49.696	1.00	83.40
	ATOM	2829	CB	SER 396	23.379	37.264	49.366	1.00	84.05
25	ATOM	2830	OG	SER 396	24.123	36.252	48.716	1.00	86.28
	ATOM	2831	C	SER 396	23.462	39.526	50.406	1.00	84.36
	ATOM	2832	O	SER 396	23.578	40.708	50.092	1.00	84.49
	ATOM	2833	N	ARG 397	22.639	39.118	51.362	1.00	86.41
	ATOM	2834	CA	ARG 397	21.812	40.070	52.090	1.00	88.71

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	ATOM	2835	CB	ARG 397	20.682	39.335	52.816	1.00	89.74
	ATOM	2836	CG	ARG 397	19.579	40.241	53.346	1.00	90.87
	ATOM	2837	CD	ARG 397	19.096	39.776	54.713	1.00	91.04
	ATOM	2838	NE	ARG 397	20.021	40.158	55.782	1.00	89.87
5	ATOM	2839	CZ	ARG 397	19.905	39.766	57.047	1.00	89.80
	ATOM	2840	NH1	ARG 397	18.906	38.971	57.409	1.00	91.15
	ATOM	2841	NH2	ARG 397	20.779	40.174	57.955	1.00	87.97
	ATOM	2842	C	ARG 397	22.653	40.847	53.102	1.00	89.74
	ATOM	2843	O	ARG 397	22.585	40.588	54.305	1.00	90.41
10	ATOM	2844	N	SER 398	23.448	41.795	52.614	1.00	90.58
	ATOM	2845	CA	SER 398	24.288	42.602	53.492	1.00	91.09
	ATOM	2846	CB	SER 398	24.903	43.782	52.718	1.00	91.14
	ATOM	2847	OG	SER 398	25.845	43.347	51.747	1.00	89.49
	ATOM	2848	C	SER 398	23.470	43.129	54.677	1.00	91.27
15	ATOM	2849	O	SER 398	22.458	43.810	54.496	1.00	91.10
	ATOM	2850	N	GLU 399	23.904	42.786	55.887	1.00	91.43
	ATOM	2851	CA	GLU 399	23.238	43.233	57.108	1.00	90.89
	ATOM	2852	CB	GLU 399	21.799	42.705	57.183	1.00	91.87
	ATOM	2853	CG	GLU 399	20.969	43.349	58.298	1.00	93.31
20	ATOM	2854	CD	GLU 399	20.726	44.836	58.064	1.00	94.22
	ATOM	2855	OE1	GLU 399	20.270	45.533	58.999	1.00	93.53
	ATOM	2856	OE2	GLU 399	20.986	45.307	56.936	1.00	94.80
	ATOM	2857	C	GLU 399	24.013	42.774	58.339	1.00	89.25
	ATOM	2858	O	GLU 399	24.987	42.029	58.236	1.00	88.96
25	ATOM	2859	N	ASP 400	23.570	43.226	59.502	1.00	87.38
	ATOM	2860	CA	ASP 400	24.214	42.883	60.754	1.00	85.70
	ATOM	2861	CB	ASP 400	23.332	43.352	61.915	1.00	88.35
	ATOM	2862	CG	ASP 400	22.861	44.795	61.743	1.00	90.64
	ATOM	2863	OD1	ASP 400	22.059	45.055	60.817	1.00	91.42

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	ATOM	2864	OD2	ASP	400	23.297	45.671	62.524	1.00	91.68
	ATOM	2865	C	ASP	400	24.496	41.385	60.853	1.00	82.94
	ATOM	2866	O	ASP	400	25.506	40.900	60.346	1.00	82.03
	ATOM	2867	N	VAL	401	23.593	40.658	61.502	1.00	79.90
5	ATOM	2868	CA	VAL	401	23.738	39.219	61.682	1.00	75.91
	ATOM	2869	CB	VAL	401	23.607	38.841	63.153	1.00	74.20
	ATOM	2870	CG1	VAL	401	24.803	39.343	63.927	1.00	73.12
	ATOM	2871	CG2	VAL	401	22.314	39.430	63.710	1.00	72.79
	ATOM	2872	C	VAL	401	22.662	38.458	60.925	1.00	74.63
10	ATOM	2873	O	VAL	401	21.489	38.846	60.942	1.00	75.56
	ATOM	2874	N	MET	402	23.063	37.365	60.278	1.00	70.61
	ATOM	2875	CA	MET	402	22.130	36.539	59.521	1.00	65.65
	ATOM	2876	CB	MET	402	22.818	35.887	58.325	1.00	62.74
	ATOM	2877	CG	MET	402	21.897	34.958	57.543	1.00	56.61
15	ATOM	2878	SD	MET	402	22.543	34.551	55.906	1.00	52.49
	ATOM	2879	CE	MET	402	23.857	33.399	56.323	1.00	49.76
	ATOM	2880	C	MET	402	21.532	35.450	60.381	1.00	65.00
	ATOM	2881	O	MET	402	22.222	34.513	60.781	1.00	65.18
	ATOM	2882	N	ARG	403	20.241	35.575	60.657	1.00	63.62
20	ATOM	2883	CA	ARG	403	19.535	34.593	61.462	1.00	61.57
	ATOM	2884	CB	ARG	403	18.418	35.275	62.262	1.00	64.83
	ATOM	2885	CG	ARG	403	18.856	36.547	62.987	1.00	70.01
	ATOM	2886	CD	ARG	403	17.691	37.205	63.724	1.00	75.36
	ATOM	2887	NE	ARG	403	17.412	36.582	65.018	1.00	80.50
25	ATOM	2888	CZ	ARG	403	16.305	36.788	65.731	1.00	83.41
	ATOM	2889	NH1	ARG	403	15.358	37.603	65.277	1.00	84.55
	ATOM	2890	NH2	ARG	403	16.147	36.187	66.907	1.00	83.64
	ATOM	2891	C	ARG	403	18.946	33.560	60.504	1.00	57.99
	ATOM	2892	O	ARG	403	17.775	33.639	60.135	1.00	58.57



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	ATOM	2893	N	ILE 404	19.762	32.597	60.091	1.00	52.97
	ATOM	2894	CA	ILE 404	19.301	31.570	59.170	1.00	49.14
	ATOM	2895	CB	ILE 404	20.293	31.412	57.999	1.00	47.44
	ATOM	2896	CG2	ILE 404	21.538	30.680	58.458	1.00	43.94
5	ATOM	2897	CG1	ILE 404	19.629	30.649	56.854	1.00	48.45
	ATOM	2898	CD1	ILE 404	20.477	30.559	55.598	1.00	48.95
	ATOM	2899	C	ILE 404	19.126	30.222	59.879	1.00	48.34
	ATOM	2900	O	ILE 404	19.771	29.967	60.897	1.00	48.83
	ATOM	2901	N	THR 405	18.236	29.380	59.346	1.00	46.42
10	ATOM	2902	CA	THR 405	17.956	28.043	59.892	1.00	42.37
	ATOM	2903	CB	THR 405	16.451	27.838	60.222	1.00	41.93
	ATOM	2904	OG1	THR 405	16.010	28.839	61.145	1.00	43.89
	ATOM	2905	CG2	THR 405	16.227	26.475	60.849	1.00	38.85
	ATOM	2906	C	THR 405	18.332	26.990	58.857	1.00	39.95
15	ATOM	2907	O	THR 405	18.178	27.204	57.653	1.00	38.97
	ATOM	2908	N	VAL 406	18.809	25.844	59.324	1.00	38.10
	ATOM	2909	CA	VAL 406	19.195	24.776	58.414	1.00	36.64
	ATOM	2910	CB	VAL 406	20.686	24.442	58.563	1.00	35.12
	ATOM	2911	CG1	VAL 406	21.069	23.342	57.600	1.00	35.29
20	ATOM	2912	CG2	VAL 406	21.515	25.672	58.303	1.00	35.40
	ATOM	2913	C	VAL 406	18.390	23.499	58.635	1.00	35.83
	ATOM	2914	O	VAL 406	18.214	23.058	59.765	1.00	37.06
	ATOM	2915	N	GLY 407	17.895	22.915	57.549	1.00	34.50
	ATOM	2916	CA	GLY 407	17.143	21.680	57.653	1.00	32.79
25	ATOM	2917	C	GLY 407	18.074	20.522	57.353	1.00	32.90
	ATOM	2918	O	GLY 407	18.704	20.467	56.294	1.00	33.85
	ATOM	2919	N	VAL 408	18.177	19.585	58.279	1.00	31.27
	ATOM	2920	CA	VAL 408	19.064	18.466	58.054	1.00	29.57
	ATOM	2921	CB	VAL 408	20.199	18.491	59.042	1.00	29.66

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	ATOM	2922	CG1	VAL	408	21.390	17.767	58.468	1.00	31.77
	ATOM	2923	CG2	VAL	408	20.515	19.916	59.412	1.00	29.91
	ATOM	2924	C	VAL	408	18.366	17.135	58.206	1.00	29.58
	ATOM	2925	O	VAL	408	17.392	17.015	58.942	1.00	28.54
5	ATOM	2926	N	ASP	409	18.878	16.131	57.509	1.00	30.15
	ATOM	2927	CA	ASP	409	18.324	14.789	57.598	1.00	31.95
	ATOM	2928	CB	ASP	409	17.109	14.635	56.674	1.00	35.66
	ATOM	2929	CG	ASP	409	16.455	13.252	56.775	1.00	40.01
	ATOM	2930	OD1	ASP	409	15.613	12.928	55.898	1.00	40.26
10	ATOM	2931	OD2	ASP	409	16.773	12.499	57.728	1.00	39.33
	ATOM	2932	C	ASP	409	19.415	13.824	57.180	1.00	31.91
	ATOM	2933	O	ASP	409	20.352	14.208	56.484	1.00	32.39
	ATOM	2934	N	GLY	410	19.300	12.574	57.607	1.00	31.09
	ATOM	2935	CA	GLY	410	20.299	11.593	57.233	1.00	29.56
15	ATOM	2936	C	GLY	410	20.703	10.704	58.385	1.00	29.32
	ATOM	2937	O	GLY	410	20.510	11.041	59.558	1.00	28.27
	ATOM	2938	N	SER	411	21.282	9.559	58.053	1.00	28.24
	ATOM	2939	CA	SER	411	21.699	8.631	59.086	1.00	27.52
	ATOM	2940	CB	SER	411	22.018	7.253	58.481	1.00	29.46
20	ATOM	2941	OG	SER	411	23.016	7.316	57.471	1.00	31.64
	ATOM	2942	C	SER	411	22.895	9.160	59.863	1.00	25.78
	ATOM	2943	O	SER	411	22.909	9.113	61.090	1.00	25.89
	ATOM	2944	N	VAL	412	23.890	9.687	59.161	1.00	23.18
	ATOM	2945	CA	VAL	412	25.076	10.185	59.839	1.00	21.25
25	ATOM	2946	CB	VAL	412	26.099	10.669	58.841	1.00	20.56
	ATOM	2947	CG1	VAL	412	27.372	11.084	59.564	1.00	17.73
	ATOM	2948	CG2	VAL	412	26.378	9.552	57.857	1.00	20.59
	ATOM	2949	C	VAL	412	24.769	11.300	60.818	1.00	20.44
	ATOM	2950	O	VAL	412	25.182	11.262	61.983	1.00	21.51

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	ATOM	2951	N	TYR 413	24.033	12.288	60.340	1.00	16.42
	ATOM	2952	CA	TYR 413	23.659	13.409	61.171	1.00	16.41
	ATOM	2953	CB	TYR 413	23.095	14.526	60.288	1.00	16.40
	ATOM	2954	CG	TYR 413	22.700	15.762	61.051	1.00	14.37
5	ATOM	2955	CD1	TYR 413	23.645	16.707	61.434	1.00	13.43
	ATOM	2956	CE1	TYR 413	23.296	17.789	62.226	1.00	13.93
	ATOM	2957	CD2	TYR 413	21.401	15.939	61.470	1.00	13.10
	ATOM	2958	CE2	TYR 413	21.049	17.007	62.256	1.00	15.82
	ATOM	2959	CZ	TYR 413	21.994	17.927	62.638	1.00	14.65
10	ATOM	2960	OH	TYR 413	21.620	18.948	63.475	1.00	16.02
	ATOM	2961	C	TYR 413	22.626	13.007	62.233	1.00	17.41
	ATOM	2962	O	TYR 413	22.364	13.758	63.172	1.00	18.36
	ATOM	2963	N	LYS 414	22.035	11.826	62.103	1.00	18.12
	ATOM	2964	CA	LYS 414	21.033	11.426	63.083	1.00	19.00
15	ATOM	2965	CB	LYS 414	19.706	11.130	62.384	1.00	19.22
	ATOM	2966	CG	LYS 414	18.962	12.358	61.894	1.00	18.92
	ATOM	2967	CD	LYS 414	17.615	11.965	61.314	1.00	21.36
	ATOM	2968	CE	LYS 414	16.829	13.181	60.855	1.00	25.08
	ATOM	2969	NZ	LYS 414	15.567	12.829	60.132	1.00	28.46
20	ATOM	2970	C	LYS 414	21.400	10.249	63.975	1.00	20.50
	ATOM	2971	O	LYS 414	20.637	9.883	64.871	1.00	21.27
	ATOM	2972	N	LEU 415	22.565	9.655	63.753	1.00	22.22
	ATOM	2973	CA	LEU 415	22.958	8.511	64.565	1.00	23.27
	ATOM	2974	CB	LEU 415	22.679	7.218	63.784	1.00	21.47
25	ATOM	2975	CG	LEU 415	21.234	6.978	63.313	1.00	17.45
	ATOM	2976	CD1	LEU 415	21.158	5.672	62.545	1.00	16.66
	ATOM	2977	CD2	LEU 415	20.293	6.954	64.498	1.00	14.44
	ATOM	2978	C	LEU 415	24.418	8.566	65.033	1.00	25.05
	ATOM	2979	O	LEU 415	24.921	7.625	65.657	1.00	26.05

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	ATOM	2980	N	HIS 416	25.095	9.673	64.736	1.00	24.04
	ATOM	2981	CA	HIS 416	26.481	9.852	65.147	1.00	22.40
	ATOM	2982	CB	HIS 416	27.365	9.997	63.922	1.00	23.29
	ATOM	2983	CG	HIS 416	27.383	8.774	63.069	1.00	25.75
5	ATOM	2984	CD2	HIS 416	28.392	7.937	62.729	1.00	27.82
	ATOM	2985	ND1	HIS 416	26.241	8.248	62.506	1.00	26.69
	ATOM	2986	CE1	HIS 416	26.545	7.138	61.857	1.00	28.69
	ATOM	2987	NE2	HIS 416	27.844	6.926	61.977	1.00	28.20
	ATOM	2988	C	HIS 416	26.577	11.080	66.027	1.00	21.63
10	ATOM	2989	O	HIS 416	26.808	12.184	65.558	1.00	22.44
	ATOM	2990	N	PRO 417	26.386	10.898	67.331	1.00	21.25
	ATOM	2991	CD	PRO 417	26.126	9.627	68.015	1.00	22.18
	ATOM	2992	CA	PRO 417	26.440	11.991	68.297	1.00	22.07
	ATOM	2993	CB	PRO 417	26.447	11.258	69.627	1.00	21.52
15	ATOM	2994	CG	PRO 417	25.565	10.108	69.340	1.00	23.41
	ATOM	2995	C	PRO 417	27.655	12.874	68.113	1.00	22.46
	ATOM	2996	O	PRO 417	27.519	14.076	67.878	1.00	22.18
	ATOM	2997	N	SER 418	28.835	12.262	68.221	1.00	20.96
	ATOM	2998	CA	SER 418	30.105	12.959	68.064	1.00	18.32
20	ATOM	2999	CB	SER 418	31.264	11.962	68.076	1.00	20.88
	ATOM	3000	OG	SER 418	32.419	12.512	67.460	1.00	24.12
	ATOM	3001	C	SER 418	30.099	13.720	66.757	1.00	15.71
	ATOM	3002	O	SER 418	30.269	14.935	66.742	1.00	16.10
	ATOM	3003	N	PHE 419	29.905	13.010	65.656	1.00	11.39
25	ATOM	3004	CA	PHE 419	29.864	13.683	64.379	1.00	10.22
	ATOM	3005	CB	PHE 419	29.243	12.789	63.335	1.00	5.53
	ATOM	3006	CG	PHE 419	29.035	13.468	62.034	1.00	1.42
	ATOM	3007	CD1	PHE 419	29.814	13.137	60.942	1.00	3.13
	ATOM	3008	CD2	PHE 419	28.080	14.449	61.893	1.00	1.00

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	ATOM	3009	CE1	PHE	419	29.648	13.773	59.712	1.00	1.47
	ATOM	3010	CE2	PHE	419	27.909	15.088	60.670	1.00	2.68
	ATOM	3011	CZ	PHE	419	28.699	14.746	59.575	1.00	1.00
	ATOM	3012	C	PHE	419	29.037	14.965	64.472	1.00	12.48
5	ATOM	3013	O	PHE	419	29.520	16.048	64.156	1.00	12.11
	ATOM	3014	N	LYS	420	27.785	14.838	64.900	1.00	15.88
	ATOM	3015	CA	LYS	420	26.917	16.000	64.994	1.00	20.63
	ATOM	3016	CB	LYS	420	25.525	15.610	65.522	1.00	21.26
	ATOM	3017	CG	LYS	420	24.470	16.730	65.361	1.00	22.35
10	ATOM	3018	CD	LYS	420	23.045	16.288	65.686	1.00	22.81
	ATOM	3019	CE	LYS	420	22.942	15.740	67.102	1.00	25.24
	ATOM	3020	NZ	LYS	420	21.616	15.092	67.350	1.00	27.51
	ATOM	3021	C	LYS	420	27.505	17.099	65.866	1.00	24.04
	ATOM	3022	O	LYS	420	27.533	18.260	65.465	1.00	23.74
15	ATOM	3023	N	GLU	421	27.978	16.733	67.053	1.00	29.67
	ATOM	3024	CA	GLU	421	28.550	17.701	67.999	1.00	34.96
	ATOM	3025	CB	GLU	421	29.075	16.972	69.244	1.00	36.76
	ATOM	3026	CG	GLU	421	29.292	17.843	70.480	1.00	40.52
	ATOM	3027	CD	GLU	421	29.895	17.047	71.638	1.00	43.55
20	ATOM	3028	OE1	GLU	421	30.981	16.467	71.445	1.00	47.03
	ATOM	3029	OE2	GLU	421	29.294	16.990	72.734	1.00	43.28
	ATOM	3030	C	GLU	421	29.680	18.512	67.369	1.00	36.40
	ATOM	3031	O	GLU	421	29.689	19.745	67.442	1.00	38.37
	ATOM	3032	N	ARG	422	30.629	17.816	66.751	1.00	35.66
25	ATOM	3033	CA	ARG	422	31.755	18.477	66.124	1.00	35.13
	ATOM	3034	CB	ARG	422	32.801	17.449	65.684	1.00	38.76
	ATOM	3035	CG	ARG	422	33.277	16.525	66.811	1.00	46.51
	ATOM	3036	CD	ARG	422	33.915	17.286	67.980	1.00	51.67
	ATOM	3037	NE	ARG	422	35.322	17.578	67.732	1.00	57.41

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	ATOM	3038	CZ	ARG 422	36.269	16.649	67.625	1.00	60.70
	ATOM	3039	NH1	ARG 422	35.956	15.364	67.749	1.00	60.82
	ATOM	3040	NH2	ARG 422	37.529	17.002	67.380	1.00	61.68
	ATOM	3041	C	ARG 422	31.256	19.278	64.942	1.00	33.47
5	ATOM	3042	O	ARG 422	31.585	20.450	64.803	1.00	35.28
	ATOM	3043	N	PHE 423	30.446	18.654	64.096	1.00	32.46
	ATOM	3044	CA	PHE 423	29.901	19.348	62.930	1.00	30.30
	ATOM	3045	CB	PHE 423	28.949	18.423	62.165	1.00	27.32
	ATOM	3046	CG	PHE 423	28.188	19.106	61.063	1.00	23.75
10	ATOM	3047	CD1	PHE 423	26.891	19.552	61.270	1.00	22.33
	ATOM	3048	CD2	PHE 423	28.765	19.293	59.814	1.00	23.98
	ATOM	3049	CE1	PHE 423	26.178	20.169	60.245	1.00	22.83
	ATOM	3050	CE2	PHE 423	28.061	19.909	58.784	1.00	22.46
	ATOM	3051	CZ	PHE 423	26.769	20.347	59.001	1.00	22.73
15	ATOM	3052	C	PHE 423	29.185	20.663	63.280	1.00	29.75
	ATOM	3053	O	PHE 423	29.328	21.652	62.568	1.00	27.58
	ATOM	3054	N	HIS 424	28.415	20.694	64.363	1.00	30.19
	ATOM	3055	CA	HIS 424	27.743	21.936	64.692	1.00	32.48
	ATOM	3056	CB	HIS 424	26.754	21.760	65.835	1.00	32.75
20	ATOM	3057	CG	HIS 424	25.412	21.279	65.387	1.00	31.94
	ATOM	3058	CD2	HIS 424	24.980	20.860	64.176	1.00	29.85
	ATOM	3059	ND1	HIS 424	24.341	21.147	66.243	1.00	32.28
	ATOM	3060	CE1	HIS 424	23.308	20.661	65.580	1.00	30.67
	ATOM	3061	NE2	HIS 424	23.670	20.477	64.323	1.00	30.19
25	ATOM	3062	C	HIS 424	28.737	23.011	65.048	1.00	35.15
	ATOM	3063	O	HIS 424	28.689	24.102	64.487	1.00	36.91
	ATOM	3064	N	ALA 425	29.636	22.711	65.979	1.00	36.32
	ATOM	3065	CA	ALA 425	30.652	23.675	66.395	1.00	36.74
	ATOM	3066	CB	ALA 425	31.542	23.058	67.444	1.00	35.43

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	ATOM	3067	C	ALA 425	31.492	24.149	65.201	1.00	37.82
	ATOM	3068	O	ALA 425	31.420	25.316	64.809	1.00	38.66
	ATOM	3069	N	SER 426	32.274	23.243	64.617	1.00	37.75
	ATOM	3070	CA	SER 426	33.113	23.576	63.466	1.00	37.83
5	ATOM	3071	CB	SER 426	33.602	22.289	62.782	1.00	38.67
	ATOM	3072	OG	SER 426	34.440	22.560	61.667	1.00	37.85
	ATOM	3073	C	SER 426	32.390	24.461	62.445	1.00	37.21
	ATOM	3074	O	SER 426	33.025	25.151	61.657	1.00	37.08
	ATOM	3075	N	VAL 427	31.064	24.443	62.450	1.00	37.84
10	ATOM	3076	CA	VAL 427	30.321	25.269	61.510	1.00	38.87
	ATOM	3077	CB	VAL 427	28.935	24.667	61.194	1.00	39.38
	ATOM	3078	CG1	VAL 427	28.000	25.744	60.633	1.00	37.50
	ATOM	3079	CG2	VAL 427	29.092	23.534	60.188	1.00	36.83
	ATOM	3080	C	VAL 427	30.138	26.655	62.090	1.00	39.54
15	ATOM	3081	O	VAL 427	30.578	27.639	61.512	1.00	40.58
	ATOM	3082	N	ARG 428	29.483	26.724	63.238	1.00	40.14
	ATOM	3083	CA	ARG 428	29.247	27.993	63.897	1.00	42.86
	ATOM	3084	CB	ARG 428	28.603	27.739	65.258	1.00	42.72
	ATOM	3085	CG	ARG 428	27.288	26.982	65.186	1.00	43.31
20	ATOM	3086	CD	ARG 428	27.139	26.044	66.378	1.00	46.03
	ATOM	3087	NE	ARG 428	25.802	25.461	66.485	1.00	47.83
	ATOM	3088	CZ	ARG 428	24.690	26.173	66.648	1.00	48.39
	ATOM	3089	NH1	ARG 428	24.757	27.499	66.716	1.00	47.35
	ATOM	3090	NH2	ARG 428	23.516	25.559	66.756	1.00	47.34
25	ATOM	3091	C	ARG 428	30.561	28.768	64.064	1.00	44.67
	ATOM	3092	O	ARG 428	30.577	30.001	64.060	1.00	45.05
	ATOM	3093	N	ARG 429	31.663	28.037	64.195	1.00	45.77
	ATOM	3094	CA	ARG 429	32.972	28.652	64.378	1.00	46.48
	ATOM	3095	CB	ARG 429	33.849	27.738	65.244	1.00	52.63

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	ATOM	3096	CG	ARG 429	33.260	27.471	66.648	1.00	59.36
	ATOM	3097	CD	ARG 429	33.828	26.199	67.328	1.00	64.53
	ATOM	3098	NE	ARG 429	35.247	26.286	67.677	1.00	66.23
	ATOM	3099	CZ	ARG 429	35.963	25.274	68.159	1.00	66.80
5	ATOM	3100	NH1	ARG 429	35.398	24.083	68.357	1.00	66.02
	ATOM	3101	NH2	ARG 429	37.249	25.455	68.435	1.00	68.38
	ATOM	3102	C	ARG 429	33.657	28.954	63.049	1.00	44.06
	ATOM	3103	O	ARG 429	34.885	28.943	62.954	1.00	43.92
	ATOM	3104	N	LEU 430	32.847	29.221	62.029	1.00	41.46
10	ATOM	3105	CA	LEU 430	33.333	29.551	60.692	1.00	40.12
	ATOM	3106	CB	LEU 430	33.495	28.300	59.830	1.00	35.57
	ATOM	3107	CG	LEU 430	34.755	27.468	60.042	1.00	34.48
	ATOM	3108	CD1	LEU 430	34.764	26.279	59.101	1.00	32.77
	ATOM	3109	CD2	LEU 430	35.965	28.332	59.806	1.00	33.57
15	ATOM	3110	C	LEU 430	32.332	30.468	60.029	1.00	42.10
	ATOM	3111	O	LEU 430	32.503	30.868	58.880	1.00	42.67
	ATOM	3112	N	THR 431	31.280	30.797	60.763	1.00	44.70
	ATOM	3113	CA	THR 431	30.238	31.658	60.239	1.00	48.98
	ATOM	3114	CB	THR 431	28.923	30.928	60.113	1.00	49.80
20	ATOM	3115	OG1	THR 431	28.533	30.463	61.410	1.00	50.69
	ATOM	3116	CG2	THR 431	29.048	29.758	59.159	1.00	51.11
	ATOM	3117	C	THR 431	29.999	32.820	61.174	1.00	51.66
	ATOM	3118	O	THR 431	28.986	32.868	61.881	1.00	52.07
	ATOM	3119	N	PRO 432	30.935	33.774	61.190	1.00	52.95
25	ATOM	3120	CD	PRO 432	32.179	33.719	60.403	1.00	51.90
	ATOM	3121	CA	PRO 432	30.886	34.980	62.020	1.00	52.47
	ATOM	3122	CB	PRO 432	32.135	35.733	61.587	1.00	54.48
	ATOM	3123	CG	PRO 432	33.073	34.623	61.176	1.00	54.21
	ATOM	3124	C	PRO 432	29.620	35.783	61.739	1.00	52.15



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	ATOM	3125	O	PRO 432	29.257	35.981	60.582	1.00	49.70
	ATOM	3126	N	SER 433	28.955	36.243	62.793	1.00	53.82
	ATOM	3127	CA	SER 433	27.734	37.042	62.652	1.00	57.56
	ATOM	3128	CB	SER 433	28.055	38.372	61.952	1.00	59.89
5	ATOM	3129	OG	SER 433	28.537	38.176	60.633	1.00	62.34
	ATOM	3130	C	SER 433	26.570	36.340	61.926	1.00	57.57
	ATOM	3131	O	SER 433	25.907	36.923	61.056	1.00	57.63
	ATOM	3132	N	CYS 434	26.327	35.088	62.306	1.00	56.67
	ATOM	3133	CA	CYS 434	25.256	34.275	61.738	1.00	54.67
10	ATOM	3134	CB	CYS 434	25.805	33.375	60.634	1.00	54.21
	ATOM	3135	SG	CYS 434	26.729	34.213	59.354	1.00	55.95
	ATOM	3136	C	CYS 434	24.657	33.390	62.832	1.00	54.71
	ATOM	3137	O	CYS 434	25.381	32.663	63.513	1.00	54.74
	ATOM	3138	N	GLU 435	23.344	33.454	63.011	1.00	54.63
15	ATOM	3139	CA	GLU 435	22.681	32.621	64.009	1.00	54.57
	ATOM	3140	CB	GLU 435	21.529	33.383	64.681	1.00	59.73
	ATOM	3141	CG	GLU 435	21.927	34.615	65.511	1.00	64.17
	ATOM	3142	CD	GLU 435	20.717	35.479	65.902	1.00	67.96
	ATOM	3143	OE1	GLU 435	20.905	36.554	66.521	1.00	68.24
20	ATOM	3144	OE2	GLU 435	19.574	35.079	65.584	1.00	69.98
	ATOM	3145	C	GLU 435	22.134	31.378	63.289	1.00	51.70
	ATOM	3146	O	GLU 435	21.058	31.412	62.685	1.00	51.14
	ATOM	3147	N	ILE 436	22.889	30.288	63.350	1.00	47.61
	ATOM	3148	CA	ILE 436	22.497	29.046	62.702	1.00	43.09
25	ATOM	3149	CB	ILE 436	23.719	28.331	62.118	1.00	38.65
	ATOM	3150	CG2	ILE 436	23.278	27.138	61.300	1.00	38.13
	ATOM	3151	CG1	ILE 436	24.502	29.286	61.234	1.00	34.79
	ATOM	3152	CD1	ILE 436	25.768	28.686	60.710	1.00	34.08
	ATOM	3153	C	ILE 436	21.798	28.088	63.664	1.00	42.96

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	ATOM	3154	O	ILE 436	22.403	27.608	64.621	1.00	43.46
	ATOM	3155	N	THR 437	20.521	27.821	63.402	1.00	41.73
	ATOM	3156	CA	THR 437	19.724	26.910	64.218	1.00	39.10
	ATOM	3157	CB	THR 437	18.384	27.553	64.638	1.00	37.86
5	ATOM	3158	OG1	THR 437	18.182	28.763	63.899	1.00	37.22
	ATOM	3159	CG2	THR 437	18.370	27.856	66.130	1.00	37.07
	ATOM	3160	C	THR 437	19.430	25.672	63.380	1.00	38.74
	ATOM	3161	O	THR 437	18.979	25.784	62.238	1.00	39.10
	ATOM	3162	N	PHE 438	19.696	24.494	63.936	1.00	36.24
10	ATOM	3163	CA	PHE 438	19.449	23.257	63.210	1.00	33.18
	ATOM	3164	CB	PHE 438	20.556	22.256	63.491	1.00	30.88
	ATOM	3165	CG	PHE 438	21.905	22.742	63.093	1.00	32.48
	ATOM	3166	CD1	PHE 438	22.597	23.652	63.887	1.00	31.95
	ATOM	3167	CD2	PHE 438	22.489	22.301	61.913	1.00	32.85
15	ATOM	3168	CE1	PHE 438	23.857	24.118	63.507	1.00	31.30
	ATOM	3169	CE2	PHE 438	23.745	22.758	61.522	1.00	32.28
	ATOM	3170	CZ	PHE 438	24.432	23.668	62.320	1.00	31.80
	ATOM	3171	C	PHE 438	18.102	22.648	63.563	1.00	33.15
	ATOM	3172	O	PHE 438	17.662	22.729	64.705	1.00	34.90
20	ATOM	3173	N	ILE 439	17.450	22.049	62.570	1.00	31.06
	ATOM	3174	CA	ILE 439	16.150	21.412	62.738	1.00	28.59
	ATOM	3175	CB	ILE 439	15.010	22.347	62.321	1.00	26.74
	ATOM	3176	CG2	ILE 439	15.268	22.879	60.937	1.00	27.91
	ATOM	3177	CG1	ILE 439	13.683	21.591	62.312	1.00	27.91
25	ATOM	3178	CD1	ILE 439	12.545	22.406	61.776	1.00	26.70
	ATOM	3179	C	ILE 439	16.113	20.190	61.837	1.00	29.76
	ATOM	3180	O	ILE 439	16.208	20.310	60.618	1.00	29.55
	ATOM	3181	N	GLU 440	15.977	19.014	62.434	1.00	30.76
	ATOM	3182	CA	GLU 440	15.934	17.781	61.666	1.00	32.34

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	ATOM	3183	CB	GLU 440	16.028	16.592	62.609	1.00	34.09
	ATOM	3184	CG	GLU 440	17.272	16.583	63.458	1.00	38.93
	ATOM	3185	CD	GLU 440	17.339	15.367	64.353	1.00	43.10
	ATOM	3186	OE1	GLU 440	16.378	15.162	65.131	1.00	44.22
5	ATOM	3187	OE2	GLU 440	18.346	14.623	64.277	1.00	44.99
	ATOM	3188	C	GLU 440	14.648	17.687	60.854	1.00	33.11
	ATOM	3189	O	GLU 440	13.703	18.445	61.086	1.00	31.25
	ATOM	3190	N	SER 441	14.613	16.764	59.896	1.00	34.70
	ATOM	3191	CA	SER 441	13.416	16.587	59.086	1.00	37.07
10	ATOM	3192	CB	SER 441	13.738	15.904	57.761	1.00	34.79
	ATOM	3193	OG	SER 441	14.159	14.579	57.988	1.00	34.61
	ATOM	3194	C	SER 441	12.452	15.724	59.889	1.00	40.43
	ATOM	3195	O	SER 441	12.866	14.964	60.773	1.00	38.99
	ATOM	3196	N	GLU 442	11.168	15.855	59.571	1.00	43.31
15	ATOM	3197	CA	GLU 442	10.099	15.135	60.254	1.00	45.59
	ATOM	3198	CB	GLU 442	8.764	15.638	59.724	1.00	46.37
	ATOM	3199	CG	GLU 442	7.575	15.244	60.549	1.00	49.47
	ATOM	3200	CD	GLU 442	6.653	16.421	60.794	1.00	52.25
	ATOM	3201	OE1	GLU 442	5.425	16.199	60.895	1.00	52.44
20	ATOM	3202	OE2	GLU 442	7.160	17.568	60.894	1.00	53.16
	ATOM	3203	C	GLU 442	10.165	13.607	60.174	1.00	47.69
	ATOM	3204	O	GLU 442	10.828	13.035	59.314	1.00	47.21
	ATOM	3205	N	GLU 443	9.435	12.964	61.076	1.00	50.15
	ATOM	3206	CA	GLU 443	9.382	11.508	61.210	1.00	52.79
25	ATOM	3207	CB	GLU 443	8.911	11.204	62.623	1.00	55.86
	ATOM	3208	CG	GLU 443	9.468	12.183	63.635	1.00	61.71
	ATOM	3209	CD	GLU 443	10.948	11.962	63.877	1.00	66.19
	ATOM	3210	OE1	GLU 443	11.689	11.746	62.886	1.00	68.22
	ATOM	3211	OE2	GLU 443	11.365	12.006	65.058	1.00	67.57

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	ATOM	3212	C	GLU 443	8.521	10.711	60.218	1.00	53.03
	ATOM	3213	O	GLU 443	7.344	10.999	60.025	1.00	54.82
	ATOM	3214	N	GLY 444	9.116	9.702	59.593	1.00	52.26
	ATOM	3215	CA	GLY 444	8.373	8.861	58.667	1.00	52.32
5	ATOM	3216	C	GLY 444	7.966	9.389	57.302	1.00	53.07
	ATOM	3217	O	GLY 444	6.767	9.460	57.003	1.00	52.97
	ATOM	3218	N	SER 445	8.961	9.750	56.483	1.00	52.71
	ATOM	3219	CA	SER 445	8.760	10.239	55.104	1.00	50.05
	ATOM	3220	CB	SER 445	7.836	11.464	55.084	1.00	51.01
10	ATOM	3221	OG	SER 445	6.487	11.084	55.318	1.00	46.84
	ATOM	3222	C	SER 445	10.076	10.545	54.356	1.00	46.51
	ATOM	3223	O	SER 445	11.123	10.710	54.976	1.00	45.30
	ATOM	3224	N	GLY 446	10.013	10.603	53.026	1.00	43.17
	ATOM	3225	CA	GLY 446	11.207	10.842	52.235	1.00	40.08
15	ATOM	3226	C	GLY 446	11.199	12.057	51.330	1.00	39.05
	ATOM	3227	O	GLY 446	11.414	13.164	51.803	1.00	42.74
	ATOM	3228	N	ARG 447	10.940	11.873	50.039	1.00	37.60
	ATOM	3229	CA	ARG 447	10.956	13.000	49.098	1.00	37.46
	ATOM	3230	CB	ARG 447	11.549	12.546	47.747	1.00	45.51
20	ATOM	3231	CG	ARG 447	10.793	11.401	47.014	1.00	53.91
	ATOM	3232	CD	ARG 447	11.521	10.902	45.743	1.00	58.18
	ATOM	3233	NE	ARG 447	12.939	10.598	45.975	1.00	63.62
	ATOM	3234	CZ	ARG 447	13.399	9.623	46.769	1.00	66.02
	ATOM	3235	NH1	ARG 447	12.560	8.825	47.425	1.00	67.97
25	ATOM	3236	NH2	ARG 447	14.711	9.447	46.924	1.00	69.08
	ATOM	3237	C	ARG 447	9.642	13.737	48.848	1.00	32.93
	ATOM	3238	O	ARG 447	9.122	14.416	49.741	1.00	29.46
	ATOM	3239	N	GLY 448	9.150	13.625	47.607	1.00	30.52
	ATOM	3240	CA	GLY 448	7.902	14.245	47.202	1.00	26.03

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	ATOM	3241	C	GLY 448	6.845	13.828	48.200	1.00	25.25
	ATOM	3242	O	GLY 448	5.752	14.378	48.244	1.00	24.59
	ATOM	3243	N	ALA 449	7.186	12.840	49.018	1.00	23.74
	ATOM	3244	CA	ALA 449	6.282	12.362	50.035	1.00	20.54
5	ATOM	3245	CB	ALA 449	6.611	10.917	50.410	1.00	18.12
	ATOM	3246	C	ALA 449	6.340	13.251	51.282	1.00	22.37
	ATOM	3247	O	ALA 449	5.307	13.782	51.693	1.00	22.56
	ATOM	3248	N	ALA 450	7.524	13.443	51.881	1.00	22.28
	ATOM	3249	CA	ALA 450	7.605	14.261	53.088	1.00	20.98
10	ATOM	3250	CB	ALA 450	9.056	14.432	53.535	1.00	9.63
	ATOM	3251	C	ALA 450	6.937	15.594	52.872	1.00	20.66
	ATOM	3252	O	ALA 450	6.417	16.168	53.826	1.00	19.81
	ATOM	3253	N	LEU 451	6.943	16.109	51.702	1.00	19.91
	ATOM	3254	CA	LEU 451	6.279	17.379	51.602	1.00	22.22
15	ATOM	3255	CB	LEU 451	6.586	18.056	50.279	1.00	26.74
	ATOM	3256	CG	LEU 451	6.089	19.496	50.144	1.00	34.07
	ATOM	3257	CD1	LEU 451	6.894	20.425	51.040	1.00	37.55
	ATOM	3258	CD2	LEU 451	6.160	19.955	48.696	1.00	36.19
	ATOM	3259	C	LEU 451	4.774	17.157	51.686	1.00	23.24
20	ATOM	3260	O	LEU 451	4.136	17.474	52.699	1.00	21.18
	ATOM	3261	N	VAL 452	4.212	16.613	50.608	1.00	26.44
	ATOM	3262	CA	VAL 452	2.798	16.405	50.557	1.00	26.90
	ATOM	3263	CB	VAL 452	2.454	15.179	49.666	1.00	28.65
	ATOM	3264	CG1	VAL 452	3.082	15.353	48.300	1.00	26.01
25	ATOM	3265	CG2	VAL 452	2.933	13.886	50.313	1.00	31.22
	ATOM	3266	C	VAL 452	2.217	16.308	51.935	1.00	26.69
	ATOM	3267	O	VAL 452	1.181	16.878	52.234	1.00	24.86
	ATOM	3268	N	SER 453	2.880	15.579	52.769	1.00	26.07
	ATOM	3269	CA	SER 453	2.377	15.346	54.125	1.00	26.79

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	ATOM	3270	CB	SER 453	3.058	14.127	54.756	1.00	28.88
	ATOM	3271	OG	SER 453	2.553	13.881	56.057	1.00	37.16
	ATOM	3272	C	SER 453	2.571	16.558	55.028	1.00	26.82
	ATOM	3273	O	SER 453	1.658	17.301	55.377	1.00	26.28
5	ATOM	3274	N	ALA 454	3.831	16.701	55.389	1.00	26.83
	ATOM	3275	CA	ALA 454	4.250	17.807	56.177	1.00	23.37
	ATOM	3276	CB	ALA 454	5.719	18.128	55.937	1.00	17.54
	ATOM	3277	C	ALA 454	3.381	19.002	55.866	1.00	21.80
	ATOM	3278	O	ALA 454	3.194	19.883	56.714	1.00	21.02
10	ATOM	3279	N	VAL 455	2.848	19.044	54.656	1.00	21.59
	ATOM	3280	CA	VAL 455	2.020	20.156	54.281	1.00	25.32
	ATOM	3281	CB	VAL 455	2.313	20.557	52.841	1.00	28.03
	ATOM	3282	CG1	VAL 455	1.676	19.583	51.871	1.00	29.06
	ATOM	3283	CG2	VAL 455	1.813	21.961	52.577	1.00	29.98
15	ATOM	3284	C	VAL 455	0.528	19.890	54.469	1.00	27.69
	ATOM	3285	O	VAL 455	-0.202	20.783	54.911	1.00	28.10
	ATOM	3286	N	ALA 456	0.061	18.681	54.142	1.00	30.51
	ATOM	3287	CA	ALA 456	-1.367	18.349	54.318	1.00	31.54
	ATOM	3288	CB	ALA 456	-1.666	16.937	53.836	1.00	25.20
20	ATOM	3289	C	ALA 456	-1.702	18.505	55.797	1.00	31.77
	ATOM	3290	O	ALA 456	-2.853	18.713	56.176	1.00	33.11
	ATOM	3291	N	CYS 457	-0.673	18.384	56.625	1.00	31.33
	ATOM	3292	CA	CYS 457	-0.843	18.538	58.049	1.00	33.33
	ATOM	3293	CB	CYS 457	0.262	17.815	58.811	1.00	36.53
25	ATOM	3294	SG	CYS 457	1.040	16.448	57.890	1.00	44.65
	ATOM	3295	C	CYS 457	-0.903	19.990	58.438	1.00	34.59
	ATOM	3296	O	CYS 457	-1.745	20.391	59.237	1.00	34.67
	ATOM	3297	N	LYS 458	0.005	20.779	57.881	1.00	37.14
	ATOM	3298	CA	LYS 458	0.060	22.199	58.190	1.00	38.61

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	ATOM	3299	CB	LYS	458	1.363	22.799	57.669	1.00	37.21
	ATOM	3300	CG	LYS	458	2.573	22.474	58.538	1.00	37.81
	ATOM	3301	CD	LYS	458	2.501	23.206	59.874	1.00	38.84
	ATOM	3302	CE	LYS	458	3.820	23.143	60.639	1.00	38.18
5	ATOM	3303	NZ	LYS	458	3.812	24.023	61.851	1.00	36.51
	ATOM	3304	C	LYS	458	-1.128	22.920	57.596	1.00	40.24
	ATOM	3305	O	LYS	458	-1.377	24.079	57.898	1.00	39.64
	ATOM	3306	N	LYS	459	-1.869	22.223	56.752	1.00	43.69
	ATOM	3307	CA	LYS	459	-3.036	22.820	56.147	1.00	50.66
10	ATOM	3308	CB	LYS	459	-3.242	22.248	54.747	1.00	55.88
	ATOM	3309	CG	LYS	459	-4.657	22.405	54.183	1.00	63.64
	ATOM	3310	CD	LYS	459	-5.037	23.850	53.856	1.00	66.97
	ATOM	3311	CE	LYS	459	-6.431	23.941	53.226	1.00	68.86
	ATOM	3312	NZ	LYS	459	-7.531	23.519	54.152	1.00	71.25
15	ATOM	3313	C	LYS	459	-4.262	22.562	57.018	1.00	52.41
	ATOM	3314	O	LYS	459	-5.132	23.425	57.132	1.00	51.90
	ATOM	3315	N	ALA	460	-4.322	21.380	57.634	1.00	54.96
	ATOM	3316	CA	ALA	460	-5.449	20.997	58.495	1.00	57.72
	ATOM	3317	CB	ALA	460	-5.201	19.620	59.111	1.00	54.90
20	ATOM	3318	C	ALA	460	-5.736	22.018	59.596	1.00	60.41
	ATOM	3319	O	ALA	460	-6.773	21.950	60.261	1.00	60.54
	ATOM	3320	N	CYS	461	-4.815	22.965	59.776	1.00	63.50
	ATOM	3321	CA	CYS	461	-4.961	24.022	60.776	1.00	66.18
	ATOM	3322	CB	CYS	461	-3.580	24.489	61.252	1.00	67.98
25	ATOM	3323	SG	CYS	461	-3.604	26.041	62.185	1.00	75.61
	ATOM	3324	C	CYS	461	-5.727	25.217	60.200	1.00	65.92
	ATOM	3325	O	CYS	461	-6.940	25.348	60.490	1.00	65.70
	ATOM	3326	OXT	CYS	461	-5.099	26.001	59.454	1.00	65.20
	ATOM	3327	S	SO4	600	20.241	7.477	54.655	1.00	35.04

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	ATOM	3328	01	S04	600	19.370	7.951	53.566	1.00	33.14
	ATOM	3329	02	S04	600	20.343	8.532	55.683	1.00	32.80
	ATOM	3330	03	S04	600	19.690	6.249	55.260	1.00	33.32
	ATOM	3331	04	S04	600	21.572	7.178	54.108	1.00	33.97
5	ATOM	3332	S	S04	601	22.953	22.471	69.199	1.00	77.32
	ATOM	3333	01	S04	601	21.971	21.759	68.356	1.00	76.19
	ATOM	3334	02	S04	601	22.411	23.803	69.553	1.00	77.48
	ATOM	3335	03	S04	601	23.205	21.698	70.433	1.00	77.23
	ATOM	3336	04	S04	601	24.224	22.628	68.461	1.00	77.19
10	ATOM	3337	NA+1	NA1	602	17.158	10.244	54.280	1.00	10.17
	ATOM	3338	OH2	HOH	603	19.770	14.543	47.159	1.00	1.00
	ATOM	3340	OH2	HOH	604	20.723	24.387	67.178	1.00	17.94
	ATOM	3341	OH2	HOH	605	10.880	33.802	37.628	1.00	1.00
	ATOM	3342	OH2	HOH	606	22.743	28.762	37.147	1.00	31.78
15	ATOM	3343	OH2	HOH	607	38.906	1.328	74.611	1.00	37.76
	ATOM	3344	OH2	HOH	608	1.237	30.510	46.162	1.00	32.40
	ATOM	3345	OH2	HOH	609	34.702	-1.731	56.455	1.00	62.03
	END									

- 20      なお、表 2 は、当業者によって慣用されているプロテイン・データ・バンクの表記方法に準拠して作成されている。表 2 中、HOH は水分子を表す。

本発明においては、配列番号 5、及び／又は配列番号 8 と実質的に同一のアミノ酸配列を有し、グルコキナーゼ活性を有するタンパク質の結晶は本発明の  
 25      範囲内である。そのような結晶としては、例えば、表 1、及び／又は表 2 に記載の三次元構造座標データの少なくとも一つのデータを変更した三次元構造座標データにおいて、表 1、及び／又は表 2 に記載の三次元構造座標データで示されるアミノ酸の主鎖の原子（C $\alpha$  原子）と、該 C $\alpha$  原子と対応する前記変更した三次元構造座標データで示される C $\alpha$  原子との平均二乗偏差が、0。



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6 オングストローム以下である結晶が挙げられる。原子の位置を表す座標の数値が異なっても、構造座標に含まれる対応する原子の位置を重ね合わせることができる二つの構造座標は、同一の三次元構造を表すものである。

- 5     なお、表 1、及び／又は表 2 に記載の GK タンパク質の三次元構造座標は、ドラッグデザインのための重要な情報であり、必要に応じて、コンピュータ読み取り可能な記憶媒体に保存され、コンピュータでこの情報を処理してドラッグデザインを行う。したがって、本発明の別の態様によれば、コンピュータを、表 1、及び／又は表 2 に記載のアミノ酸残基の三次元座標を記憶する三次元座標記憶手段として機能させるためのプログラムを記録したコンピュータ読み取り可能な記録媒体が提供される。

- 10     また、本発明の別の態様によれば、コンピュータを、表 1、及び／又は表 2 に記載のアミノ酸残基の三次元座標に関する情報を記憶した三次元座標記憶手段と、前記三次元座標記憶手段に記憶された表 1、及び／又は表 2 に記載のアミノ酸残基の三次元座標を用いて配列番号 5、及び／又は配列番号 8 で表されるアミノ酸配列を有するタンパク質の化合物結合部位を推測する結合部位推測手段と、タンパク質と結合する化合物の種類と、当該化合物の三次元構造に関する情報を記憶した結合化合物記憶手段と、少なくとも、前記結合部位推測手段によって推測された配列番号 5、及び／又は配列番号 8 で表されるアミノ酸配列を有するタンパク質の化合物結合部位の三次元構造に関する情報と、前記結合化合物記憶手段に記憶された化合物の三次元構造に関する情報とを用いて前記配列表の配列番号 1 で表されるアミノ酸配列を有するタンパク質の化合物結合部位に適合する化合物の候補を選択する結合化合物候補選択手段、として機能させるプログラムを記録したコンピュータ読み取り可能な記録媒体が提供される。さらに、本発明の別の態様によれば、上記各手段を備えるコンピュータも提供される。

(GK タンパク質とそれに結合する化合物との複合体の結晶)

次に、本発明の別の態様によれば、配列番号 5、又は配列番号 8 に記載のア

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ミノ酸配列又はそのアミノ酸配列と実質的に同一のアミノ酸配列を含むタンパク質と該タンパク質に結合可能な化合物との複合体を含む結晶及びその製造方法が提供される。

GKタンパク質と結合する化合物が得られた場合は、まず、GKタンパク質とその化合物を、例えば、水溶液中で混合し、複合体を形成する。このような複合体の結晶は、共結晶法、ソーキング法などの公知の共結晶の製造方法が用いられる。結晶化条件、結晶化方法については、上述した方法が参照される。

GKタンパク質と結合する化合物は、例えば、上記式（I）で表される化合物群から選択される。

10     ここで、上記式（I）のハロゲン原子としては、フッ素原子、塩素原子、臭素原子、ヨウ素原子などが例示され、これらの中でも塩素原子が好ましい。

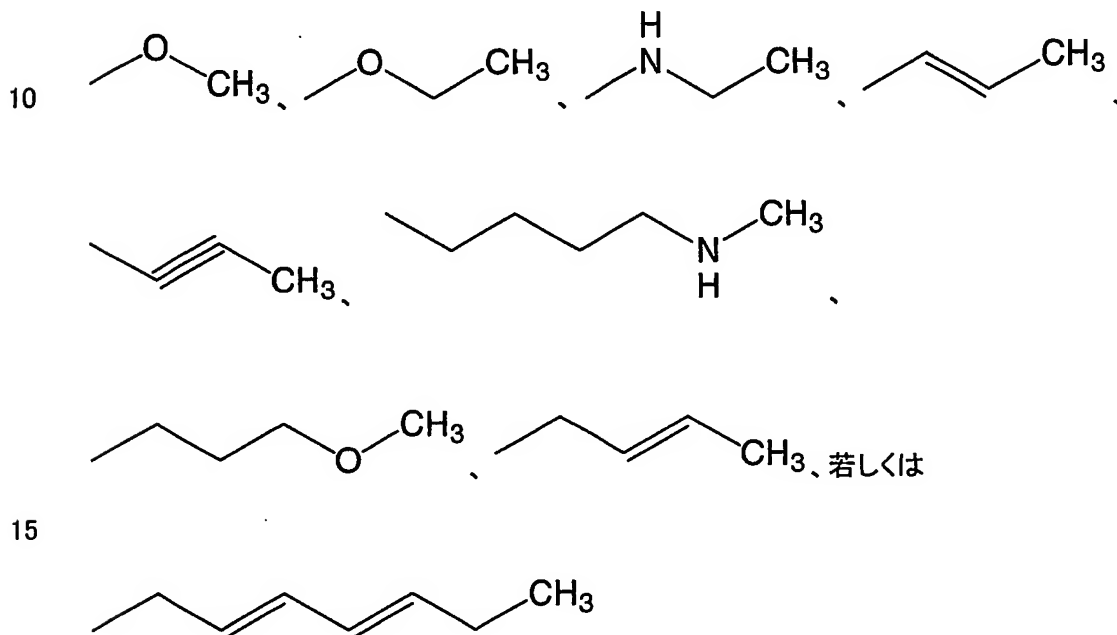
また、上記式（I）のA、B及び式（I I）のヘテロアリール基における置換基としては、アミノ基、カルバモイル基、カルバモイルアミノ基、カルバモイルオキシ基、カルボキシ基、シアノ基、スルファモイル基、トリフルオロメチル基、ハロゲン原子、ヒドロキシ基、ホルミル基、直鎖の $C_1-C_6$ アルキル基、環状の $C_3-C_6$ 炭化水素基、アラルキル基、N-アラルキルアミノ基、N, N-ジアラルキルアミノ基、アラルキルオキシ基、アラルキルカルボニル基、N-アラルキルカルバモイル基、アリール基、アリールチオ基、N-アリールアミノ基、アリールオキシ基、アリールスルホニル基、アリールスルホニルオキシ基、N-アリールスルホニルアミノ基、アリールスルファモイル基、N-アリールカルバモイル基、アロイル基、アロキシ基、 $C_2-C_6$ アルカノイル基、N- $C_2-C_6$ アルカノイルアミノ基、 $C_1-C_6$ アルキルチオ基、N- $C_1-C_6$ アルキルスルファモイル基、N, N-ジ- $C_1-C_6$ アルキルスルファモイル基、 $C_1-C_6$ アルキルスルフィニル基、 $C_1-C_6$ アルキルスルホニル基、N- $C_1-C_6$ アルキルスルホニルアミノ基、 $C_1-C_6$ アルコキシ基、 $C_1-C_6$ アルコキシカルボニル基又は $C_1-C_6$ アルキルアミノ基を示す）などが挙げられる。ここで用いられる好ましい置換基は、アミノ基、カルバモイル基、カルバモイルアミノ基、カルバモイルオキシ基、カルボキシ基、シアノ基、スルファモイル基、トリフルオロメチル基、ハロゲン原子、ヒドロキシ基、ホルミ

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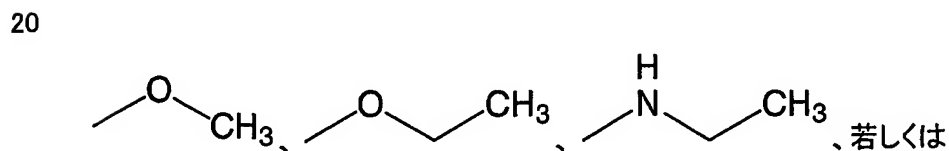
ル基、直鎖のC<sub>1</sub>－C<sub>6</sub>アルキル基などが例示される。

- ここで、「炭化水素基」は、炭素数1乃至6の直鎖のアルキル基を示すか、又は該アルキル基を構成する炭素原子のうち、1又は2の、好ましくは1の炭素原子が窒素原子、硫黄原子又は酸素原子で置き換わっていてもよいが、及び
- 5 /又は該炭素数1乃至6の直鎖のアルキル基中の炭素原子同士が二重結合又は三重結合で結合されていてもよい基である。該二重結合又は三重結合の数は、1又は2であることが好ましく、1であることがより好ましい。

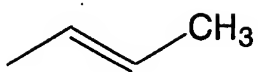
該炭化水素基としては、具体的には、メチル基、エチル基、プロピル基若しくはイソプロピル基、ブチル基又は下記式



で表される基であることが好ましい。より好ましい炭化水素基は、メチル基、エチル基、プロピル基、イソプロピル基又は下記式



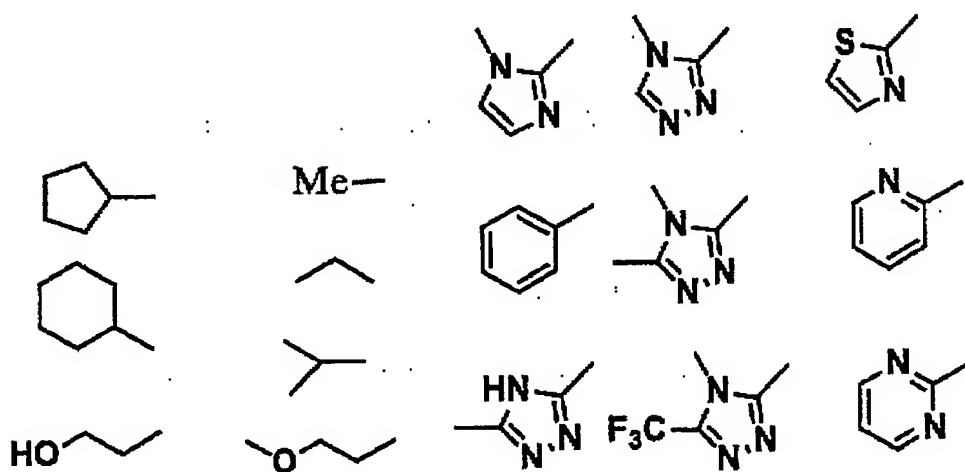
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で表される基である。

好ましいAとしては (p=0 の場合)、例えば、次の基が挙げられる。

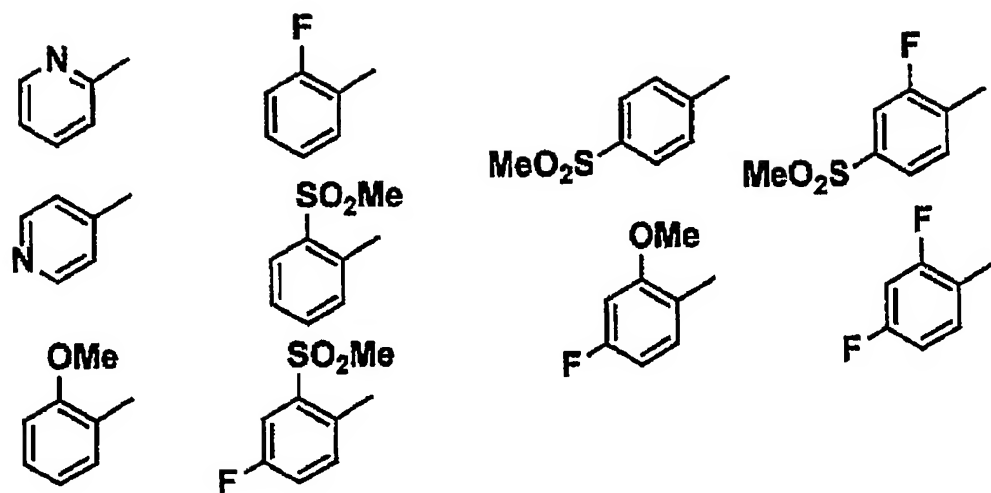
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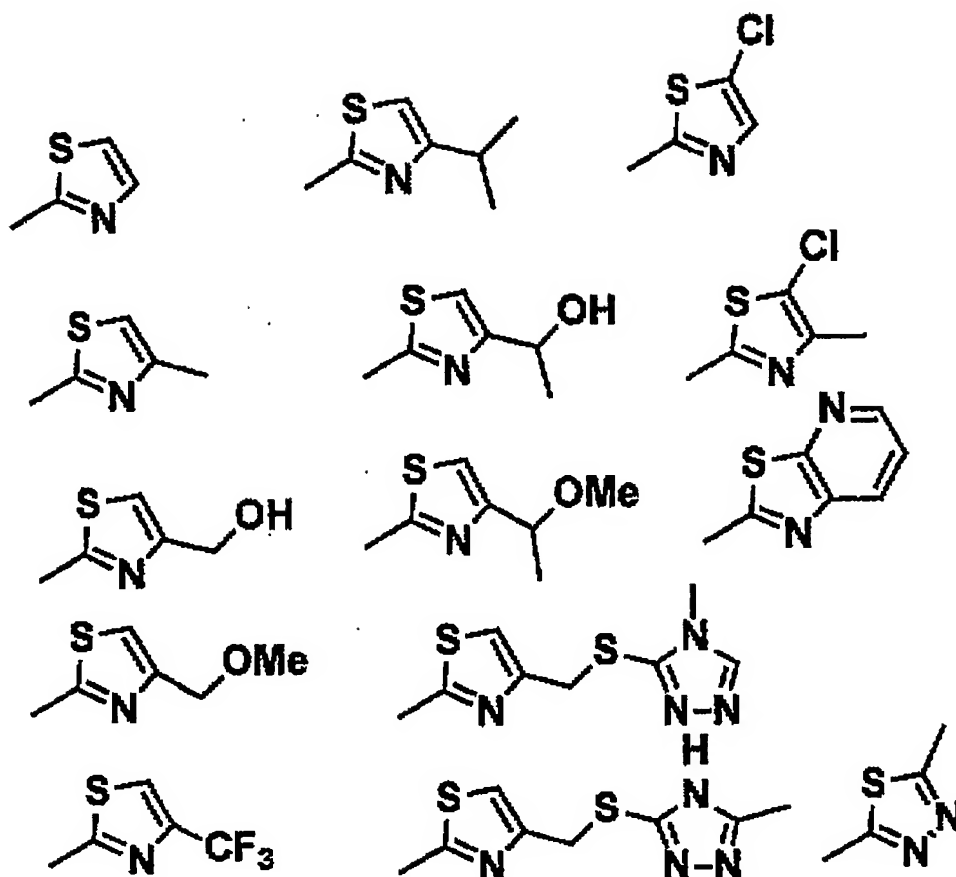
好ましいBとしては、例えば、次の基が挙げられる。

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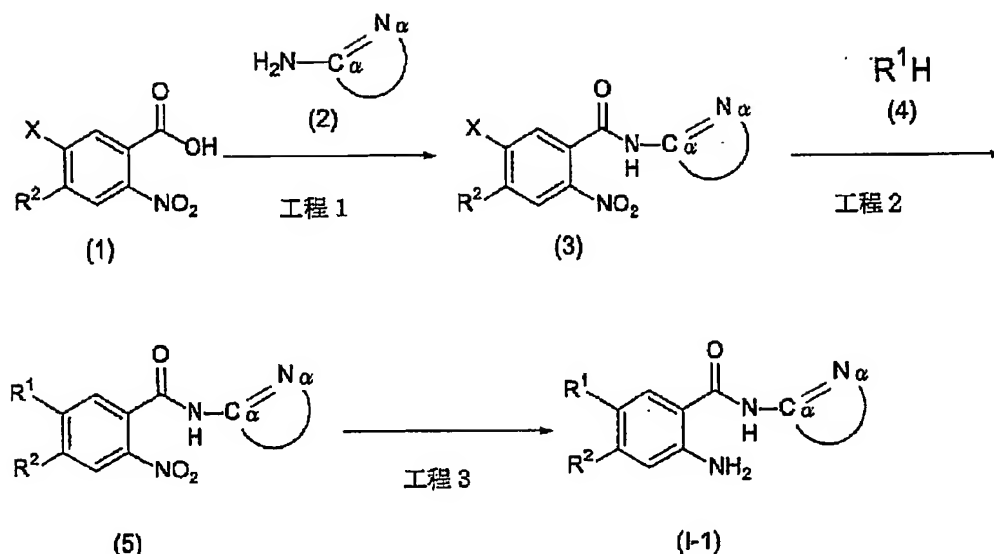
式 (I I) で示されるヘテロアリール基としては、例えば、次の複素環基が  
5 挙げられる。



5      なお、特に好ましい化合物は、上述した式(IIIa)～式(IIIc)で表される  
       いずれかの化合物である。

      本発明の化合物(I)は、公知の反応手段を用いるか、或いは公知の方法に  
       従って容易に製造することができる。なお、本発明の一般式(I)の化合物は、  
       通常、液相における合成のみならず、近年発達が目覚ましい例えばコンビナトリ  
       アル合成法やパラレル合成法等の固相を用いた合成によっても製造することが  
 10      できる。好ましくは例えば以下の方法により製造することができる。

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[式中、各記号は前記定義に同じ]

## (工程 1)

- 5 本工程は、カルボン酸化合物 (1) 又はその反応性誘導体と前記式 (2) で表される置換されていてもよい単環の、又は双環のヘテロアリール基を有するアミノ化合物又はその塩とを反応させて、化合物 (3) を製造する方法である。本反応は文献記載の方法 (例えば、ペプチド合成の基礎と実験、泉屋信夫他、丸善、1983年、コンプリヘンシブ オーガニック シンセシス (Comprehensive Organic Synthesis)、第6巻、Pergamon Press社、1991年、等)、それに準じた方法又はこれらと常法とを組み合わせることにより、通常のアミド形成反応を行えばよく、即ち、当業者に周知の縮合剤を用いて行うか、或いは、当業者に利用可能なエステル活性化方法、混合酸無水物法、酸クロリド法、カルボジイミド法等により行うことができる。このようなアミド形成試薬としては、例えば塩化チオニル、N, N-ジシクロヘキシルカルボジイミド、1-メチル-2-プロモピリジニウムアイオダイド、N, N'-カルボニルジイミダゾール、ジフェニルフォスフォルルクロリド、ジフェニルフォスフォルルアジド、N, N'-ジスク
- 10
- 15

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- シニミジルカルボネート、N, N'-ジスクシニミジルオキザレート、1-エチル-3-(3-ジメチルアミノプロピル)カルボジイミド塩酸塩、クロロギ酸エチル、クロロギ酸イソブチル又はベンゾトリアゾ-1-リル-オキシートリス(ジメチルアミノ)フォスフォニウムヘキサフルオロフォスフェイト等
- 5 が挙げられ、中でも例えば塩化チオニル、N, N-ジシクロヘキシルカルボジイミド又はベンゾトリアゾ-1-リル-オキシートリス(ジメチルアミノ)フォスフォニウムヘキサフルオロフォスフェイト等が好適である。またアミド形成反応においては、上記アミド形成試薬と共に塩基、縮合補助剤を用いてもよい。
- 10 用いられる塩基としては、例えばトリメチルアミン、トリエチルアミン、N, N-ジイソプロピルエチルアミン、N-メチルモルホリン、N-メチルピロリジン、N-メチルピペリジン、N, N-ジメチルアニリン、1, 8-ジアザビシクロ[5. 4. 0]ウンデカ-7-エン(DBU)、1, 5-アザビシクロ[4. 3. 0]ノナ-5-エン(DBN)等の第3級脂肪族アミン;例えばピ
- 15 リジン、4-ジメチルアミノピリジン、ピコリン、ルチジン、キノリン又はイソキノリン等の芳香族アミン等が挙げられ、中でも例えば第3級脂肪族アミン等が好ましく、特に例えばトリエチルアミン又はN, N-ジイソプロピルエチルアミン等が好適である。

- 用いられる縮合補助剤としては、例えばN-ヒドロキシベンゾトリアゾール
- 20 水和物、N-ヒドロキシスクシンイミド、N-ヒドロキシ-5-ノルボルネン-2, 3-ジカルボキシイミド又は3-ヒドロキシ-3, 4-ジヒドロ-4-オキソ-1, 2, 3-ベンゾトリアゾール等が挙げられ、中でも例えばN-ヒドロキシベンゾトリアゾール等が好適である。

- 用いられるアミノ化合物(2)の量は、用いられる化合物及び溶媒の種類そ
- 25 の他の反応条件により異なるが、通常カルボン酸化合物(1)又はその反応性誘導体1当量に対して、0.02乃至50当量、好ましくは0.2乃至2当量である。ここにおいて、反応性誘導体としては、通常有機化学の分野において用いられる、例えば活性エステル誘導体、活性アミド誘導体等が挙げられる。

用いられるアミド形成試薬の量は、用いられる化合物及び溶媒の種類その他



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の反応条件により異なるが、通常カルボン酸化合物（１）又はその反応性誘導体 1 当量に対して、1 乃至 50 当量、好ましくは 1 乃至 5 当量である。

用いられる縮合補助剤の量は、用いられる化合物及び溶媒の種類その他の反応条件により異なるが、通常カルボン酸化合物（１）又はその反応性誘導体 1  
5 当量に対して、1 乃至 50 当量、好ましくは 1 乃至 5 当量である。

用いられる塩基の量は、用いられる化合物及び溶媒の種類その他の反応条件により異なるが、通常 1 乃至 50 当量、好ましくは 3 乃至 5 当量である。

本工程において用いられる反応溶媒としては、例えば不活性有機溶媒であり、反応に支障のない限り、特に限定されないが、具体的には、例えば塩化メチレン、クロロホルム、1, 2-ジクロロエタン、トリクロロエタン、N, N-ジメチルホルムアミド、酢酸エチルエステル、酢酸メチルエステル、アセトニトリル、ベンゼン、キシレン、トルエン、1, 4-ジオキサン、テトラヒドロフラン、ジメトキシエタン又はそれらの混合溶媒が挙げられるが、好適な反応温度確保の点から、特に例えば塩化メチレン、クロロホルム、1, 2-ジクロロエタン、アセトニトリル又は N, N-ジメチルホルムアミド等が好適である。  
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反応温度は、-100℃乃至溶媒の沸点温度、好ましくは 0 乃至 30℃である。

反応時間は、0.5 乃至 96 時間、好ましくは 3 乃至 24 時間である。

本工程 1 で用いられる塩基、アミド形成試薬、縮合補助剤は、一種又はそれ  
20 以上組み合わせて使用することができる。

化合物（３）が保護基を有している場合には、適宜当該保護基を除去することが可能である。当該補助基の除去は、文献記載の方法（プロテクティブ グループス イン オーガニック シンセシス (Protective Groups in Organic Synthesis)、T. W. Green 著、  
25 第 2 版、John Wiley & Sons 社、1991 年、等）、それに準じた方法又はこれらと常法とを組み合わせることにより行うことができる。

このようにして得られる化合物（３）は、公知の分離精製手段、例えば濃縮、減圧濃縮、結晶化、溶媒抽出、再沈殿、クロマトグラフィー等により単離精製するか又は単離精製することなく次工程に付すことができる。

## (工程 2)

本工程は、上記工程 1 で得られたアミド化合物 (3) と化合物 (4) とを反応させることにより化合物 (5) を製造する方法である。

- 5 本反応においては、反応系中に必要に応じて塩基を加えてもよい。用いられる化合物 (4) としては、好ましくはフェノール誘導体又はチオール誘導体为好ましい。該フェノール誘導体又はチオール誘導体としては、例えばフェノール、チオフェノール、チオイミダゾール、チオトリアゾール等が挙げられる。
- 10 用いられる化合物 (4) の量は、用いられる化合物及び溶媒の種類その他の反応条件により異なるが、通常アミノ誘導体 (3) 1 当量に対して、2 乃至 50 当量、好ましくは 2 乃至 5 当量である。用いられる塩基としては、例えばトリメチルアミン、トリエチルアミン、N, N-ジイソプロピルエチルアミン、N-メチルモルホリン、N-メチルピロリジン、N-メチルピペリジン、N, N-ジメチルアニリン、1, 8-ジアザビシクロ [5. 4. 0] ウンデカ-7-エン (DBU)、1, 5-アザビシクロ [4. 3. 0] ノナ-5-エン (DBN) 等の第 3 級脂肪族アミン；例えばピリジン、4-ジメチルアミノピリジン、ピコリン、ルチジン、キノリン又はイソキノリン等の芳香族アミン；例えば金属カリウム、金属ナトリウム、金属リチウム等のアルカリ金属；例えば水素化ナトリウム、水素化カリウム等のアルカリ金属水素化物；例えばブチルリチウム等のアルカリ金属アルキル化物；例えばカリウム-tert-ブチラート、ナトリウムエチラート又はナトリウムメチラート等のアルカリ金属アルコキシド；例えば水酸化カリウム、水酸化ナトリウム等のアルカリ金属水酸化物；例えば炭酸カリウム等のアルカリ金属炭酸塩等が挙げられ、中でも例えば第 3 級脂肪族アミン、アルカリ金属水素化物又はアルカリ金属炭酸塩が好ましく、特
- 20 25 に例えばトリエチルアミン、N, N-ジイソプロピルエチルアミン、水素化ナトリウム又は炭酸カリウムが好適である。

用いられる当該塩基の量は、用いられる化合物及び溶媒の種類その他の反応条件により異なるが、アミド化合物 (3) 1 当量に対して通常 0 乃至 50 当量、好ましくは 2 乃至 10 当量である。該塩基は、必要に応じて一種又は 2 種以上

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用いることができる。

用いられる不活性有機溶媒としては、反応に支障のないものであれば、特に限定されないが、具体的には、例えば塩化メチレン、クロロホルム、1, 2-ジクロロエタン、トリクロロエタン、N, N-ジメチルホルムアミド、N, N-ジメチルアセトアミド、酢酸エチルエステル、酢酸メチルエステル、アセトニトリル、ベンゼン、キシレン、水、トルエン、1, 4-ジオキサン、テトラヒドロフラン又はこれらの混合溶媒等が挙げられる。

このようにして得られる化合物(5)は、公知の分離精製手段、例えば濃縮、減圧濃縮、結晶化、溶媒抽出、再沈殿、クロマトグラフィー等により単離精製

10 することができる。

### (工程3)

本工程は化合物(5)を還元して、本発明で用いる化合物(I)を製造する方法である。本工程において用いられる還元反応は、当業者に周知の方法が用

15 いられる。本工程においてもいられる還元反応としては、具体的には、例えば(1)水素、蟻酸、蟻酸アンモニウム、ヒドラジン水和物とパラジウム、白金、ニッケル触媒を用いる接触還元法、(2)塩酸、塩化アンモニウムと鉄を用いる還元法、(3)メタノールと塩化スズを用いる還元法等が挙げられる。

上記還元反応において用いられる還元剤の量は、用いられる化合物及び溶媒

20 の種類その他の反応条件により異なるが、化合物(5) 1当量に対して通常1乃至50当量、好ましくは2乃至20当量である。

用いられる反応溶媒としては、反応に支障のない限り、特に限定されないが、例えばジクロロメタン、クロロホルム等のハロゲン化炭化水素類、例えばジエチルエーテル、tert-ブチルメチルエーテル、テトラヒドロフラン等のエーテル類、例えばN, N-ジメチルホルムアミド、N, N-ジメチルアセトアミド等のアミド類、例えばジメチルスルホキシド等のスルホキシド類、例えばアセトニトリル等のニトリル類、例えばメタノール、エタノール、プロパノール等のアルコール類、例えばベンゼン、トルエン、キシレン等の芳香族炭化水素類、水或いはこれらの混合溶媒を用いることができる。

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反応温度及び反応時間は特に限定されないが、 $-10$ 乃至 $100^{\circ}\text{C}$ 程度、好ましくは $0$ 乃至 $50^{\circ}\text{C}$ 程度の反応温度で $1$ 乃至 $20$ 時間程度、好ましくは $1$ 乃至 $5$ 時間程度反応を行う。

このようにして得られる本発明で用いる化合物(I)は、公知の分離精製手段、例えば濃縮、減圧濃縮、結晶化、溶媒抽出、再沈殿、クロマトグラフィー等により単離精製するか又は単離精製することなく、次工程に付すことができる。

上記各工程の化合物は、各置換基上に保護基を有していてもよい。当該保護基は、各工程において適宜、公知の方法これに準じた方法、又はこれらと常法とを組み合わせた方法により除去することができる。除去の態様は、化合物、反応の種類その他の反応条件により、適宜の除去反応が可能であるが、個別に各保護基を除去する場合、各保護基を同時に除去する場合等が考えられ、当業者が適宜選択可能である。当該保護基としては、例えばヒドロキシ基の保護基、アミノ基の保護基、カルボキシル基の保護基、アルデヒドの保護基、ケト基の保護基等が挙げられる。また、当該保護基の除去順序は、特に限定されるものではない。

ヒドロキシ基の保護基としては、例えばtert-ブチルジメチルシリル基、tert-ブチルジフェニルシリル基等の低級アルキルシリル基、例えばメトキシメチル基、2-メトキシエトキシメチル基等の低級アルコキシメチル基、例えばベンジル基、p-メトキシベンジル基等のアラルキル基、例えばホルミル基、アセチル基等のアシル基等が挙げられ、これらのうち、特にtert-ブチルジメチルシリル基、アセチル基等が好ましい。

アミノ基の保護基としては、例えばベンジル基、p-ニトロベンジル基等のアラルキル基、例えばホルミル基、アセチル基等のアシル基、例えばエトキシカルボニル基、tert-ブトキシカルボニル基等の低級アルコキシカルボニル基、例えばベンジロキシカルボニル基、p-ニトロベンジロキシカルボニル基等のアラルキロキシカルボニル基等が挙げられ、これらのうち、特にニトロベンジル基、tert-ブトキシカルボニル基、ベンジロキシカルボニル基等が好ましい。

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カルボキシル基の保護基としては、例えばメチル基、エチル基、tert-ブチル基等の低級アルキル基、例えばベンジル基、p-メトキシベンジル基等のアラルキル基等が挙げられ、これらのうち、特にメチル基、エチル基、tert-ブチル基、ベンジル基等が好ましい。

- 5     ケト基の保護基としては、例えばジメチルケタール基、1, 3-ジオキシラン基、1, 3-ジオキソラン基、1, 3-ジチアン基、1, 3-ジチオラン基等が挙げられ、これらのうち、ジメチルケタール基、1, 3-ジオキソラン基等がより好ましい。

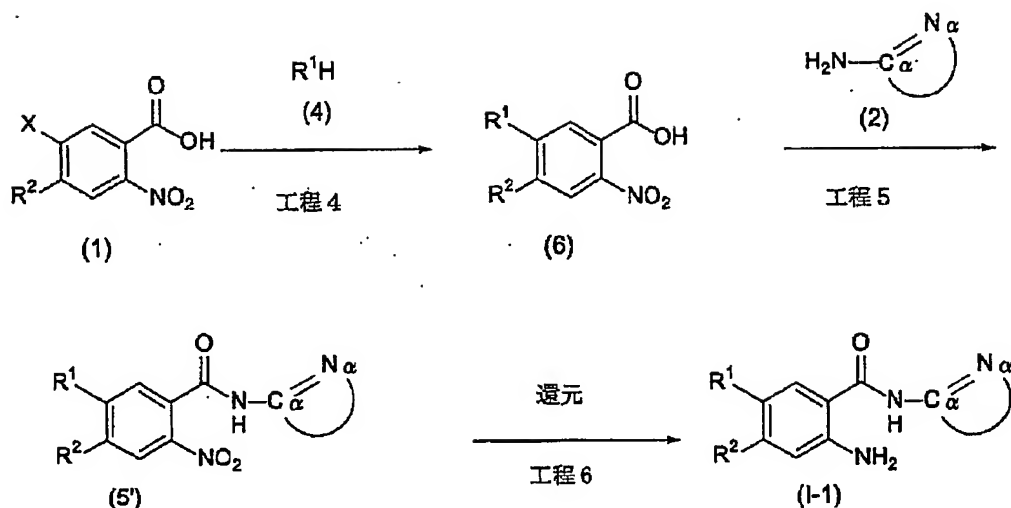
- 10    アルデヒド基の保護基としては、例えば、ジメチルアセタール基、1, 3-ジオキシラン基、1, 3-ジオキソラン基、1, 3-ジチアン基、1, 3-ジチオラン基等が挙げられ、これらのうちジメチルアセタール基、1, 3-ジオキソラン基等がより好ましい。

- 15    本発明で用いる化合物を製造するに当たっては、反応を効率よく進行させるために、官能基に保護基を導入する場合もある。これらの保護基の導入は、当業者に適宜選択可能であり、当該保護基の除去は、前記記載のプロテクティブグループス イン オーガニックシンセシス等の方法、これに準じた方法又はこれらと常法とを組み合わせることにより行うことができる。なお、保護基の除去の順序についても、当業者が適宜選択可能である。

- 20    このようにして得られる化合物(I)は、公知の分離精製手段、例えば濃縮、減圧濃縮、結晶化、再沈殿、溶媒抽出、クロマトグラフィー等により単離精製するか又は単離精製することなく次工程に付すことができる。

また、本発明で用いる化合物である(I)は、下記の工程によっても製造することができる。

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[式中各記号は前記定義に同じ]

上記工程 4、工程 5 及び工程 6 については、試薬の量、反応溶媒、反応温度  
 5 等その他の反応条件は、前記工程 2、工程 1 及び工程 3 と同様にして行うことができる。

$R^2$ に保護基が必要な場合には、前記記載のプロテクティブグループス イン  
 ンオーガニックシンセシス等の方法、それに準じた方法又はこれらと常法とを  
 組み合わせることにより、当業者が保護基を適宜選択することによって行うこ  
 10 とができる。

このようにして得られる化合物 (6)、(5') は、公知の分離精製手段、  
 例えば濃縮、減圧濃縮、結晶化、再沈殿、溶媒抽出等により単離精製するか、  
 又は単離精製することなく次工程に付すことができる。

本発明で用いる化合物 (I) は、公知の分離精製手段、例えば濃縮、減圧濃  
 15 縮、結晶化、再沈殿、溶媒抽出等により単離精製することができる。

上記工程 1 乃至 6 において、保護基の除去は、当該保護基の種類及び化合物  
 の安定性により異なるが、前記記載のプロテクティブ グループス イン  
 ーガニック シンセシス (Protective Groups in O

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rganic Synthesis)、T. W. Green著 第2版、John Wiley & Sons社、1991年、等)、それに準じた方法又はこれらと常法とを組み合わせることにより行うことができる。例えば酸又は塩基を用いる加溶媒分解、水素化金属錯体等を用いる化学的還元又はパラジウム炭素触媒、ラネーニッケル等を用いる接触還元等により行うことができる。

5 本発明によって提供されるベンズアミド化合物は、薬学的に許容される塩として存在することができる。当該塩は、常法に従って製造することができる。具体的には、上記化合物(I)が、当該分子内に例えばアミノ基、ピリジル基等に由来する塩基性基を有している場合には、当該化合物を酸で処理することにより、相当する薬学的に許容される塩に変換することができる。

当該酸付加塩としては、例えば塩酸塩、フッ化水素酸塩、臭化水素酸塩、ヨウ化水素酸塩等のハロゲン化水素酸塩；硝酸塩、過塩素酸塩、硫酸塩、リン酸塩、炭酸塩等の無機酸塩；メタンスルホン酸塩、トリフルオロメタンスルホン酸塩、エタンスルホン酸塩等の低級アルキルスルホン酸塩；ベンゼンスルホン酸塩、  
15 p-トルエンスルホン酸塩等のアリールスルホン酸塩；フマル酸塩、コハク酸塩、クエン酸塩、酒石酸塩、シュウ酸塩、マレイン酸塩等の有機酸塩；及びグルタミン酸塩、アスパラギン酸塩等のアミノ酸等の有機酸である酸付加塩を挙げることができる。また、本発明の化合物が酸性基を当該基内に有している場合、例えばカルボキシル基等を有している場合には、当該化合物を塩基で処理  
20 することによっても、相当する薬学的に許容される塩に変換することができる。当該塩基付加塩としては、例えば例えばナトリウム、カリウム等のアルカリ金属塩、カルシウム、マグネシウム等のアルカリ土類金属塩、アンモニウム塩、グアニジン、トリエチルアミン、ジシクロヘキシルアミン等の有機塩基による塩が挙げられる。さらに本発明の化合物は、遊離化合物又はその塩の任意の水  
25 和物又は溶媒和物として存在してもよい。

本発明においては、実施例の記載にて詳述するように、配列番号5に示すアミノ酸配列を有するGKタンパク質と上記式(IIIa)～式(IIIc)との化合物の複合体の結晶が得られている。これらの、結晶の3次元構造座標を解析することによって、配列番号5で示すGKタンパク質においては、化合物結合部位

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が、チロシン61～セリン69、グルタミン酸96～グルタミン98、イソロイシン159、メチオニン210～チロシン215、ヒスチジン218～グルタミン酸221、メチオニン235、アルギニン250、ロイシン451～リジン459のアミノ酸残基から構成されることが解明されている。

5

なお、本発明の別の態様によれば、配列番号2に記載のアミノ酸配列を有するタンパク質から、上述のようにN末端側、および/またはC末端側の所定の数のアミノ酸残基を欠損したアミノ酸配列を有するタンパク質を製造するタンパク質製造工程と、前記タンパク質製造工程で得られたタンパク質と結合する化合物と、前記タンパク質製造工程で得られたタンパク質とを反応させる工程を含む、タンパク質及びそのタンパク質と結合する化合物の複合体を含む結晶を製造する方法が提供される。

上記タンパク質製造工程において製造されるタンパク質としては、結晶内で隣接するGKタンパク質との間で立体的な障害がなくなる範囲であればその数は限定されない。具体的には、例えば、配列番号2で表されるアミノ酸配列において、N末端側の1～50個、好ましくは3～30個、より好ましくは5～25個、さらに好ましくは8～18個、特に好ましくは11～15個のアミノ酸残基を欠失させたアミノ酸配列などが挙げられる。また、C末端側の1～8個、好ましくは1～7個、より好ましくは2～6個のアミノ酸残基を欠失させたアミノ酸配列などが挙げられる。

#### (3次元構造座標を用いるドラッグデザイン方法)

上記のようにして得られる本発明のGKタンパク質の3次元構造は、CARD D (Computer Aided Rational Drug Design) による創薬システムのための重要な情報である。このGKタンパク質の活性中心、及びアロステリック部位を明らかにし、その部位に適合し、GKタンパク質と相互作用することにより、GKタンパク質を阻害、または活性化する物質を検索することは、GKタンパク質をターゲットとする創薬開発の重要なステップである。

すなわち、本発明の別の態様によれば、タンパク質の立体構造情報に基づい



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て該タンパク質に結合する化合物の構造をデザインするドラッグデザイン方法であって、該タンパク質の立体構造情報が、上述のようにして得られる結晶を解析することによって得られる情報であることを特徴とする、ドラッグデザイン方法が提供される。このようなドラッグデザイン方法としては、エネルギー計算、若しくはこれに類似する活性予測値、又はファルマコフォアを用いてドラッグデザインする手法と、コンピュータグラフィックスの技術を用いて視覚的にドラッグデザインをする手法がある。

エネルギー計算、若しくはこれに類する活性予測値、又はファルマコフォアを用いる手法による方法としては、(1) 上述したようにして得られる立体構造情報に基づいて、上記タンパク質の化合物結合部位を推測する結合部位推測工程と、前記結合部位推測工程で推測された化合物結合部位に適合する化合物を、化合物ライブラリより選択する選択工程とを含むことを特徴とするドラッグデザイン方法、(2) 前記立体構造情報に基づいて、前記タンパク質の化合物結合部位を推測する結合部位推測工程と、前記結合部位推測工程で推測された化合物結合部位に適合する化合物の構造を構築する化合物構造構築工程とを含むことを特徴とする、ドラッグデザイン方法などが例示される。

上記タンパク質の化合物結合部位を推測する方法としては、例えば、化合物との共結晶においてリガンドが結合している部位をコンピュータのディスプレイ上で目視で確認して特定する方法の他、リガンドが結合していない状態で解かれたタンパク質結晶構造に対してリガンドが結合しそうな部位を推定して特定する方法が挙げられる。いずれの方法においても公知の方法や市販のコンピュータソフトウェアを用いることができる。前者の方法においては、例えば、InsightII (Accelrys Inc.), SYBYL (Tripos Inc.), MOE (Chemical Computing Group) 等のソフトウェアを用いることができる。一方、後者の方法においては、例えば、Cavity search: an algorithm for the isolation and display of cavity-like binding regions. (Journal of Computer-Aided Molecular Design. 4(4):337-54, 1990) 等の公知の手法を用いることができ、SiteID (Tripos Inc.) 等のソフトウェアを用いて実施することができる。

タンパク質における化合物との結合部位が推測できたら、その推測された結

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合部位に適合し得る化合物を選択する。この化合物候補を選択する方法としては、既存の化合物ライブラリからの化合物の構造情報を入手して、そのライブラリ中の化合物の構造情報と上記のようにして推測された結合部位の構造情報とを比較することによって、結合可能化合物候補を選択する。

- 5 より具体的には、配列番号 5 に示すアミノ酸配列のアミノ酸残基（チロシン 61～セリン 69、グルタミン酸 96～グルタミン 98、イソロイシン 159、メチオニン 210～チロシン 215、ヒスチジン 218～グルタミン酸 221、メチオニン 235、アルギニン 250、ロイシン 451～リジン 459）から 1 つないしは 2 つ以上の残基もしくは複合体中のリガンドの官能基から形成される水素結合性または疎水性などのファルマコフォアと、蛋白構造またはその一部の側鎖の配向を改変させた構造から作成される蛋白表面を検索条件として、化合物ライブラリより各化合物の配座、配向を網羅的に探索しながら条件を満たすかどうかを判断して選択する。

- 15 他の代替方法として、化合物ライブラリより各化合物の配座、配向を網羅的に探索しながら、アミノ酸残基（チロシン 61～セリン 69、グルタミン酸 96～グルタミン 98、イソロイシン 159、メチオニン 210～チロシン 215、ヒスチジン 218～グルタミン酸 221、メチオニン 235、アルギニン 250、ロイシン 451～リジン 459）から構成されるリガンド結合部位の構造またはその一部の側鎖の配向を改変させた構造に対して候補化合物をバーチャルでドッキングさせ、
- 20 アミノ酸残基（チロシン 61～セリン 69、グルタミン酸 96～グルタミン 98、イソロイシン 159、メチオニン 210～チロシン 215、ヒスチジン 218～グルタミン酸 221、メチオニン 235、アルギニン 250、ロイシン 451～リジン 459）から 1 つないしは 2 つ以上の残基と 4 オングストローム以下で近接した相互作用を形成したものを選択したり、エネルギー評価関数を用いた選択を行う。

- 25 一方、候補化合物は、上記のようにして推測された結合部位の構造情報に基づいて結合可能化合物を設計することによっても選択することができる。より具体的には、配列番号 5 に示すアミノ酸配列のアミノ酸残基（チロシン 61～セリン 69、グルタミン酸 96～グルタミン 98、イソロイシン 159、メチオニン 210～チロシン 215、ヒスチジン 218～グルタミン酸 221、メチオニン 235、ア

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ルギニン 250、ロイシン 451～リジン 459) から構成される化合物結合部位の構造またはその一部の側鎖の配向を改変させた構造に対して、1つないしは2つ以上の残基と相互作用するように各種原子種、官能基を種々つなぎ合わせて化合物構造を構築する。この方法としては、メチル、エチル等の化学基を  
5 活性部位に並べて適合する化合物を探す方法と、原子を活性部位にコンピュータプログラムを用いて結合させていく方法とが知られている。

なお、コンピュータによるエネルギー評価による方法では、例えば分子力場計算を用いて化合物と、GKタンパク質との結合のエネルギーを求める方法が挙げられる。その計算をデータベースの中の各化合物に適用し、安定に結合で  
10 きる化合物候補を、ライブラリ化合物の中から求める。Insight II のLudiなどコンピュータプログラムによっては、蛋白質分子において相互作用するアミノ酸残基の3次元構造座標を与えると、自動的に結合可能な化合物の候補を選択し出力するものもあり、好適に利用することができる。

また、分子の3次元構造に基づくドラッグデザインについては、医薬品の開発・第7巻「分子設計」(廣川書店)をはじめとして数多くの文献が知られて  
15 いる。具体的には、第一にFlexiDock、FlexX等のフレキシブルリガンドバインディングシミュレーションソフトウェアを用いて、低分子(分子量1000以下)化合物のライブラリ(たとえば約150000種)をコンピュータでスクリーニングすることができる。このライブラリ内の化学物質はCONCORD等のプログラ  
20 ムで3次元構造を構築し、活性部位に適合する化合物を選択することができる。

一方、目視的によりドラッグデザインする方法としては、前記立体構造情報に基づいて、前記タンパク質の化合物結合部位を推測する結合部位推測工程と、前記結合部位推測工程で推測された化合物結合部位と該化合物結合部位に適合  
25 する化合物とが相互作用するように化合物の構造を目視によりデザインするデザイン工程とを含むことを特徴とする、ドラッグデザイン方法が挙げられる。例えば、配列番号5に示すアミノ酸配列のアミノ酸残基(チロシン61～セリン69、グルタミン酸96～グルタミン98、イソロイシン159、メチオニン210～チロシン215、ヒスチジン218～グルタミン酸221、メチオニン235、アルギ

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ニン 250、ロイシン 451～リジン 459) から構成されるリガンド結合部位の構造またはその一部の側鎖の配向を改変させた構造に対して、これらの残基のうち 1 つないしは 2 つ以上の残基と相互作用するように目視による構造構築、もしくは構造改変を行う。

- 5     具体的には、視覚的方法では、まずコンピュータの画面上に GK タンパク質とそれに結合する化合物との複合体の結晶の構造を、得られた構造座標に従って表示する。そして、コンピュータ上で化学的相互作用を考慮しながら、ライブラリ中にある化合物と GK タンパク質との結合可能性を順次検討する。ここで考慮すべき化学的相互作用は静電相互作用、疎水性相互作用、水素結合、ファンデルワールス相互作用などである。すなわち、該化合物の 3 次元空間での構造が、その官能基群においてカルボキシル基、ニトロ基、ハロゲン基などの陰性電荷を運びやすい基が、GK タンパク質のリジン、アルギニン、ヒスチジンといった正電荷を持つアミノ酸残基に相互作用するように、アミノ基、イミノ基、グアニジル基などの陽性電荷を運びやすい基が、GK タンパク質のグルタミン酸、アスパラギン酸といった負電荷を持つアミノ酸残基に相互作用するように、脂肪族基や芳香族基といった疎水性の官能基が、アラニン、ロイシン、イソロイシン、バリン、プロリン、フェニルアラニン、トリプトファン及びメチオニンといった疎水性のアミノ酸残基と相互作用するように、水酸基、アミド基などの水素結合に関与する基が、GK タンパク質の主鎖や側鎖部分と水素結合ができるように、更には、該化合物と GK タンパク質の結合において立体的な障害が生じないように、また、更には、空隙部分ができるべくできないように空隙部分が充填され、ファンデルワールス相互作用が大きくなるようになど、相互作用に好ましい構造になっているかを総合的に考慮する。このように、静電相互作用、疎水性相互作用、ファンデルワールス相互作用、水素結合などの
- 20    因子を、コンピュータ画面上で視覚的に総合的に考慮して、最終的に候補化合物が GK タンパク質に結合し得るか否かの判断を行う。

このように目視によって化合物候補を選択するプログラムとしては、Insight II や MOE 等のシミュレーションプログラムが例示される。GK タンパク質と相互作用する化合物の有力候補を挙げるために、候補化合物と GK タ

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ンパク質と接触させ、GKタンパク質の活性を測定する。有力候補化合物を実際にGKタンパク質と混合し、結晶化し適合するかどうかを検討する。更に適合した複合物を有機合成を用いて修飾することにより、より望ましい構造とする。

- 5     なお、視覚的手法と、エネルギーを考慮した手法は、適宜組合わせて用いることもできる。そのようなコンピュータソフトウェアとしては、FlexiDock (Tripos Inc.)、FlexX (Tripos Inc.)、SYBYL (Tripos Inc.)、Insight II (Accelrys Inc.)、MOE (Chemical Computing Group Inc.) などが挙げられる。
- 10    なお、本発明においては、上述したドラッグデザイン方法によって選択された化合物を実際に合成し、これらの化合物群を化合物アレイ（又は化合物ライブラリ）として提供することができる。このような化合物アレイを利用すれば、ハイスループットスクリーニングの技術などを用いて、一度に大量の候補化合物をアッセイすることができるので、グルコキナーゼの活性化剤又は阻害剤を
- 15    効率良くスクリーニングすることができる。

（本発明の方法によって得られる化合物及びそれを含む治療剤）

- 上記のドラッグデザイン方法によって設計される化合物は、グルコキナーゼと結合する能力を有するので、グルコキナーゼの活性化化合物又はグルコキナーゼ阻害化合物として用いることができる。また、このような化合物を含有する治療剤又は医薬組成物は、グルコキナーゼ活性が関与する疾患の治療剤（例えば、糖尿病治療剤）として有効に用いることができる。
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- 上記医薬組成物は、本発明のグルコキナーゼと結合する化合物を有効成分として、その薬学的有効量を、適当な薬学的に許容される担体ないし希釈剤と共に含有する。上記医薬組成物（医薬製剤）に利用できる薬学的に許容できる担体としては、製剤の使用形態に応じて通常使用される、充填剤、増量剤、結合剤、付湿剤、崩壊剤、表面活性剤、滑沢剤などの希釈剤或は賦形剤などが例示される。これらの担体は、得られる製剤の投与単位形態に応じて適宜選択使用される。
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本発明の医薬組成物の投与単位形態としては、各種の形態が治療目的に応じて選択でき、その代表的なものとしては、錠剤、丸剤、散剤、粉末剤、顆粒剤、カプセル剤などの固体投与形態や、溶液、懸濁剤、乳剤、シロップ、エリキシルなどの液剤投与形態が含まれ、これらは更に投与経路に応じて経口剤、非経口剤、経鼻剤、経膈剤、坐剤、舌下剤、軟膏剤などに分類され、それぞれ通常の方法に従い、調合、成形、調製することができる。例えば、錠剤の形態に成形するに際しては、上記製剤担体として例えば乳糖、白糖、塩化ナトリウム、ブドウ糖、尿素、デンプン、炭酸カルシウム、カオリン、結晶セルロース、ケイ酸、リン酸カリウムなどの賦形剤、水、エタノール、プロパノール、単シロップ、ブドウ糖液、デンプン液、ゼラチン溶液、カルボキシメチルセルロース、ヒドロキシプロピルセルロース、メチルセルロース、ポリビニルピロリドンなどの結合剤、カルボキシメチルセルロースナトリウム、カルボキシメチルセルロースカルシウム、低置換度ヒドロキシプロピルセルロース、乾燥デンプン、アルギン酸ナトリウム、カンテン末、ラミナラン末、炭酸水素ナトリウム、炭酸カルシウムなどの崩壊剤、ポリオキシエチレンソルビタン脂肪酸エステル類、ラウリル硫酸ナトリウム、ステアリン酸モノグリセリドなどの界面活性剤、白糖、ステアリン、カカオバター、水素添加油などの崩壊抑制剤、第4級アンモニウム塩基、ラウリル硫酸ナトリウムなどの吸収促進剤、グリセリン、デンプンなどの保湿剤、デンプン、乳糖、カオリン、ベントナイト、コロイド状ケイ酸などの吸着剤、精製タルク、ステアリン酸塩、ホウ酸末、ポリエチレングリコールなどの滑沢剤などを使用できる。更に錠剤は必要に応じ通常の剤皮を施した錠剤、例えば糖衣錠、ゼラチン被包錠、腸溶被錠、フィルムコーティング錠とすることができ、また二重錠ないしは多層錠とすることもできる。

丸剤の形態に成形するに際しては、製剤担体として例えばブドウ糖、乳糖、デンプン、カカオ脂、硬化植物油、カオリン、タルクなどの賦形剤、アラビアゴム末、トラガント末、ゼラチン、エタノールなどの結合剤、ラミナラン、カンテンなどの崩壊剤などを使用できる。

カプセル剤は、常法に従い通常本発明の有効成分を上記で例示した各種の製剤担体と混合して硬質ゼラチンカプセル、軟質カプセルなどに充填して調整さ

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れる。

経口投与用液体投与形態は、慣用される不活性希釈剤、例えば水、を含む医薬的に許容される溶液、エマルジョン、懸濁液、シロップ、エリキシルなどを包含し、更に湿潤剤、乳剤、懸濁剤などの助剤を含ませることができ、これらは常法に従い調製される。

非経口投与用の液体投与形態、例えば滅菌水性乃至非水性溶液、エマルジョン、懸濁液などへの調製に際しては、希釈剤として例えば水、エチルアルコール、プロピレングリコール、ポリエチレングリコール、エトキシ化イソステアリルアルコール、ポリオキシ化イソステアリルアルコール、ポリオキシエチレンソルビタン脂肪酸エステル及びオリーブ油などの植物油などを使用でき、また注入可能な有機エステル類、例えばオレイン酸エチルなどを配合できる。これらには更に通常の溶解補助剤、緩衝剤、湿潤剤、乳化剤、懸濁剤、保存剤、分散剤などを添加することもできる。滅菌は、例えばバクテリア保留フィルターを通過させる濾過操作、殺菌剤の配合、照射処理及び加熱処理などにより実施できる。また、これらは使用直前に滅菌水や適当な滅菌可能媒体に溶解することのできる滅菌固体組成物形態に調製することもできる。

坐剤や腔投与用製剤の形態に成形するに際しては、製剤担体として、例えばポリエチレングリコール、カカオ脂、高級アルコール、高級アルコールのエステル類、ゼラチン及び半合成グリセライドなどを使用できる。

ペースト、クリーム、ゲルなどの軟膏剤の形態に成形するに際しては、希釈剤として、例えば白色ワセリン、パラフィン、グリセリン、セルロース誘導体、プロピレングリコール、ポリエチレングリコール、シリコン、ベントナイト及びオリーブ油などの植物油などを使用できる。

経鼻又は舌下投与用組成物は、周知の標準賦形剤を用いて、常法に従い調製することができる。

尚、本発明薬剤中には、必要に応じて着色剤、保存剤、香料、風味剤、甘味剤などや他の医薬品などを含有させることもできる。

上記医薬製剤中に含有されるべき有効成分の量及びその投与量は、特に限定されず、所望の治療効果、投与法、治療期間、患者の年齢、性別その他の条件

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などに応じて広範囲より適宜選択される。一般的には、投与量は、通常、1日  
当たり体重60kg当り、約0.01mg~1000mg、好ましくは約1mg  
~100mgとするのがよく、1日に1~数回に分けて投与することができる。

- 5 本明細書の配列表の配列番号は、以下の配列を示す。

〔配列番号：1〕

ヒト由来肝臓型グルコキナーゼをコードするDNAの塩基配列を示す。

〔配列番号：2〕

ヒト由来肝臓型グルコキナーゼのアミノ酸配列を示す。

- 10 〔配列番号：3〕

ヒト由来β細胞グルコキナーゼのアミノ酸配列を示す。

〔配列番号：4〕

ヒト由来肝臓型グルコキナーゼのN末端側のアミノ酸残基11個を欠失させ  
たタンパク質をコードするDNAの塩基配列を示す。

- 15 〔配列番号：5〕

ヒト由来肝臓型グルコキナーゼのN末端側のアミノ酸残基11個を欠失させ  
たタンパク質のアミノ酸配列を示す。

〔配列番号：6〕

- 20 以下の実施例1におけるPCR反応で使用した、プライマー1の塩基配列を  
示す。

〔配列番号：7〕

以下の実施例1におけるPCR反応で使用した、プライマー2の塩基配列を  
示す。

〔配列番号：8〕

- 25 ヒト由来肝臓型グルコキナーゼのN末端側のアミノ酸残基15個を欠失させ  
たタンパク質のアミノ酸配列を示す。

〔配列番号：9〕

以下の実施例6におけるPCR反応で使用した、プライマーの塩基配列を示  
す。



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〔配列番号：10〕

以下の実施例6におけるPCR反応で使用した、プライマーの塩基配列を示す。

## 5 (実施例)

以下、本発明を、実施例を用いて具体的に説明する。

(変異型酵素の精製方法)

Human グルコキナーゼには、プロモーターの違いによって肝臓型と脾臓型が存在し、N末端の15残基が異なる。三次元構造解析を目的に結晶化を行うため  
10 に、この部分の一部あるいはすべてを欠損した変異型酵素を以下の方法で作成した。

pCR2.1 (INTROGEN 社製) 上にクローニングされた Human 肝臓型グルコキナーゼの cDNA と 2 種のプライマーセット

5' - gtcacaaggagccagaagccttatggccttgactctggtag- 3' (配列番号6) 及び  
15 5' -gaagccccacgacattgttcccttctgc - 3' (配列番号7) の組み合わせ、ならびに、

5' - ccaggcccagacagccaagccttatggtagagcagatcc- 3'、 (配列番号9) 及び

5' -gaagccccacgacattgttcccttctgc 3' (配列番号10)

を用いてPCR反応を行った。得られたPCR産物のHind III、ClaI断片を  
20 pFLAG・CTC ベクター (Eastman Kodak) のHind III、Eco RI 部位にクローニングされていた肝臓型GKのHind III - Cla I 領域と置換することで、肝臓型GKの1~11残基を欠損する変異型GK ( $\Delta 1-11$ )、及び1~15残基を欠損する変異型GK ( $\Delta 1-15$ ) をコードするcDNAを得た。得られたcDNAの配列を確認した後、これらのベクターを発現ベクターとし、大腸菌DH5 $\alpha$ 株 (宝  
25 酒造社製) を形質変換した。

形質変換体をLB培地で600nmの吸収が0.8になるまで37℃で培養した後、終濃度が0.4mMになるようにイソプロピルー1-チオール $\beta$ -D-ガラクトシド (和光純薬社製) を加え、25℃で16時間、タンパク質の生産誘導を行った。

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培養された大腸菌を遠心機で収集し、以下の成分を含む緩衝液 (50 mM リン酸カリ (Potassium Phosphate) pH7.5, 50mM NaCl, 2 mM DTT, 0.5 mM Pefabloc SC (関東化学社製)、a proteinase inhibitor mixture (Roche 社製)) に懸濁した。

- 5 収集した大腸菌は、超音波破碎法によって破碎し、可溶化画分を上記の緩衝液に対して透析した後、HiTrapQ カラム (アマシャム社製) により精製した。HiTrap Q カラムより塩化カリウムのグラジエントにより溶出された GK 画分を希釈により塩濃度 50mM に希釈した。

- 希釈された GK 画分を論文 (Preparative Biochemistry, 20 (2), 163-178 (1990)) に示されている方法で作製した Glucosamin Sepharose カラムにより精製した。GK 画分を Glucosamin Sepharose カラムに吸着させ 100mM 塩化ナトリウムで不純物を除いた後、1M のグルコースにより溶出させた。

- 溶出された GK 画分は、MonoQ10/10 カラムにより精製した。MonoQ10/10 カラム (アマシャム社製) より塩化ナトリウムのグラジエントにより溶出された GK 画分を、移動層として 50mM Tris-Cl pH7.2, 50mM NaCl 緩衝液を用いて、Superdex200 カラム (アマシャム社製) により精製した。

(結晶化方法)

(変異型 GK ( $\Delta 1-11$ ) / グルコース / 化合物複合体の結晶)

- 20 変異型 GK ( $\Delta 1-11$ ) / グルコース / 化合物複合体の結晶は、以下に示す蒸気拡散の手法を用いて得た。なお、変異型 GK ( $\Delta 1-11$ ) は、配列番号 5 で表されるアミノ酸配列を有するグルコキナーゼを意味する。

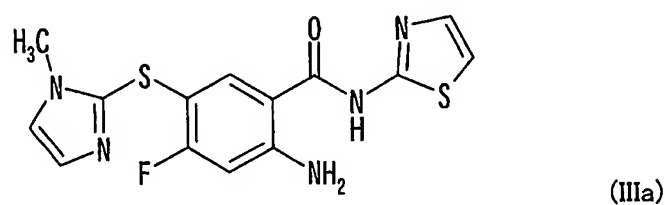
- すなわち、高純度に精製された変異型 GK を濃縮し、最終的に 10mg/ml 程度の変異型 GK の溶液 (25 mM Tris-Cl, 50 mM NaCl, 5 mM TCEP) とした。これに最終濃度 20mM のグルコース、及び最終濃度 0.3 mM の GK を活性化する下記化合物 1 (式 IIIa の化合物) を加え、結晶化に用いた。タンパク質溶液 1~5  $\mu$ l に結晶化溶液として 28~30% PEG 1500、0.1 M Hepes - NaOH (pH6.6) を等量加えて混合した溶液を 0.5~1ml の結晶化溶液を入れた密閉容器に、両溶液が触れ合わないよう収め、20℃で静置した。およそ 3 日~1 ヶ月の静置の

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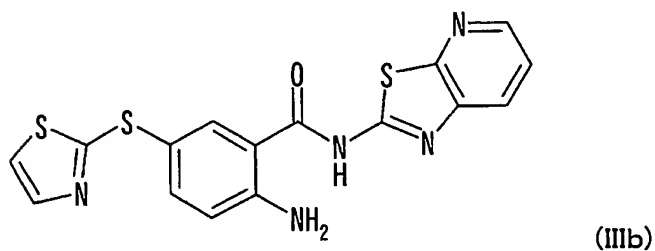
後に、試料溶液中に最大 0.4 mm×0.4 mm×0.7 mm 程度の結晶が得られた（実施例 1）。

さらに上記の方法で得られた結晶を下記化合物 2（式 III b で表される化合物）が 0.3 mM の濃度で含まれるようにして、28～30% PEG 1500、0.1 M Hepes - NaOH (pH 6.6) 溶液に 3～7 日程度浸透することによって、下記化合物 2 と上

記変異型 GK の複合体結晶を得た（実施例 2）。



10 化合物 2

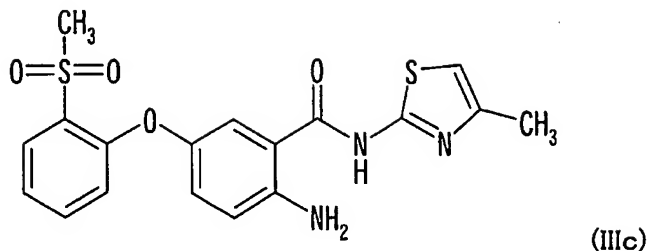


また、前記化合物 1 に代えて化合物 3（式 III c で表される化合物）を用いた以外は、実施例 1 と同様にして結晶化を試みた結果、それぞれ実施例 1 と同

15 様な結晶が得られた（実施例 3）。

化合物 3

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- 得られた結晶を 10 % のグリセロールを加えた結晶化溶液に浸し、続いて液体窒素中で急速に凍結した。シンクロトロン施設 KEK-PF の BL6B において振動法により、凍結した結晶の X 線回折データを 100K 窒素気流中で収集した。得られた回折像から、DENZO/SCALEPACK (HKL 社製) を用いて回折強度を数値化し、結晶構造因子を求めた。この段階で結晶は六方晶系で空間群は  $P6_322$  あるいは  $P6_122$  を有し、結晶の単位格子は、 $a = b = 79.9$  オングストローム、 $c = 322.2$  オングストローム、 $\alpha = \beta = 90^\circ$ 、 $\gamma = 120^\circ$  であるとわかった。
- 10 得られた構造因子と Human ヘキソキナーゼ タイプ 1 の 3 次元構造座標を用いて分子置換法を行い構造を解析した。計算には 8 オングストロームから 4 オングストロームの分解能のデータを用い、CCP4 (Council for the Central laboratory of the Research Councils) の Amore プログラムにより行った。計算により得られた構造の R 因子は、53.7% であり、結晶の空間群は  $P6_322$  で非対称単位に変異型 GK 一分子を含むことが分かった。この構造と構造因子から電子密度マップを得て、プログラム 0 (Dat-ONO 社製) を用いて変異型グルコキナーゼの構造を決定した。
- 15

- 次に CNX (Accelrys Inc.) を用いてアミノ酸の位置の精密化を行い、プログラム 0 を用いてアミノ酸残基の同定を行った。この操作を繰り返し行い、変異型グルコキナーゼのスレオニン 14 からシステイン 461 までの 448 アミノ酸残基の構造座標、1 分子のグルコース分子、1 分子の化合物 A、1 個のナトリウムイオン、及び 149 個の水分子を同定し構造座標を決定した。最終的に決定された構造の正確さの指標とされる R 因子は、30 オングストロームから 2.3 オングストロームの分解能のデータに対して  $R=23.2\%$  であり、構造の精密化の段階で計算に用いなかったデータに対する R 因子 ( $R_{\text{free}}$ ) は 27.4% であった。
- 25

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ラマチャンドラン・プロットで確認したところ許容されない構造を持ったアミノ酸残基はなかった。

決定された変異型グルコキナーゼの構造は、アイソザイムであるヘキソキナーゼの構造と似たものであったが、グルコキナーゼを活性化する化合物 1 (式 IIIa の化合物) の結合している部位の構造は異なっていた。この構造の相違は、現在の計算化学の能力で予想できうるものでなく、今回の構造解析により、この部位がアクティベーターの結合部位であること、そしてその詳細な立体構造が初めて明らかとなった。図 1 a は、ここで解明されたグルコキナーゼの三次元構造を示すリボン図である。図 1 a に示されるように、新規に見つかった  
5  
10  
15  
アクティベーター結合部位は、ラージドメインとスモールドメインの間に位置しており、基質であるグルコースが結合しているグルコキナーゼの活性中心から、約 20 オングストローム離れていた。アクティベーター結合部位を構成しているグルコキナーゼのアミノ酸残基は以下のとおりであった。チロシン 61～セリン 69、グルタミン酸 96～グルタミン 98、イソロイシン 159、メチオニン 210～チロシン 215、ヒスチジン 218～グルタミン酸 221、メチオニン 235、アルギニン 250、ロイシン 451～リジン 459。

また、この結合部位に対する化合物 1 (式 IIIa の化合物) の結合様式を図 2 に、グルコキナーゼの結合部位の構造を図 3 に示す。チアゾール環は、バリ  
20  
25  
ン 62、バリン 452、バリン 455 のそれぞれのアミノ酸側鎖の分子とファンデルワールス接触をしており、またチアゾール環上の窒素原子がアルギニン 63 の主鎖の窒素原子と水素結合をしていた。化合物 1 上のアミドの窒素原子は、アルギニン 63 の主鎖の酸素原子と水素結合をしていた。化合物 1 のベンゼン環部分はイソロイシン 211 とファンデルワールス接触をしており、ベンゼン環に置換したフッ素原子はチロシン 214 の側鎖とファンデルワールス接触をしていた。化合物 1 のアニリン構造は、チロシン 215 の側鎖の酸素原子と水素結合を形成していた。硫黄を介してベンゼン環と結合しているイミダゾール環部分は、メチオニン 210、メチオニン 235、チロシン 214 のアミノ酸側鎖部分とファンデルワールス接触をしていた。ラージドメインとスモールドメインを結んでい  
る、セリン 64～セリン 69 の部分は、溶液に露出した構造をしており、化合物

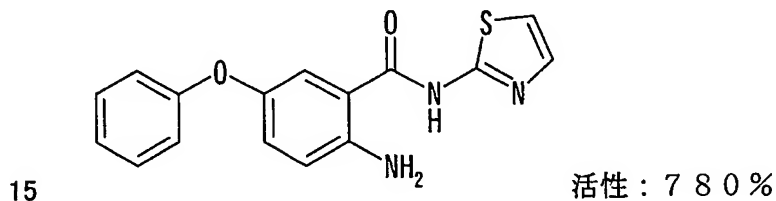
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1 は、この部分が形作るアーチ状構造の下部に結合していた（図 3）。

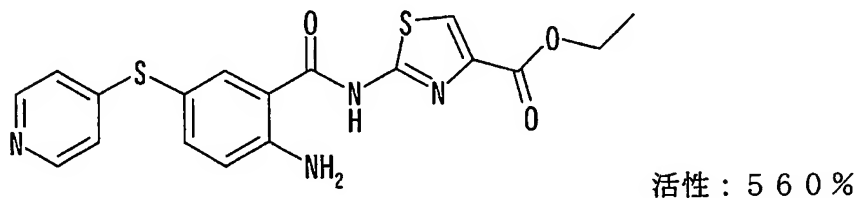
（実施例 4：ドラッグデザインの実施例）

ソフトウェア UNITY（トライボス社製）を用い、Arg63 の主鎖 NH、CO からそれぞれ発生させた水素結合アクセプター、水素結合ドナーのファルマコフォアと、複合体を形成するリガンドのアニン部分のフェニル基に相当する空間に形成された疎水性のファルマコフォア、および蛋白の構造を元に作成した蛋白表面を検索条件としてライブラリ化合物をスクリーニングし、下記化合物 4、及び化合物 5 が得られ、アッセイを行ったところ、それぞれ 780%、および 560% の活性が認められた。なお活性が 780% とは、グルコキナーゼの活性をコントロールを 100% としたときに、これらの化合物によって 780% まで増強されたことを示す（グルコース 2.5M 及びリガンド 10 $\mu$ M を使用）。

化合物 4



化合物 5



20 （実施例 5）

（変異型 GK（ $\Delta 1-15$ ）の結晶）

変異型 GK（ $\Delta 1-15$ ）（配列番号 8 で表されるアミノ酸配列を有するグルコキナーゼ）の単体の結晶は、以下に示す蒸気拡散の手法を用いて得た。

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すなわち、高純度に精製された変異型 GK を濃縮し、最終的に 10mg/ml 程度の変異型 GK の溶液 (25 mM Tris-Cl pH7.2, 50 mM NaCl, 5 mM TCEP) とした。タンパク質溶液 1~5  $\mu$ l に結晶化溶液 (1.5 ~ 1.6 M 硫酸アンモニウム、50mM NaCl、0.1 M Bicine NaOH (pH8.7)) を等量加えて混合した溶液を 0.5~

5 1ml の結晶化溶液が入った密閉容器に、両溶液が触れ合わないよう収め、20℃で静置した。およそ 3 日~1 ヶ月の静置の後に、試料溶液中に最大 0.07mm  $\times$  0.07mm  $\times$  0.5mm 程度の大きさの結晶が得られた。

- 得られた結晶を 20% のグリセロールを加えた結晶化溶液に浸し、続いて液体窒素中で急速に凍結した。シンクロトロン施設 Spring-8 の BL32B2 において、
- 10 振動法により、凍結した結晶の X 線回折データを 100K 窒素気流中で収集した。得られた回折像から、Mosflm を用いて回折強度を数値化し、結晶構造因子を求めた。この段階で結晶は六方晶系であり、空間群は  $P6_522$  あるいは  $P6_122$  を有し、結晶の単位格子は、 $a = b = 103.2 \text{ \AA}$ ,  $c = 281.0 \text{ \AA}$ ,  $\alpha = \beta = 90^\circ$ ,  $\gamma = 120^\circ$  であることが明らかとなった。
- 15 次に、得られた構造因子をもちいて分子置換法を行い、構造を解析した。立体構造のモデルとして、変異型 GK ( $\Delta 1-11$ ) / グルコース / 化合物複合体結晶により決定されたグルコキナーゼの各ドメインの 3 次元構造座標をそれぞれ別々に用いた。計算は、8~4 オングストロームの分解能のデータを用いて、CCP4 (Council for the Central laboratory of the Research Councils)
- 20 の Amore プログラムにより行った。結晶の空間群は  $P6_522$  であり、非対称単位に変異型 GK ( $\Delta 1-15$ ) 一分子を含むことが分かった。この構造と構造因子から電子密度マップを得て、プログラム 0 (Dat-ON0 社製) を用いて変異型 GK ( $\Delta 1-15$ ) 単体の構造を決定した。

- 次に、CNX (モレキュラーシミュレーション社製) を用いてアミノ酸の位置
- 25 の精密化を行い、プログラム 0 を用いてアミノ酸残基の同定を行った。この操作を繰り返し行い、変異型グルコキナーゼのメチオニン 15 からヒスチジン 156 とアスパラギン 180 からシステイン 461 までの 424 アミノ酸残基の構造座標、2 分子の硫酸イオン、1 個のナトリウムイオン、及び 7 個の水分子を同定し構造座標を決定した。最終的に決定された構造の正確さの指標とされる R 因

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子は、50~3.4 オングストロームの分解能のデータに対して R=23.8% であり、構造の精密化の段階で計算に用いなかったデータに対する R 因子 (Rfree) は 30.6% であった。ラマチャンドラン・プロットで確認したところ、許容されない構造を持ったアミノ酸残基はなかった。

- 5 図 1 a 及び図 1 b に、それぞれグルコキナーゼ ( $\Delta 1-11$ ) / グルコース / 化合物 1 の構造を示すリボン図、及びグルコキナーゼ ( $\Delta 1-15$ ) 単体の構造を示すリボン図を示す。なお、右図は、左図を回転した図である。決定された変異型 GK ( $\Delta 1-15$ ) 単体の構造においてラージドメイン及びスモールドメインの主要部分の構造は、変異型 GK ( $\Delta 1-11$ ) / グルコース / 化合物複合体結晶により決定されたグルコキナーゼにおけるそれぞれの構造と似たものであったが、2つのドメインの相対位置が大きく異なっていた。変異型 GK ( $\Delta 1-15$ ) 単体構造においてスモールドメインの主要部分は、変異型 GK ( $\Delta 1-11$ ) / グルコース / 化合物複合体構造におけるスモールドメインの位置からおよそ 99 度回転していた。また、グルコキナーゼの C 末端領域に位置し
- 10 変異型 GK ( $\Delta 1-11$ ) / グルコース / 化合物複合体構造においてはスモールドメインを構成していた  $\alpha 13$  ヘリックスは、変異型 GK ( $\Delta 1-15$ ) 単体構造においてはもはやスモールドメインを構成せず、両ドメイン間に位置していた。さらに、変異型 GK ( $\Delta 1-11$ ) / グルコース / 化合物複合体構造における基質グルコースの結合部位及び活性化剤結合部位はどちらも 2つのドメイン間に存在していたため、新たに決定した構造ではそれらの部位の構造は大きく変化していた。変異型 GK ( $\Delta 1-15$ ) 単体構造では酵素活性に重要な役割を果たすアミノ酸残基が活性部位を形成しておらず、今回解析した変異型 GK ( $\Delta 1-15$ ) 単体の構造は、グルコキナーゼの不活性状態の構造であった。また、変異型 GK ( $\Delta 1-15$ ) 単体の構造において活性化剤結合部位
- 15 は、完全に消失していた。変異型 GK ( $\Delta 1-11$ ) / グルコース / 化合物複合体構造および変異型 GK ( $\Delta 1-15$ ) 単体構造により観測されたグルコキナーゼの構造変化 (約 99 度のドメインの回転) は、今まで知られていたヘキソキナーゼの構造変化 (約 12 度のドメインの回転) と比較してはるかに大きな
- 20
- 25



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ものであり、現在の計算化学の能力で予想でき得るものではなく、今回の構造解析により初めて明らかとなったものである。

- また、不活性型である変異型 GK ( $\Delta 1-15$ ) 単体構造への構造変化を阻害する目的として、変異型 GK ( $\Delta 1-11$ ) / グルコース / 化合物複合体構造で示された化合物結合部位に結合する化合物を設計することにより、グルコキナーゼの活性化剤を設計できることが明らかとなった。

#### 産業上の利用可能性

- 以上説明したように、本発明によれば、従来は結晶化が困難であったグルコキナーゼタンパク質の結晶を得ることができた。この結晶の構造を解析することによって得られる三次元構造座標は、グルコキナーゼに結合する化合物を設計するために好適に用いることができる。また、このようにして設計される化合物は、グルコキナーゼに結合するので、グルコキナーゼ活性化剤又は阻害剤として、グルコキナーゼ活性が関与する疾患の治療剤（例えば、糖尿病治療剤）として用いることができる。

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## 請求の範囲

1. 結晶化に用いることを特徴とする、グルコキナーゼタンパク質。
2. 配列番号 5 に記載のアミノ酸配列からなることを特徴とする、請求項 1
- 5 に記載のタンパク質。
3. 配列番号 5 に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同一のアミノ酸配列からなることを特徴とするタンパク質の結晶。
4. 前記タンパク質がグルコキナーゼタンパク質である、請求項 3 に記載の結晶。
- 10 5. 配列番号 5 に記載のアミノ酸配列を有するタンパク質の結晶である、請求項 3 に記載の結晶。
6. 格子定数が、下記式 (1) ~ (4) :  

$$a=b=79.9\pm 4\text{オングストローム} \quad \cdots (1)$$

$$c=322.2\pm 15\text{オングストローム} \quad \cdots (2)$$
15 
$$\alpha=\beta=90^\circ \quad \cdots (3)$$

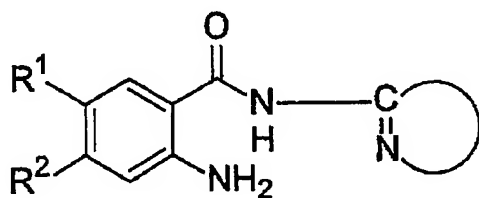
$$\gamma=120^\circ \quad \cdots (4)$$
を満たす、請求項 3 に記載の結晶。
7. 空間群が  $P6_522$  である、請求項 6 に記載の結晶。
8. 表 1 に記載の三次元構造座標データによって特定されるタンパク質の結
- 20 晶。
9. 表 1 に記載の三次元構造座標データの少なくとも一つのデータを変更した三次元構造座標データにおいて、表 1 に記載の三次元構造座標データで示されるアミノ酸の主鎖の原子 ( $C\alpha$  原子) と、該  $C\alpha$  原子と対応する前記変更した三次元構造座標データで示される  $C\alpha$  原子との平均二乗偏差が、0.6 オン
- 25 グストローム以下である結晶。
10. 化合物結合部位が、配列番号 5 に示すアミノ酸配列における、チロシン 61 ~ セリン 69、グルタミン酸 96 ~ グルタミン 98、イソロイシン 159、メチオニン 210 ~ チロシン 215、ヒスチジン 218 ~ グルタミン酸 221、メチオニン 235、アルギニン 250、ロイシン 451 ~ リジン 459

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のアミノ酸残基の少なくともひとつによって構成されている、請求項 3～9 のいずれかに記載の結晶。

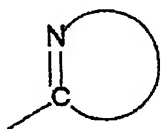
- 1 1. 配列番号 5 に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同一のアミノ酸配列からなるタンパク質と該タンパク質に結合可能な化合物との複合体を含む結晶。

- 1 2. 前記化合物が、式 (I) で表される、請求項 1 1 に記載の結晶。



(I)

- 10 [式中、R<sup>1</sup>は、ハロゲン原子、-S-(O)<sub>p</sub>-A、-S-(O)<sub>q</sub>-B又は-O-Bを示し（ここで、p及びqは同一又は異なって、0～2の整数を示し、Aは置換されていてもよい直鎖のC<sub>1</sub>-C<sub>6</sub>アルキル基を示し、Bは置換されていてもよい五員環又は六員環のアリール基又はヘテロアリール基を示し、R<sup>2</sup>は水素原子又はハロゲン原子を示し、



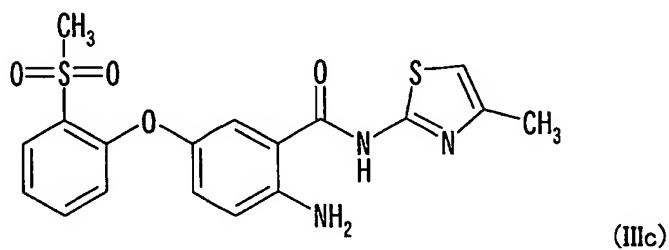
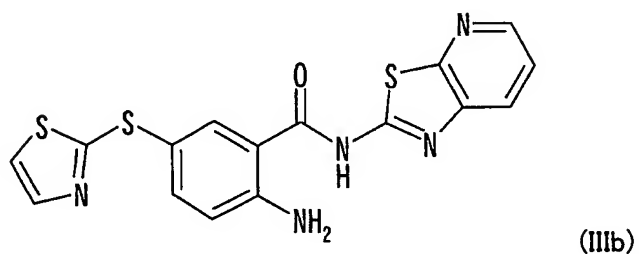
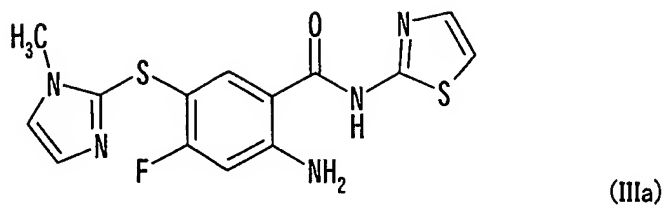
(II)

15

は、アミド基に結合した炭素原子の隣に窒素原子を有する、置換されていてもよい単環の又は双環のヘテロアリール基を示す)

- 1 3. 前記化合物が、式 (IIIa)～式 (IIIc) で表されるいずれかの化合物である請求項 1 2 に記載の結晶。

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5

- 1 4. 配列番号 8 に記載のアミノ酸配列からなることを特徴とする、請求項 1 に記載のタンパク質。
- 1 5. 配列番号 8 に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同一のアミノ酸配列からなることを特徴とするタンパク質の結晶。
- 1 6. 前記タンパク質がグルコキナーゼタンパク質である、請求項 1 5 に記載の結晶。
- 1 7. 配列番号 8 に記載のアミノ酸配列を有するタンパク質の結晶である、請求項 1 5 に記載の結晶。
- 15 1 8. 格子定数が、下記式
 
$$a=b=103.2\pm5 \text{ オングストローム} \quad \cdots (5)$$

$$c=281.0\pm7 \text{ オングストローム} \quad \cdots (6)$$

$$\alpha=\beta=90^\circ \quad \cdots (7)$$

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$$\gamma=120^\circ \quad \cdots (8)$$

を満たす、請求項 15 に記載の結晶。

19. 空間群が  $P6_522$  である、請求項 18 に記載の結晶。

20. 表 2 に記載の三次元構造座標データによって特定されるタンパク質の  
5 結晶。

21. 表 2 に記載の三次元構造座標データの少なくとも一つのデータを変更  
した三次元構造座標データにおいて、表 2 に記載の三次元構造座標データで示  
されるアミノ酸の主鎖の原子 ( $C\alpha$  原子) と、該  $C\alpha$  原子と対応する前記変更  
した三次元構造座標データで示される  $C\alpha$  原子との平均二乗偏差が、0.6 オ  
10 ングストローム以下である結晶。

22. 配列番号 2 に記載のアミノ酸配列を有するタンパク質の N 末端、C 末  
端のいずれかまたは両方から、1~50 個のアミノ酸残基を欠損したアミノ酸  
配列を有するタンパク質を製造するタンパク質製造工程と、

前記タンパク質製造工程で得られたタンパク質と結合する化合物と、前記タ  
15 ンパク質製造工程で得られたタンパク質とを反応させるタンパク質反応工程と  
を含む、

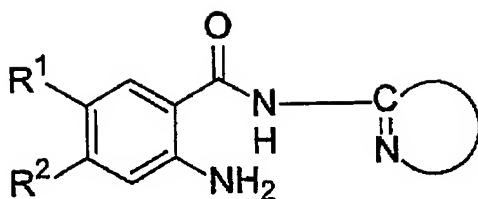
タンパク質及びそのタンパク質と結合する化合物の複合体を含む結晶の製造  
方法。

23. タンパク質の結晶を製造する方法であって、

20 配列番号 5 に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同一のア  
ミノ酸配列を含みグルコキナーゼ活性を有するタンパク質、及び該タンパク質  
に結合可能な化合物を用いることを特徴とする、結晶の製造方法。

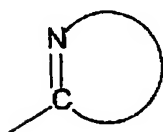
24. 前記タンパク質に結合可能な化合物が、式 (I) で表される化合物で  
あることを特徴とする、請求項 23 に記載のタンパク質の結晶の製造方法。

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(I)

[式中、 $R^1$ は、ハロゲン原子、 $-S-(O)_p-A$ 、 $-S-(O)_q-B$ 又は $-O-B$ を示し（ここで、 $p$ 及び $q$ は同一又は異なって、 $0 \sim 2$ の整数を示し、 $A$ は置換されていてもよい直鎖の $C_1-C_6$ アルキル基を示し、 $B$ は置換されていてもよい五員環又は六員環のアリール基又はヘテロアリール基を示し、 $R^2$ は水素原子又はハロゲン原子を示し、



(II)

は、アミド基に結合した炭素原子の隣に窒素原子を有する、置換されていてもよい単環の又は双環のヘテロアリール基を示す)

25. 共結晶法又はソーキング法による、請求項23、又は請求項24に記載の結晶の製造方法。

26. タンパク質の立体構造情報に基づいて該タンパク質に結合する化合物の構造をデザインするドラッグデザイン方法であって、

15 該タンパク質の立体構造情報が、請求項3～13、請求項15～21のうちのいずれか一項に記載の結晶を解析することによって得られる情報であることを特徴とする、ドラッグデザイン方法。

27. 前記立体構造情報に基づいて、前記タンパク質の化合物結合部位を推測する結合部位推測工程と、

20 前記結合部位推測工程で推測された化合物結合部位に適合する化合物を、化合

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物ライブラリより選択する選択工程と、

を含むことを特徴とする、請求項 26 に記載のドラッグデザイン方法。

28. 前記立体構造情報に基づいて、前記タンパク質の化合物結合部位を推測する結合部位推測工程と、

5 前記結合部位推測工程で推測された化合物結合部位に適合する化合物の構造を構築する化合物構造構築工程と、

を含むことを特徴とする、請求項 26 に記載のドラッグデザイン方法。

29. 前記立体構造情報に基づいて、前記タンパク質の化合物結合部位を推測する結合部位推測工程と、

10 前記結合部位推測工程で推測された化合物結合部位と該化合物結合部位に適合する化合物とが相互作用するように化合物の構造を目視によりデザインするデザイン工程と、

を含むことを特徴とする、請求項 26 に記載のドラッグデザイン方法。

30. 前記化合物結合部位が、配列番号 5 に示すアミノ酸配列における、チロシン 61～セリン 69、グルタミン酸 96～グルタミン 98、イソロイシン 159、メチオニン 210～チロシン 215、ヒスチジン 218～グルタミン酸 221、メチオニン 235、アルギニン 250、ロイシン 451～リジン 459 のアミノ酸残基の少なくともひとつによって構成されている、請求項 26～29 のうちのいずれか一項に記載のドラッグデザイン方法。

20 31. さらに、前記化合物結合部位に適合すると推定される候補化合物の生理活性を測定する工程を含む、請求項 26～30 のいずれか一項に記載のドラッグデザイン方法。

32. さらに、前記化合物結合部位に適合すると推定される候補化合物と、配列番号 5 に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同一のアミノ酸配列を含むタンパク質とを接触させ、その候補化合物が該タンパク質に結合するか否かを判定する結合判定工程を含む、請求項 26～30 のいずれか一項に記載のドラッグデザイン方法。

33. 請求項 26～30 のいずれか一項に記載のドラッグデザイン方法によって選択された化合物群を化合物アレイとして組み合わせることを含む化合物

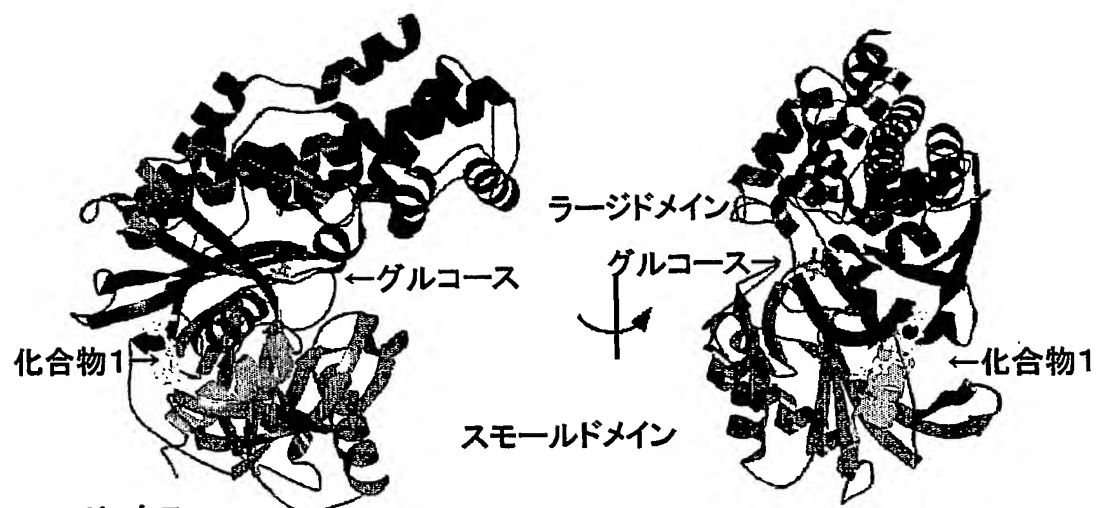
- 299 -

アレイの製造方法。



図1

a



b

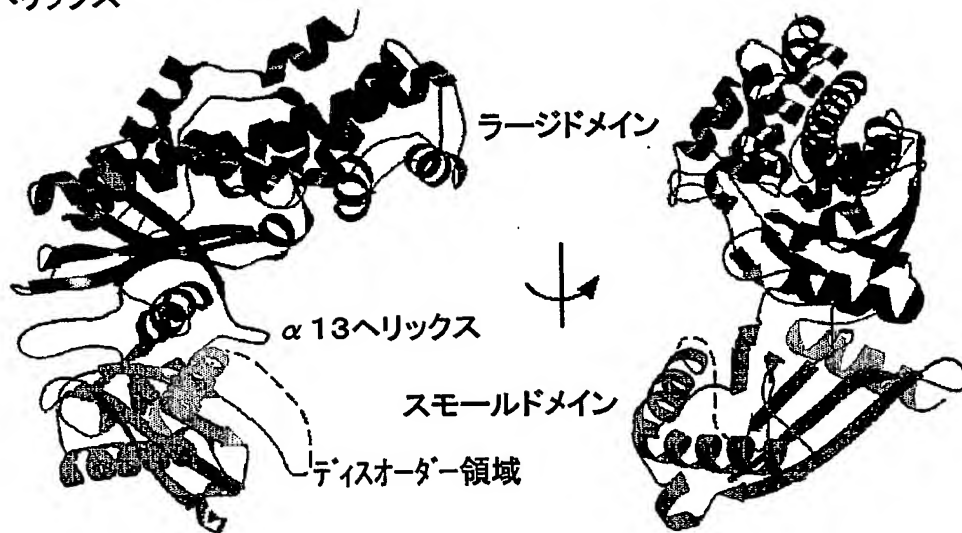
 $\alpha$  13ヘリックス

図2

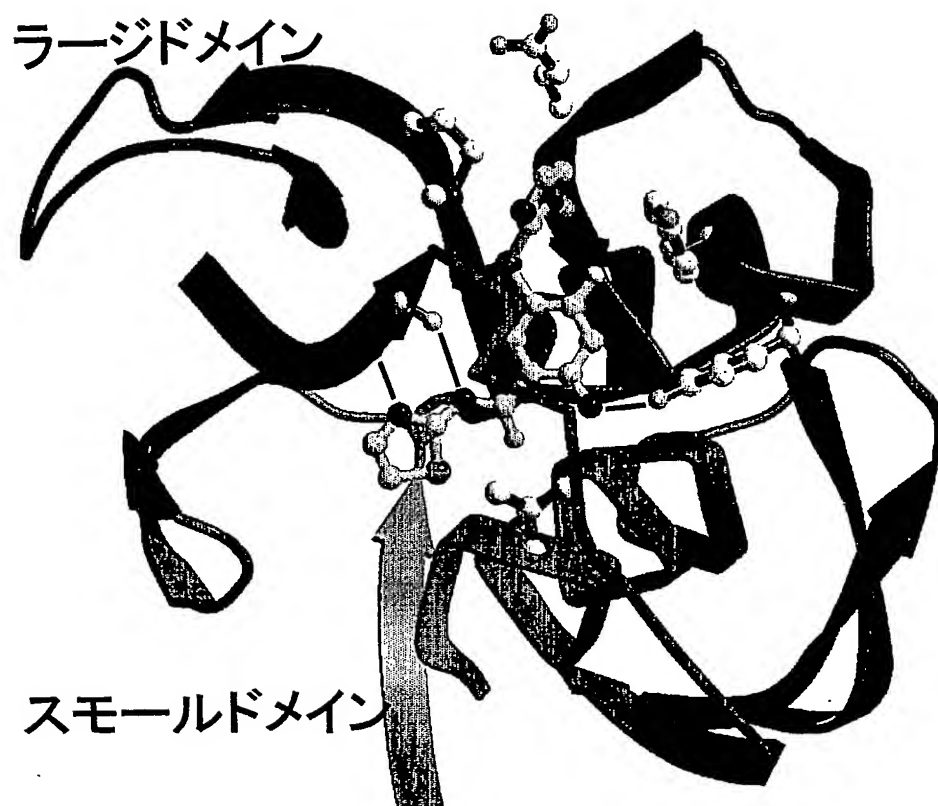
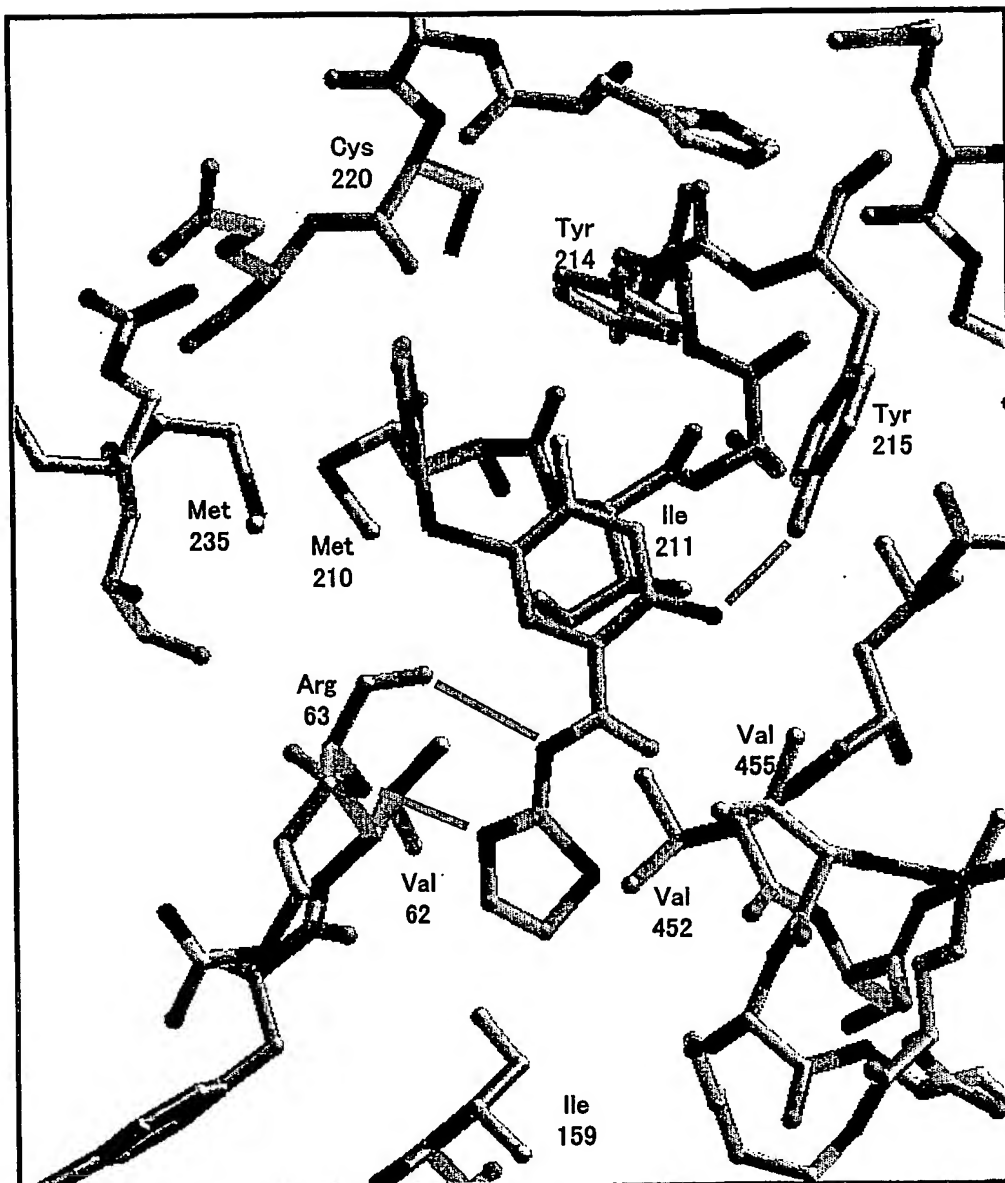


図3



1/15  
SEQUENCE LISTING

&lt;110&gt; Banyu Pharmaceutical Co., Ltd.

<120> Crystal of Glucokinase Protein and Drug Desing Method  
Using Thereof

&lt;130&gt; P03-0064PCT

&lt;140&gt;

&lt;141&gt;

&lt;150&gt; JP2002-142232

&lt;151&gt; 2002-05-16

&lt;160&gt; 10

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1401

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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2/15

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&lt;210&gt; 2

&lt;211&gt; 466

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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 20 25 30

Lys Val Met Arg Arg Met Gln Lys Glu Met Asp Arg Gly Leu Arg Leu  
 35 40 45

Glu Thr His Glu Glu Ala Ser Val Lys Met Leu Pro Thr Tyr Val Arg  
 50 55 60

Ser Thr Pro Glu Gly Ser Glu Val Gly Asp Phe Leu Ser Leu Asp Leu  
 65 70 75 80

Gly Gly Thr Asn Phe Arg Val Met Leu Val Lys Val Gly Glu Gly Glu  
85 90 95

Glu Gly Gln Trp Ser Val Lys Thr Lys His Gln Met Tyr Ser Ile Pro  
100 105 110

Glu Asp Ala Met Thr Gly Thr Ala Glu Met Leu Phe Asp Tyr Ile Ser  
115 120 125

Glu Cys Ile Ser Asp Phe Leu Asp Lys His Gln Met Lys His Lys Lys  
130 135 140

Leu Pro Leu Gly Phe Thr Phe Ser Phe Pro Val Arg His Glu Asp Ile  
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Asp Lys Gly Ile Leu Leu Asn Trp Thr Lys Gly Phe Lys Ala Ser Gly  
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Ala Glu Gly Asn Asn Val Val Gly Leu Leu Arg Asp Ala Ile Lys Arg  
180 185 190

Arg Gly Asp Phe Glu Met Asp Val Val Ala Met Val Asn Asp Thr Val  
195 200 205

Ala Thr Met Ile Ser Cys Tyr Tyr Glu Asp His Gln Cys Glu Val Gly  
210 215 220

Met Ile Val Gly Thr Gly Cys Asn Ala Cys Tyr Met Glu Glu Met Gln  
225 230 235 240

Asn Val Glu Leu Val Glu Gly Asp Glu Gly Arg Met Cys Val Asn Thr  
245 250 255

Glu Trp Gly Ala Phe Gly Asp Ser Gly Glu Leu Asp Glu Phe Leu Leu  
260 265 270

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Glu Tyr Asp Arg Leu Val Asp Glu Ser Ser Ala Asn Pro Gly Gln Gln  
275 280 285

Leu Tyr Glu Lys Leu Ile Gly Gly Lys Tyr Met Gly Glu Leu Val Arg  
290 295 300

Leu Val Leu Leu Arg Leu Val Asp Glu Asn Leu Leu Phe His Gly Glu  
305 310 315 320

Ala Ser Glu Gln Leu Arg Thr Arg Gly Ala Phe Glu Thr Arg Phe Val  
325 330 335

Ser Gln Val Glu Ser Asp Thr Gly Asp Arg Lys Gln Ile Tyr Asn Ile  
340 345 350

Leu Ser Thr Leu Gly Leu Arg Pro Ser Thr Thr Asp Cys Asp Ile Val  
355 360 365

Arg Arg Ala Cys Glu Ser Val Ser Thr Arg Ala Ala His Met Cys Ser  
370 375 380

Ala Gly Leu Ala Gly Val Ile Asn Arg Met Arg Glu Ser Arg Ser Glu  
385 390 395 400

Asp Val Met Arg Ile Thr Val Gly Val Asp Gly Ser Val Tyr Lys Leu  
405 410 415

His Pro Ser Phe Lys Glu Arg Phe His Ala Ser Val Arg Arg Leu Thr  
420 425 430

Pro Ser Cys Glu Ile Thr Phe Ile Glu Ser Glu Glu Gly Ser Gly Arg  
435 440 445

Gly Ala Ala Leu Val Ser Ala Val Ala Cys Lys Lys Ala Cys Met Leu  
450 455 460

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Gly Gln

465

&lt;210&gt; 3

&lt;211&gt; 465

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

Met	Leu	Asp	Asp	Arg	Ala	Arg	Met	Glu	Ala	Ala	Lys	Lys	Glu	Lys	Val
1				5				10					15		

Glu	Gln	Ile	Leu	Ala	Glu	Phe	Gln	Leu	Gln	Glu	Glu	Asp	Leu	Lys	Lys
			20				25						30		

Val	Met	Arg	Arg	Met	Gln	Lys	Glu	Met	Asp	Arg	Gly	Leu	Arg	Leu	Glu
		35					40					45			

Thr	His	Glu	Glu	Ala	Ser	Val	Lys	Met	Leu	Pro	Thr	Tyr	Val	Arg	Ser
	50						55				60				

Thr	Pro	Glu	Gly	Ser	Glu	Val	Gly	Asp	Phe	Leu	Ser	Leu	Asp	Leu	Gly
65					70					75				80	

Gly	Thr	Asn	Phe	Arg	Val	Met	Leu	Val	Lys	Val	Gly	Glu	Gly	Glu	Glu
				85					90					95	

Gly	Gln	Trp	Ser	Val	Lys	Thr	Lys	His	Gln	Met	Tyr	Ser	Ile	Pro	Glu
			100					105					110		

Asp	Ala	Met	Thr	Gly	Thr	Ala	Glu	Met	Leu	Phe	Asp	Tyr	Ile	Ser	Glu
		115					120					125			

Cys	Ile	Ser	Asp	Phe	Leu	Asp	Lys	His	Gln	Met	Lys	His	Lys	Lys	Leu
130							135				140				



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Pro Leu Gly Phe Thr Phe Ser Phe Pro Val Arg His Glu Asp Ile Asp  
145 150 155 160

Lys Gly Ile Leu Leu Asn Trp Thr Lys Gly Phe Lys Ala Ser Gly Ala  
165 170 175

Glu Gly Asn Asn Val Val Gly Leu Leu Arg Asp Ala Ile Lys Arg Arg  
180 185 190

Gly Asp Phe Glu Met Asp Val Val Ala Met Val Asn Asp Thr Val Ala  
195 200 205

Thr Met Ile Ser Cys Tyr Tyr Glu Asp His Gln Cys Glu Val Gly Met  
210 215 220

Ile Val Gly Thr Gly Cys Asn Ala Cys Tyr Met Glu Glu Met Gln Asn  
225 230 235 240

Val Glu Leu Val Glu Gly Asp Glu Gly Arg Met Cys Val Asn Thr Glu  
245 250 255

Trp Gly Ala Phe Gly Asp Ser Gly Glu Leu Asp Glu Phe Leu Leu Glu  
260 265 270

Tyr Asp Arg Leu Val Asp Glu Ser Ser Ala Asn Pro Gly Gln Gln Leu  
275 280 285

Tyr Glu Lys Leu Ile Gly Gly Lys Tyr Met Gly Glu Leu Val Arg Leu  
290 295 300

Val Leu Leu Arg Leu Val Asp Glu Asn Leu Leu Phe His Gly Glu Ala  
305 310 315 320

Ser Glu Gln Leu Arg Thr Arg Gly Ala Phe Glu Thr Arg Phe Val Ser  
325 330 335

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Gln Val Glu Ser Asp Thr Gly Asp Arg Lys Gln Ile Tyr Asn Ile Leu  
 340 345 350

Ser Thr Leu Gly Leu Arg Pro Ser Thr Thr Asp Cys Asp Ile Val Arg  
 355 360 365

Arg Ala Cys Glu Ser Val Ser Thr Arg Ala Ala His Met Cys Ser Ala  
 370 375 380

Gly Leu Ala Gly Val Ile Asn Arg Met Arg Glu Ser Arg Ser Glu Asp  
 385 390 395 400

Val Met Arg Ile Thr Val Gly Val Asp Gly Ser Val Tyr Lys Leu His  
 405 410 415

Pro Ser Phe Lys Glu Arg Phe His Ala Ser Val Arg Arg Leu Thr Pro  
 420 425 430

Ser Cys Glu Ile Thr Phe Ile Glu Ser Glu Glu Gly Ser Gly Arg Gly  
 435 440 445

Ala Ala Leu Val Ser Ala Val Ala Cys Lys Lys Ala Cys Met Leu Gly  
 450 455 460

Gln  
 465

&lt;210&gt; 4

&lt;211&gt; 1368

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

atggccttga ctctggtaga gcagatcctg gcagagttcc agctgcagga ggaggacctg 60

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aagaaggatga tgagacggat gcagaaggag atggaccgcg gcctgaggct ggagacccat 120
gaagaggcca gtgtgaagat gctgccacc tacgtgcgct ccaccccaga aggctcagaa 180
gtcggggact tcctctccct ggacctgggt ggcactaact tcagggtgat gctggigaag 240
gtgggagaag gtgaggagg gcagtggagc gtgaagacca aacaccagat gtactccatc 300
cccaggagc ccatgaccgg cactgctgag atgctcttcg actacatctc tgagtgcac 360
tccgacttcc tggacaagca tcagatgaaa cacaagaagc tgcccctggg cttcaccttc 420
tcctttcctg tgaggcacga agacatcgat aagggcatcc ttctcaactg gaccaagggc 480
ttcaaggcct caggagcaga agggaacaat gtcgtggggc ttctgcgaga cgctatcaaa 540
cggagagggg actttgaaat ggatgtgggt gcaatggtga atgacacggt ggccacgatg 600
atctcctgct actacgaaga ccatcagtcg gaggtcggca tgatcgtggg cacgggctgc 660
aatgccctgct acatggagga gatgcagaat gtggagctgg tggaggggga cgagggccg 720
atgtgcgtca ataccgagtg gggcgccctc ggggactccg gcgagctgga cgagttcctg 780
ctggagtatg accgcctggt ggacgagagc tctgcaaacc ccggtcagca gctgtatgag 840
aagctcatag gtggcaagta catgggcgag ctgggtgcggc ttgtgctgct caggctcgtg 900
gacgaaaacc tgctcttcca cggggaggcc tccgagcagc tgcgcacacg cggagccctc 960
gagacgcgct tcgtgtcgca ggtggagagc gacacgggcg accgcaagca gatctacaac 1020
atcctgagca cgctggggct gcgaccctcg accaccgact gcgacatcgt gcgccgcgcc 1080
tgcgagagcg tgtctacgcg cgctgcgcac atgtgctcgg cggggctggc gggcgtcatc 1140
aaccgcatgc gcgagagccg cagcgaggac gtaatgcgca tcactgtggg cgtggatggc 1200
tccgtgtaca agctgcaccc cagcttcaag gagcggttcc atgccagcgt gcgcaggctg 1260
acgccagct gcgagatcac ctcatcgag tcggaggagg gcagtggccg gggcgcggcc 1320
ctggctcctg cggtagcctg taagaaggcc tgtatgctgg gccagtga 1368

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&lt;210&gt; 5

&lt;211&gt; 455

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

Met Ala Leu Thr Leu Val Glu Gln Ile Leu Ala Glu Phe Gln Leu Gln

1

5

10

15

Glu Glu Asp Leu Lys Lys Val Met Arg Arg Met Gln Lys Glu Met Asp

20

25

30

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Arg Gly Leu Arg Leu Glu Thr His Glu Glu Ala Ser Val Lys Met Leu  
                   35                                  40                                  45

Pro Thr Tyr Val Arg Ser Thr Pro Glu Gly Ser Glu Val Gly Asp Phe  
                   50                                  55                                  60

Leu Ser Leu Asp Leu Gly Gly Thr Asn Phe Arg Val Met Leu Val Lys  
                   65                                  70                                  75                                  80

Val Gly Glu Gly Glu Glu Gly Gln Trp Ser Val Lys Thr Lys His Gln  
                                   85                                  90                                  95

Met Tyr Ser Ile Pro Glu Asp Ala Met Thr Gly Thr Ala Glu Met Leu  
                   100                                  105                                  110

Phe Asp Tyr Ile Ser Glu Cys Ile Ser Asp Phe Leu Asp Lys His Gln  
                   115                                  120                                  125

Met Lys His Lys Lys Leu Pro Leu Gly Phe Thr Phe Ser Phe Pro Val  
                   130                                  135                                  140

Arg His Glu Asp Ile Asp Lys Gly Ile Leu Leu Asn Trp Thr Lys Gly  
                   145                                  150                                  155                                  160

Phe Lys Ala Ser Gly Ala Glu Gly Asn Asn Val Val Gly Leu Leu Arg  
                                   165                                  170                                  175

Asp Ala Ile Lys Arg Arg Gly Asp Phe Glu Met Asp Val Val Ala Met  
                   180                                  185                                  190

Val Asn Asp Thr Val Ala Thr Met Ile Ser Cys Tyr Tyr Glu Asp His  
                   195                                  200                                  205

Gln Cys Glu Val Gly Met Ile Val Gly Thr Gly Cys Asn Ala Cys Tyr  
                   210                                  215                                  220

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Met Glu Glu Met Gln Asn Val Glu Leu Val Glu Gly Asp Glu Gly Arg  
 225 230 235 240

Met Cys Val Asn Thr Glu Trp Gly Ala Phe Gly Asp Ser Gly Glu Leu  
 245 250 255

Asp Glu Phe Leu Leu Glu Tyr Asp Arg Leu Val Asp Glu Ser Ser Ala  
 260 265 270

Asn Pro Gly Gln Gln Leu Tyr Glu Lys Leu Ile Gly Gly Lys Tyr Met  
 275 280 285

Gly Glu Leu Val Arg Leu Val Leu Leu Arg Leu Val Asp Glu Asn Leu  
 290 295 300

Leu Phe His Gly Glu Ala Ser Glu Gln Leu Arg Thr Arg Gly Ala Phe  
 305 310 315 320

Glu Thr Arg Phe Val Ser Gln Val Glu Ser Asp Thr Gly Asp Arg Lys  
 325 330 335

Gln Ile Tyr Asn Ile Leu Ser Thr Leu Gly Leu Arg Pro Ser Thr Thr  
 340 345 350

Asp Cys Asp Ile Val Arg Arg Ala Cys Glu Ser Val Ser Thr Arg Ala  
 355 360 365

Ala His Met Cys Ser Ala Gly Leu Ala Gly Val Ile Asn Arg Met Arg  
 370 375 380

Glu Ser Arg Ser Glu Asp Val Met Arg Ile Thr Val Gly Val Asp Gly  
 385 390 395 400

Ser Val Tyr Lys Leu His Pro Ser Phe Lys Glu Arg Phe His Ala Ser  
 405 410 415

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Val Arg Arg Leu Thr Pro Ser Cys Glu Ile Thr Phe Ile Glu Ser Glu  
420 425 430

Glu Gly Ser Gly Arg Gly Ala Ala Leu Val Ser Ala Val Ala Cys Lys  
435 440 445

Lys Ala Cys Met Leu Gly Gln  
450 455

&lt;210&gt; 6

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:Primer

&lt;400&gt; 6

gtcacaagga gccagaagct tatggcctga ctctggtag

39

&lt;210&gt; 7

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:Primer

&lt;400&gt; 7

gaagcccccac gacattgttc ccttctgc

28

&lt;210&gt; 8

&lt;211&gt; 451

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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

Met Val Glu Gln Ile Leu Ala Glu Phe Gln Leu Gln Glu Glu Asp Leu  
1 5 10 15

Lys Lys Val Met Arg Arg Met Gln Lys Glu Met Asp Arg Gly Leu Arg  
20 25 30

Leu Glu Thr His Glu Glu Ala Ser Val Lys Met Leu Pro Thr Tyr Val  
35 40 45

Arg Ser Thr Pro Glu Gly Ser Glu Val Gly Asp Phe Leu Ser Leu Asp  
50 55 60

Leu Gly Gly Thr Asn Phe Arg Val Met Leu Val Lys Val Gly Glu Gly  
65 70 75 80

Glu Glu Gly Gln Trp Ser Val Lys Thr Lys His Gln Met Tyr Ser Ile  
85 90 95

Pro Glu Asp Ala Met Thr Gly Thr Ala Glu Met Leu Phe Asp Tyr Ile  
100 105 110

Ser Glu Cys Ile Ser Asp Phe Leu Asp Lys His Gln Met Lys His Lys  
115 120 125

Lys Leu Pro Leu Gly Phe Thr Phe Ser Phe Pro Val Arg His Glu Asp  
130 135 140

Ile Asp Lys Gly Ile Leu Leu Asn Trp Thr Lys Gly Phe Lys Ala Ser  
145 150 155 160

Gly Ala Glu Gly Asn Asn Val Val Gly Leu Leu Arg Asp Ala Ile Lys  
165 170 175

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Arg Arg Gly Asp Phe Glu Met Asp Val Val Ala Met Val Asn Asp Thr  
180 185 190

Val Ala Thr Met Ile Ser Cys Tyr Tyr Glu Asp His Gln Cys Glu Val  
195 200 205

Gly Met Ile Val Gly Thr Gly Cys Asn Ala Cys Tyr Met Glu Glu Met  
210 215 220

Gln Asn Val Glu Leu Val Glu Gly Asp Glu Gly Arg Met Cys Val Asn  
225 230 235 240

Thr Glu Trp Gly Ala Phe Gly Asp Ser Gly Glu Leu Asp Glu Phe Leu  
245 250 255

Leu Glu Tyr Asp Arg Leu Val Asp Glu Ser Ser Ala Asn Pro Gly Gln  
260 265 270

Gln Leu Tyr Glu Lys Leu Ile Gly Gly Lys Tyr Met Gly Glu Leu Val  
275 280 285

Arg Leu Val Leu Leu Arg Leu Val Asp Glu Asn Leu Leu Phe His Gly  
290 295 300

Glu Ala Ser Glu Gln Leu Arg Thr Arg Gly Ala Phe Glu Thr Arg Phe  
305 310 315 320

Val Ser Gln Val Glu Ser Asp Thr Gly Asp Arg Lys Gln Ile Tyr Asn  
325 330 335

Ile Leu Ser Thr Leu Gly Leu Arg Pro Ser Thr Thr Asp Cys Asp Ile  
340 345 350

Val Arg Arg Ala Cys Glu Ser Val Ser Thr Arg Ala Ala His Met Cys  
355 360 365



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Ser Ala Gly Leu Ala Gly Val Ile Asn Arg Met Arg Glu Ser Arg Ser  
 370 375 380

Glu Asp Val Met Arg Ile Thr Val Gly Val Asp Gly Ser Val Tyr Lys  
 385 390 395 400

Leu His Pro Ser Phe Lys Glu Arg Phe His Ala Ser Val Arg Arg Leu  
 405 410 415

Thr Pro Ser Cys Glu Ile Thr Phe Ile Glu Ser Glu Glu Gly Ser Gly  
 420 425 430

Arg Gly Ala Ala Leu Val Ser Ala Val Ala Cys Lys Lys Ala Cys Met  
 435 440 445

Leu Gly Gln  
 450

&lt;210&gt; 9

&lt;211&gt; 38

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:Primer

&lt;400&gt; 9

ccaggcccag acagccaagc ttatggtaga gcagatcc

38

&lt;210&gt; 10

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

15/15

<220>

<223> Description of Artificial Sequence:Primer

<400> 10

gaagccccac gacattgttc cttctgc

28

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/JP03/06054

A. CLASSIFICATION OF SUBJECT MATTER  
Int.Cl<sup>7</sup> C12N9/12, C12Q1/48

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)  
Int.Cl<sup>7</sup> C12N9/12, C12Q1/48

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
CA (STN), BIOSIS (DIALOG), WPI (DIALOG),  
SwissProt/PIR/Genbank/EMBL/DDBJ/GeneSeq

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X A	TANIZAWA, Y. et al., Human Liver Glucokinase Gene: Cloning and Sequence Determination of Two Alternatively Spliced cDNAs, Proc.Natl.Acad.Sci. USA., 1991, Vol.88, pages 7294 to 7297	<u>1</u> 2-25
A	MAHALINGAM B. et al., Structural model of human glucokinase in complex with glucose and ATP., Diabetes, 1999, Vol.48, pages 1698 to 1705	1-25
A	WILLSON M. et al., Yeast hexokinase inhibitors designed from the 3-D enzyme structure rebuilding. J. Enzyme Inhib., 1997, Vol.12, No.2, pages 101 to 121	1-25

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E" earlier document but published on or after the international filing date	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&" document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means	
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search  
12 June, 2003 (12.06.03)

Date of mailing of the international search report  
24 June, 2003 (24.06.03)

Name and mailing address of the ISA/  
Japanese Patent Office

Authorized officer

Facsimile No.

Telephone No.

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP03/06054

## Box I Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 26 to 33

because they relate to subject matter not required to be searched by this Authority, namely:

Inventions according to said claims relate to subject matters not required to be searched by this Authority in accordance with PCT Article 17 (2) (a) and PCT Rule 39.1. (see extra sheet for details)

2. ☐ Claims Nos.:

because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:

because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.  
☐ No protest accompanied the payment of additional search fees.

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP03/06054

Continuation of Box No.I-1 of continuation of first sheet(1)

"Method for drug design" according to the present invention relates to the design of a compound to be bonded to a protein, on the basis of the information on the three-dimensional structure of the protein. The design according to the present invention involves the work of the inventor to estimate a suitable compound by his mental acts, and such work is considered to correspond to the performance of purely mental acts.

A. 発明の属する分野の分類 (国際特許分類 (IPC)) Int. Cl <sup>7</sup> C12N9/12, C12Q1/48		
B. 調査を行った分野 調査を行った最小限資料 (国際特許分類 (IPC)) Int. Cl <sup>7</sup> C12N9/12, C12Q1/48		
最小限資料以外の資料で調査を行った分野に含まれるもの		
国際調査で使用した電子データベース (データベースの名称、調査に使用した用語) CA (STN), BIOSIS (DIALOG), WPI (DIALOG) SwissProt/PIR/Genbank/EMBL/DDBJ/GeneSeq		
C. 関連すると認められる文献		
引用文献の カテゴリー*	引用文献名 及び一部の箇所が関連するときは、その関連する箇所の表示	関連する 請求の範囲の番号
X A	TANIZAWA Y. Tanizawa, et al., Human Liver Glucokinase Gene: Cloning and Sequence Determination of Two Alternatively Spliced cDNAs Proc. Natl. Acad. Sci. USA., 1991, Vol. 88, p. 7294-7297	1 2-25
A	MAHALINGAM B. et al., Structural model of human glucokinase in complex with glucose and ATP. Diabetes, 1999, Vol. 48, p1698-1705	1-25
<input checked="" type="checkbox"/> C欄の続きにも文献が列挙されている。 <input type="checkbox"/> パテントファミリーに関する別紙を参照。		
* 引用文献のカテゴリー 「A」 特に関連のある文献ではなく、一般的技術水準を示すもの 「E」 国際出願日前の出願または特許であるが、国際出願日以後に公表されたもの 「L」 優先権主張に疑義を提起する文献又は他の文献の発行日若しくは他の特別な理由を確立するために引用する文献 (理由を付す) 「O」 口頭による開示、使用、展示等に言及する文献 「P」 国際出願日前で、かつ優先権の主張の基礎となる出願日の後に公表された文献 「T」 国際出願日又は優先日後に公表された文献であって出願と矛盾するものではなく、発明の原理又は理論の理解のために引用するもの 「X」 特に関連のある文献であって、当該文献のみで発明の新規性又は進歩性がないと考えられるもの 「Y」 特に関連のある文献であって、当該文献と他の1以上の文献との、当業者にとって自明である組合せによって進歩性がないと考えられるもの 「&」 同一パテントファミリー文献		
国際調査を完了した日 12.06.03	国際調査報告の発送日 24.05.03	
国際調査機関の名称及びあて先 日本国特許庁 (ISA/JPO) 郵便番号100-8915 東京都千代田区霞が関三丁目4番3号	特許庁審査官 (権限のある職員) 鈴木 恵理子 電話番号 03-3581-1101 内線 3488	4B 3037 印

C (続き) . 関連すると認められる文献		
引用文献の カテゴリー*	引用文献名 及び一部の箇所が関連するときは、その関連する箇所の表示	関連する 請求の範囲の番号
A	WILLSON M. et al., Yeast hexokinase inhibitors designed from the 3-D enzyme structure rebuilding. J.Enzyme Inhib., 1997, Vol.12, No.2, p.101-121	1-25

## 第Ⅰ欄 請求の範囲の一部の調査ができないときの意見 (第1ページの2の続き)

法第8条第3項(PCT17条(2)(a))の規定により、この国際調査報告は次の理由により請求の範囲の一部について作成しなかった。

1. ☒ 請求の範囲 26-33 は、この国際調査機関が調査することを要しない対象に係るものである。つまり、  
当該請求の範囲に記載された発明は、PCT17条(2)(a)(i)及びPCT規則39.1(ii i)の規定により、この国際調査機関が調査することを要しない対象に係るものである。  
(詳細は「特別ページ」を参照されたい)
2. ☐ 請求の範囲 \_\_\_\_\_ は、有意義な国際調査をすることができる程度まで所定の要件を満たしていない国際出願の部分に係るものである。つまり、
3. ☐ 請求の範囲 \_\_\_\_\_ は、従属請求の範囲であってPCT規則6.4(a)の第2文及び第3文の規定に従って記載されていない。

## 第Ⅱ欄 発明の単一性が欠如しているときの意見 (第1ページの3の続き)

次に述べるようにこの国際出願に二以上の発明があるとこの国際調査機関は認めた。

1. ☐ 出願人が必要な追加調査手数料をすべて期間内に納付したので、この国際調査報告は、すべての調査可能な請求の範囲について作成した。
2. ☐ 追加調査手数料を要求するまでもなく、すべての調査可能な請求の範囲について調査することができたので、追加調査手数料の納付を求めなかった。
3. ☐ 出願人が必要な追加調査手数料を一部のみしか期間内に納付しなかったので、この国際調査報告は、手数料の納付のあった次の請求の範囲のみについて作成した。
4. ☐ 出願人が必要な追加調査手数料を期間内に納付しなかったので、この国際調査報告は、請求の範囲の最初に記載されている発明に係る次の請求の範囲について作成した。

追加調査手数料の異議の申立てに関する注意

- ☐ 追加調査手数料の納付と共に出願人から異議申立てがあった。  
☐ 追加調査手数料の納付と共に出願人から異議申立てがなかった。



『第1ページの続葉(1)「第I欄1.」』の続き

本願発明に係る「ドラッグデザイン方法」は、タンパク質の立体構造情報に基づいて該タンパク質に結合する化合物の構造をデザインすることであるが、発明者がその精神活動によって適切な化合物を推測する行為を包含しており、これは純粋に精神的な行為の遂行に相当すると認められる。

## Specification

Crystal of glucokinase protein and drug design method using crystal thereof.

## The Field of Technology

This invention relates to crystal of novel glucokinase protein (hereinafter it is called "GK protein") and the drug design method or the like employing three-dimensional structure coordinates obtained by using the crystal thereof.

## Background Technique

Glucokinase (ATP: D-hexose 6-phosphotransferase, EC2.7.1.1) is one of four kinds of hexokinase isozymes of mammals (hexokinase IV). These isozymes catalyse the same reaction, however, differences exist in the  $K_m$  value with respect to glucose. In other words, the  $K_m$  value of hexokinase I, II and III being  $10^{-6}$ - $10^{-4}$  M, but on the other hand the  $K_m$  value of hexokinase IV, called glucokinase with respect to glucose is much greater at about  $10^{-2}$  M. Hexokinase is an enzyme participating in the initial stage of glycolytic pathway, and catalyses the reaction from the glucose to glucose-6-phosphate.

As for glucokinase, the expression is mainly localised in liver and pancreatic beta cell, and it plays an important role in glucose metabolism of the whole body by controlling the rate-determining step of glucose metabolism in these cells. As for the glucokinase of liver and pancreatic beta cell, the sequence of 15 amino acids at N terminal is respectively different due to splicing difference. However, the enzymatic characteristics are the same.

The hypothesis that glucokinase acts as glucose sensor of pancreatic beta cell and liver is proposed since approximately 10 years ago (Garfinkel D, et al: Am J Physiol 247 [3Pt2]: R527-536, 1984). In practice, it is becoming clear from results of recent glucokinase gene manipulation mouse, that the glucokinase plays an important role in glucose homeostasis of the whole body.

The mouse in which glucokinase gene is destroyed dies of diabetes mellitus soon after birth (Grupe A, et al: Cell 83: 69-78. 1995). On the other hand, as for the mouse which overexpressed glucokinase, the blood glucose level becomes low (Ferre T, et al: Proc Natl Acad Sci USA 93: 7225-7230. 1996). When glucokinase activity is increased by the rise in glucose concentration, although the reactions of

pancreatic beta cell and hepatocyte are different, in each case, it acts in the direction of lowering blood glucose. The pancreatic beta cell starts to secrete more insulin, the liver takes up sugar and stores as glycogen and at the same time lowers the sugar release.

In this way, the fluctuation of glucokinase enzyme activity plays an important role in glucose homeostasis of mammal through liver and pancreatic beta cell. Glucokinase gene mutation is discovered in the case that develops diabetes mellitus in youth known as MODY2 (maturity-onset diabetes of the young), and the lowering of glucokinase activity is said to be the cause of blood glucose rise (Vionnet N, et al.: Nature 356: 721-722, 1992). On the other hand, the lineage having mutation to increase glucokinase activity is also found, and such persons show hypoglycemic symptom (Glaser B, et al.: N Engl J Med 338: 226-230, 1998).

From the above, glucokinase also acts glucose sensor in human and plays an important role in glucose homeostasis. On the other hand, because the glucokinase of many type II diabetics is not mutated, the blood glucose control using glucokinase sensor system is considered possible. Because the glucokinase activator substance can be expected to have insulin secretion promotion action of pancreatic beta cell and sugar up take acceleration and sugar release suppression actions in liver, it is considered as useful therapeutic drug of type II diabetic patients.

Recently, a localised expression of pancreatic beta cell type glucokinase was found in rat brain, in particular in ventromedial hypothalamic nucleus (Ventromedial hypothalamus, VMH) which is the feeding centre. About 20 % of neurons of VMH was known as glucose responsive neuron, and it has been considered to play an important role in weight control in the past. When glucose is administered intracerebrally to rat, food consumption falls, whereas when the glucose metabolism is suppressed by administration of glucose analogue, glucosamine in brain, overeating occurs. From electrophysiological experiment, glucose responsive neurons are found to be activated in response to physiological glucose concentration changes (5-20 mM), however its activity is suppressed when the glucose metabolism is inhibited with glucosamine and the like. In glucose concentration sensing system of VMH, a mechanism through glucokinase the same as insulin secretion of pancreatic beta cells is assumed. Accordingly, there is a possibility that a substance that causes glucokinase activation of VHM in addition to liver, pancreatic beta cell is expected to correct problem of obesity which is a problem in many type II diabetic patients,

in addition to blood glucose correction effect.

On the other hand, it is described in DIABETES, vol. 48, 1698-1705, September 1999 that the stereostructure of glucokinase was predicted from hexokinase 1. However, in practice, crystallisation was not carried out, nor it was a practical one.

In accordance with the above, to elucidate three-dimensional stereostructure of glucokinase and to enable efficient discovery of a compound that interacts with glucokinase are thought to greatly contribute to the development of for example a therapeutic agent or preventative agent of diabetes, a therapeutic agent or preventative agent of chronic complication of diabetes mellitus such as retinopathy, nephropathy, neurosis, ischemic cardiac disease, arteriosclerosis or the like, a therapeutic agent or preventative agent of obesity.

Presently, CARDD (Computer Aided Rational Drug Design) using computer for the tasks such as analysis of active centre of a protein or a prediction of reaction mechanism has been employed at practical level.

In the drug creation system using CARDD, the structure of active site of protein is predicted based on the three-dimensional structure analysis data of the target protein. And information about candidate compounds which can bind to the structure of active site thereof is obtained from the compound database. Thereafter, on consideration of the three-dimensional structure and physical properties of the active site of the target protein and the candidate compound, candidate compounds which can bind to the target protein are selected. These steps are so-called in silico screening step.

Whether the compound selected by in silico screening step binds to the target protein and change the activity thereof or not, is examined by actual examination (wet experiment). And the compound that changes the activity of the target protein becomes the effective ingredient of a drug. Thereby a compound that interacts with the target protein can be efficiently screened without carrying out the procedure wherein innumerable compounds are acted on the target protein one by one and the interactions are confirmed.

In silico screening can be said as an effective means of pharmaceutical development because the

candidate compounds that bind to the target protein can be greatly narrowed down.

Three-dimensional structure analysis data by X-ray structure analysis of the target protein becomes an important information in drug creation system using CARDD. Crystal of target protein is required as analysis sample in three-dimensional structural analysis by X-ray structure analysis. Accordingly, in order to carry out development of drug creation related to GK based on the drug creation system using CARDD, the crystal of GK is required. However, as stated above, crystallisation of GK was difficult, and it could not provide information necessary for CARDD.

This invention was made on consideration of the problems of aforesaid technology of the prior art, and had objects to obtain crystal of glucokinase and to design compounds that bind to glucokinase based on the information obtained from aforesaid crystal.

#### Disclosure of the Invention

At least one of aforesaid objects is solved by the following invention.

[1] A glucokinase protein characterised in being used for crystallisation.

[2] A protein in accordance with aforesaid [1] comprising amino acid sequence in accordance with Sequence Number 5.

[3] A crystal of protein comprising amino acid sequence in accordance with Sequence Number 5 or amino acid sequence substantially the same amino acid sequence thereof.

[4] A crystal in accordance with aforesaid [3], wherein the said protein is glucokinase protein.

[5] A crystal in accordance with aforesaid [3] comprising crystals of protein containing amino acid sequence in accordance with Sequence Number 5.

[6] A crystal in accordance with aforesaid [3], wherein the lattice constant satisfies the following equations (1)-(4)

$$a = b = 79.9 \pm 4 \text{ \AA} \quad (1)$$

$$c = 322.2 \pm 15 \text{ \AA} \quad (2)$$

$$\alpha = \beta = 90^\circ \quad (3)$$

$$\gamma = 120^\circ \quad (4)$$

[7] A crystal in accordance with aforesaid [6], wherein the space group is  $P6_322$ .

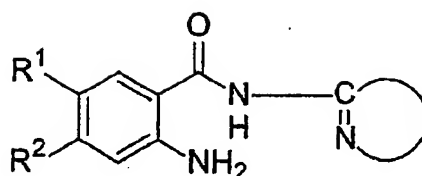
[8] A crystal of protein specified by three-dimensional structure coordinates data in accordance with Table 1.

[9] A crystal wherein in three-dimensional structure coordinates data changed in at least one data of three-dimensional structure coordinates data in accordance with Table 1, the mean square error between atoms of main chain of amino acid represented by three-dimensional structure coordinates data in accordance with Table 1 (C alpha atom) and C alpha atoms represented by the said changed three-dimensional structure coordinates data corresponding to aforesaid C alpha atoms is 0.6 Å or less.

[10] A crystal in accordance with any of [3]-[9], wherein the compound binding site is constructed by at least one of amino acid residues of tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459 in amino acid sequence shown in sequence Number 5.

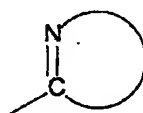
[11] A crystal including a complex of the protein comprising amino acid sequence in accordance with Sequence Number 5 or amino acid sequence substantially the same amino acid sequence thereof and a compound which can bind to the said protein.

[12] A crystal in accordance with aforesaid [11], wherein aforesaid compound is represented by formula (1).



(I)

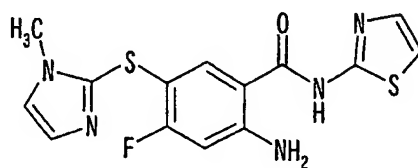
[wherein, R1 shows halogen atom, -S-(O)<sub>p</sub>-A, -S-(O)<sub>q</sub>-B or -O-B (wherein, p and q are the same or different and denote an integer of 0-2, A denotes C1-C6 alkyl group of optionally substituted straight chain, B denotes optionally substituted five-membered or six-membered ring aryl group or heteroaryl group, R2 denotes a hydrogen atom or halogen atom, and



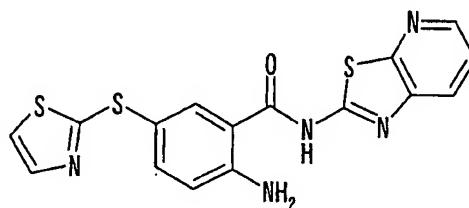
(II)

denotes an optionally substituted monocyclic or bicyclic heteroaryl group having a nitrogen atom adjacent to the carbon atom bonded to amide group].

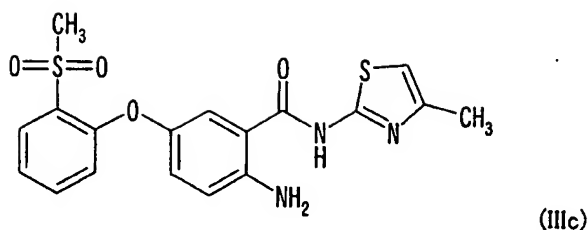
[13]. A crystal in accordance with aforesaid [12], wherein aforesaid compound is any of the compound represented by formula (IIIa)-(IIIc).



(IIIa)



(IIIb)



[14] A protein in accordance with aforesaid [1] comprising amino acid sequence in accordance with Sequence Number 8.

[15] A crystal of protein comprising amino acid sequence in accordance with Sequence Number 8 or amino acid sequence substantially the same amino acid sequence thereof.

[16] A crystal in accordance with aforesaid [15], wherein the said protein is glucokinase protein.

[17] A crystal in accordance with aforesaid [15] comprising crystals of protein containing amino acid sequence in accordance with Sequence Number 8.

[18] A crystal in accordance with aforesaid [15], wherein the lattice constant satisfies the following equations

$$a = b = 103.2 \pm 5 \text{ \AA} \quad (5)$$

$$c = 281.0 \pm 7 \text{ \AA} \quad (6)$$

$$\alpha = \beta = 90^\circ \quad (7)$$

$$\gamma = 120^\circ \quad (8)$$

[19] A crystal in accordance with aforesaid [18], wherein the space group is  $P6_322$ .

[20] A crystal of protein specified by three-dimensional structure coordinates data in accordance with Table 2.

[21] A crystal wherein in three-dimensional structure coordinates data changed at least one data of three-dimensional structure coordinates data in accordance with Table 2, the mean square error between atoms



of main chain of amino acid represented by three-dimensional structure coordinates data in accordance with Table 2 (C alpha atom) and C alpha atoms represented by the said changed three-dimensional structure coordinates data corresponding to aforesaid C alpha atoms is 0.6 Å or less.

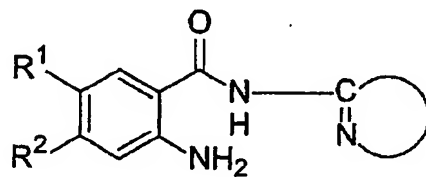
[22] A process for the production of crystal containing a complex of protein and a compound that binds to the protein thereof, including

a protein production step wherein a protein containing the amino acid sequence having deletion of 1-50 amino acid residues from either or both of N terminal and C terminal of the protein containing amino acid sequence in accordance with Sequence Number 2 is produced, and

a protein reaction step wherein a compound that binds to the protein obtained in the said protein production step and the protein obtained in the said protein production step are reacted.

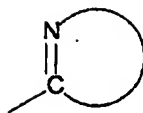
[23] A process to produce crystal of the kind wherein a crystal of a protein is produced, characterised in that a protein including amino acid sequence in accordance with Sequence Number 5 or amino acid sequence substantially the same amino acid sequence thereof and having glucokinase activity and a compound which can bind to the said protein are used.

[24] A process for the production of crystalline protein in accordance with aforesaid [23], wherein the compound which can bind to said protein is a compound represented by formula (1).



(I)

[wherein, R1 shows halogen atom, -S-(O)p-A, -S-(O)q-B or -O-B (wherein, p and q are the same or different and denote an integer of 0-2, A denotes C1-C6 alkyl group of optionally substituted straight chain, B denotes optionally substituted five-membered or six-membered ring aryl group or heteroaryl group, R2 denotes a hydrogen atom or halogen atom, and



(II)

denotes an optionally substituted monocyclic or bicyclic heteroaryl group containing nitrogen atom adjacent to the carbon atom bonded to amide group].

[25]. A process for the production of crystal in accordance with aforesaid [23] or [24] using co-crystallisation or soaking method

[26] A drug design method of the kind wherein based on stereostructural information of a protein, the structure of compound that binds to said protein is designed, characterised in that the stereostructure information of said protein is the information obtained by analysing crystal in accordance with any one of aforesaid [3]-[13] or [15]-[21].

[27] A drug design method in accordance with aforesaid [26] characterised in that  
a binding site deduction step wherein the compound binding site of said protein is deduced based on aforesaid stereostructure information, and  
a selection step wherein a compound compatible to the compound binding site deduced in aforesaid binding site deduction step is selected from compound library,  
are included.

[28] A drug design method in accordance with aforesaid [26] characterised in that  
a binding site deduction step wherein the compound binding site of said protein is deduced based on aforesaid stereostructure information, and  
a compound structure assembly step wherein the structure of compound compatible to compound binding site deduced in aforesaid binding site deduction step is constructed,  
are included.

[29] A drug design method in accordance with aforesaid [26] characterised in that

a binding site deduction step wherein the compound binding site of said protein is deduced based on aforesaid stereostructure information, and  
a design step wherein the structure of compound is designed by visual observation so that the compound binding site deduced in aforesaid binding site deduction step and a compound compatible to said compound binding site interact,  
are included.

[30] A drug design method in accordance with any of aforesaid [26]-[29], wherein aforesaid compound binding site is constituted by at least one of amino acid residue of tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459 in amino acid sequence shown in sequence Number 5.

[31] A drug design method in accordance with any of aforesaid [26]-[30] further including a step to measure physiological activity of the candidate compound predicted to be compatible to aforesaid compound binding site.

[32] A drug design method in accordance with any of aforesaid [26]-[30] further including a binding determination step wherein the candidate compound predicted to be compatible to aforesaid compound binding site and a protein including amino acid sequence in accordance with and Sequence Number 5 or amino acid sequence which is substantially the same amino acid sequence thereof are contacted, and whether the candidate compound binds to the said protein or not is assessed.

[33] A process for the production of compound array including the compound group selected by drug design method in accordance with any of aforesaid [26]-[30] is combined as compound array.

#### Brief Description of the Figures

Figure 1 is a ribbon diagram showing three-dimensional structure of glucokinase.

(Figure 1a is a ribbon diagram showing the structure of glucokinase ( $\Delta 1-11$ )/glucose/compound 1 (compound of formula IIIa). Moreover, the figure on the right is a rotated figure of the figure on the left.)

(Figure 1b is a ribbon diagram showing the simple substance of glucokinase [ $\Delta$ I-15]. Moreover, the figure on the right is a rotated figure of the figure on the left.)

Figure 2 is a figure showing coupling scheme of compound 1 (compound of formula IIIa) with respect to the binding site of glucokinase ( $\Delta$ I-11)

Figure 3 is a figure showing the structure of binding site of glucokinase ( $\Delta$ I-11).

#### Ideal form for Carrying Out the Invention

In this specification, amino acids, peptides and proteins are represented using abbreviations adopted from the IUPAC-IUB biochemistry designation committee (CBN) shown below. Moreover, the sequence of amino acid residues of peptide and protein are represented so that the N terminal to C terminal comprises from the left end to the right end and moreover the N terminal comprises the first.

Hereinafter, each embodiment of this invention is described in greater detail.

#### (Glucokinase protein).

Firstly, this invention puts forward glucokinase protein characterised in being used for crystallisation. Glucokinase protein (GK protein) is involved in extremely important sugar metabolism in vivo as described above. Accordingly, by solving the three-dimensional structure of GK protein and by elucidating active site of GK protein, it is possible to search compounds that bind to GK protein (activator or inhibitor). Therefore it is important to clarify the three-dimensional structure of GK protein.

As technique to clarify the three-dimensional structure of protein, X-ray crystal structure analysis is well known. In other words, protein is crystallised, mono-chromatised X-ray is irradiated to the crystal thereof, and three-dimensional structure of said protein is elucidated on the basis of the obtained X-ray diffraction pattern (Blundell, T.L. and Johnson, L.N, PROTEIN CRYSTALLOGRAPHY, pp. 1-565, (1976) Academic Press, New York). First GK protein needs to be crystallised in order to provide for the x-ray crystal structure analysis of GK protein.

Wherein, the "GK protein" of this invention refers to human derived liver type glucokinase having amino acid sequence shown in sequence Number 2 and a protein containing amino acid sequence which is substantially the same as Sequence Number 2. Wherein, as aforesaid protein containing amino acid sequence which is substantially the same, a species having glucokinase activity is preferable. Accordingly, in this specification, the GK protein includes not only the human derived liver type glucokinase, however also human derived pancreas type glucokinase, and non-human derived GK proteins such as mouse, rat, monkey and the like. In this invention human liver type glucokinase is preferably used. In glucokinase derived from human, 15 amino acid residues at N terminal differ in the liver type and the pancreas type. Wherein, "glucokinase activity" refers to an activity to catalyse reaction from glucose to glucose-6-phosphate.

It is generally well known that the crystallisation of protein is difficult, and the GK protein was not able to be crystallised without treatment. These inventors carried out various investigations with trial and error, as a result succeeded in crystallisation of GK protein for the first time by deletion of 11 or 15 amino acids at the N terminal side of GK protein. It was thought that the deleted region protruded from the globular GK protein molecule when the crystallisation was attempted, as a result, caused steric hindrance between adjacent GK protein molecules, and prevented the crystallisation of the GK protein. In other words, in this invention, the crystal of GK protein was obtained by using a GK protein in which 11 amino acid residues at N terminal side is deleted (Sequence Number 5) or a GK protein in which 15 amino acid residues at N terminal side is deleted (Sequence Number 8) in the glucokinase in which amino acids sequence had been known however the crystallisation had been unsuccessful. Wherein the number of amino acids is not restricted as long as it is within a range that the steric hindrance disappears between adjacent crystals. In an embodiment for example, in amino acid sequence represented by Sequence Number 2, amino acids sequence or the like in which amino acid residues of 1-50, preferably 3-30, more preferably 5-25, more preferably still 8-18, most preferably 11-15 at N terminal side are deleted, can be used in this invention. Moreover, the amino acid sequence or the like in which amino acid residues of 1-8, preferably 1-7, more preferably 2-6 at C terminal side are deleted, is used in this invention.

(Crystal of glucokinase protein and a process for the production thereof).

Next, in this invention, crystals including protein containing amino acids sequence in accordance with Sequence Number 5, and Sequence Number 8 or amino acids sequence which is substantially the same as

amino acid sequence thereof are put forward.

As described earlier, as GK protein used in crystallisation, proteins containing amino acids sequence in accordance with Sequence Number 5, and/or Sequence Number 8 or amino acids sequence which is substantially the same as amino acid sequence thereof, or the like are used.

The proteins containing amino acids sequence in accordance with Sequence Number 5, and/or Sequence Number 8 or amino acids sequence which is substantially the same as the amino acid sequence thereof (hereinafter it may be abbreviated as "GK protein" together with proteins containing amino acids sequence in accordance with Sequence Number 2 or amino acids sequence which is substantially the same as the amino acid sequence thereof) can be any as long as crystallisation is possible, and the amino acid sequence thereof is not restricted in particular. Wherein, the proteins containing amino acids sequence which is substantially the same as the amino acid sequence in accordance with Sequence Number 5, and/or Sequence Number 8 does not necessarily have glucokinase activity, and may be an inactive mutant (for example, a mutant inactivated by the presence of mutation at ATP binding site) as long as it has a crystal structure from which the information necessary for drug design can be obtained. Wherein, as proteins containing amino acids sequence which is substantially the same as the amino acid sequence in accordance with Sequence Number 2 or Sequence Number 5, amino acids sequences having about 60 % or more, preferably about 70% or more, more preferably about 80% or more, in particular preferably about 90% or more, and most preferably about 95% or more homology to the amino acids sequence in accordance with Sequence Number 2 or Sequence Number 5, or the like are nominated. Moreover, as proteins containing amino acids sequence which is substantially the same as the amino acids sequence in accordance with Sequence Number 2 or Sequence Number 5, for example, amino acids sequences in which amino acid residues of 1-10, preferably 1-5, more preferably 1-3 more preferably still 1-2 are substituted, deleted, added and/or inserted in the amino acids sequence in accordance with Sequence Number 2 or Sequence Number 5 are exemplified.

Three-dimensional structural analysis of GK protein is carried out for example as follows. Firstly, the protein is purified. And a series of steps such as crystallisation, X-ray diffraction intensity data collection, phase determination of each diffraction spot, electron density calculation, molecular model construction, refinement of structure or the like is carried out. As main equipment for performing

protein structure analysis, incubator for crystallisation, binocular microscope, X-ray diffractometer, three dimensional computer graphics apparatus or the like are used. The actual experimental process to produce protein crystals is divided into step to purify protein in large amount (several mg or more is preferred), a step to widely search conditions for obtaining crystal and a step to obtain high quality crystal suitable for X-ray analysis. Hereinafter, each step is described in concrete terms.

For crystallisation, GK protein is purified to high purity. As process for purification, well known processes can be used, and for example, column chromatography, salt precipitation, centrifugation or the like are used.

Purified GK protein is crystallised and provided as a sample for X-ray crystal structure analysis. Crystallisation is performed based on well known method such as vapor diffusion method, dialysis or the like. When obtaining protein crystals, many elements such as purity / concentration of protein, temperature, pH, concentration of the precipitant used need to be examined. Investigation of crystallisation conditions can be carried out over a wide range using commercial screening reagent, and it is preferably screened using 1-2  $\mu$ l of protein solution in protein concentration of 1-2 % per condition. In this way when microcrystals or the like are obtained, it is preferred to further refined the conditions.

Moreover, extremely many conditions must be searched in order to obtain crystal of GK protein. Accordingly, a large quantity expression system of the protein is preferably constructed also for the investigation of crystallisation condition. Generally, among proteins, many of the crystallising species are monodispersed in solution state, and polydispersed species do not crystallise in most cases. Therefore, N terminal of GK protein is successively removed, monodispersion properties of protein solution are assessed for the obtained protein using light scattering apparatus, and whether sample is suitable for crystallisation or not may be examined.

Next, using the obtained crystal of GK protein, X-ray diffraction intensity measurement is carried out. Recently, a method wherein the crystal is scooped with a ring of narrow thread or the like, is rapidly cooled to liquid nitrogen temperature, and is measured at low temperature as it is, may also be used. Usually, the intensity measurement of diffracted x-ray is performed by two-dimensional detector such as image plate or the like. Many diffraction lines generated by rotating crystal while irradiating the X-ray

are recorded on image plate, and the recorded diffraction intensities are read by shining a laser.

Next, it is preferred to prepare heavy atom iso-form replacement bodies by heavy atom soaking method or co-crystallisation method. Using this, the phase of the protein crystal can be determined by multiple isomorphous replacement method (MIR method). Instead of introducing heavy atom, the phase is also determined by multiwavelength anomalous scattering method (MAD method) based on the diffraction intensity data using complex X-rays. Molecular replacement method (MR method) in which, when a structure of molecule containing analogous structure has been already solved, the initial structure can be obtained by applying the molecular structure thereof in the crystal, Fourier synthesis diagram is drawn on the basis of this, and the structure of remaining part is elucidated, and the total structure is determined, is known as well.

Once the phase was determined by aforesaid process, electron density is determined from this. The precision of this depends on the number of reflection (resolution) and the precision of the reflection used. The resolution is expressed with the minimum plane spacing of the reflection used. Molecular model is constructed from this electron density diagram. When the molecular model is constructed, the atomic coordinates are obtained, therefore, the calculated value of structure factor is determined from this, and refinement of atomic parameters is carried out by the least-square method to approximate this size to the observed value. In this way, the most reasonable structural information is obtained.

In accordance with this invention, the crystal of GK protein shown in sequence Number 5 has been successfully prepared (cf. later described Example). The obtained crystal of GK protein had lattice constant which satisfied the following equations (1)-(4).

$$a = b = 79.9 \pm 4 \text{ \AA} \quad (1)$$

$$c = 322.2 \pm 15 \text{ \AA} \quad (2)$$

$$\alpha = \beta = 90^\circ \quad (3)$$

$$\gamma = 120^\circ \quad (4)$$

Moreover, this crystal was elucidated to have space group  $P6_522$ . Wherein, aforesaid  $a = b$  is preferably  $79.9 \pm 3 \text{ \AA}$ , more preferably  $79.9 \pm 2 \text{ \AA}$  and even more preferably  $79.9 \pm 1 \text{ \AA}$ . Moreover, aforesaid  $c$  is preferably  $322.2 \pm 10 \text{ \AA}$ , more preferably  $322.2 \pm 8 \text{ \AA}$ , and even more preferably  $322.2 \pm 5 \text{ \AA}$ .



The three-dimensional structural coordinates of the GK protein crystal obtained in this way are shown in Table 1.

### Table 1

Moreover, Table 1 is constructed in accordance with representation method of protein data bank generally used by a person skilled in the art. The GLC in Table 1 denotes glucose molecule, and CP1 denotes the compound represented by formula IIIa, and HOH denotes water molecule.

Moreover, in this invention, the crystal of GK protein shown in sequence Number 8 has been successfully prepared (cf. later described Example). The obtained crystal of GK protein had lattice constant which satisfied the following equations (5)-(8).

$$a = b = 103.2 \pm 5 \text{ \AA} \quad (5)$$

$$c = 281.0 \pm 7 \text{ \AA} \quad (6)$$

$$\alpha = \beta = 90^\circ \quad (7)$$

$$\gamma = 120^\circ \quad (8)$$

Moreover, this crystal was elucidated to have space group  $P6_322$ . Wherein, aforesaid  $a = b$  is preferably  $103.2 \pm 3 \text{ \AA}$ , more preferably  $103.2 \pm 2$ , and even more preferably  $103.2 \pm 1 \text{ \AA}$ . Moreover, aforesaid  $c$  is preferably  $281.0 \pm 6 \text{ \AA}$ , more preferably  $281.0 \pm 4 \text{ \AA}$ , and even more preferably  $281.0 \pm 2 \text{ \AA}$ .

The three-dimensional structural coordinates of the GK protein crystal obtained in this way are shown in Table 2.

### Table 2

Moreover, Table 2 is constructed in accordance with representation method of protein data bank generally used by a person skilled in the art. The HOH in Table 2 denotes water molecule.

In this invention, crystals of the protein having amino acids sequence which is substantially the same as Sequence Number 5 and/or Sequence Number 8 and having glucokinase activity are within the range of

this invention. As such crystals, for example, crystals wherein in three-dimensional structure coordinates data changed at least one data of three-dimensional structure coordinates data in accordance with Table 1 and/or 2, the mean square error between atoms of main chain of amino acid represented by three-dimensional structure coordinates data in accordance with Table 1 and/or 2 (C alpha atom) and C alpha atoms represented by the said changed three-dimensional structure coordinates data corresponding to aforesaid C alpha atoms is 0.6 Å or less, are nominated. Even if the numerical values of coordinates representing the position of atoms differ, two structural coordinates which can superimpose corresponding atoms contained in the structural coordinates on top of one another show the same three-dimensional structure.

Moreover, the three-dimensional structural coordinates of GK protein in accordance with Table 1 and/or Table 2 are important information for drug design, and stored in a storage medium that can be read by computer in accordance with requirements, this information is processed with computer, and drug design is carried out. Accordingly, in another embodiment of this invention, a computer readable recording medium which recorded a program to function a computer as three dimensional coordinate memory means that memorises three-dimensional coordinates of amino acid residue in accordance with Table 1 and/or 2 is put forward.

Moreover, according to another embodiment of this invention, a computer readable recording medium that recorded a program which functions using computer as three dimensional coordinates memory means that memorised the three-dimensional coordinates of amino acid residue in accordance with Table 1 and/or 2, as binding site deduction means that deduces compound binding site of a protein having amino acid sequence represented by Sequence Number 8 and/or Sequence Number 5 using three dimensional coordinates of amino acid residue in accordance with Table 1 and/or 2 memorised in aforesaid three-dimensional coordinates memory measure, as binding compound memory means which memorised information about the type of compounds that bind to the protein and three-dimensional structure of aforesaid compounds, and as binding compound candidate selection means for selecting candidate compounds which are compatible to the compound binding site of the protein having amino acid sequence represented by Sequence Number 1 at least using the information about the three-dimensional structure of compound binding site of protein containing amino acid sequence represented by Sequence Number 8 and/or inferred Sequence Number 5 deduced by aforesaid binding site deduction means and the

information about three-dimensional structure of compound memorised in aforesaid binding compounds memory means, is put forward. Moreover, according to another embodiment of this invention, a computer equipped with aforesaid each means, is also put forward.

(Crystal of complex of GK protein with compound that binds to this).

Next, according to another embodiment of this invention, a crystal containing a complex of protein including amino acid sequence in accordance with Sequence Number 5 or Sequence Number 8 or amino acid sequence which is substantially the same amino acid sequence thereof with the compound which can bind to the said protein and a process for the production thereof are put forward.

When a compound which binds to GK protein is obtained, firstly, the GK protein and the compound thereof are mixed for example in an aqueous solution, and a complex is formed. As for the crystal of such complex, well known processes for the production of co-crystals such as co-crystallisation, soaking method or the like are used. As for the crystallisation condition and crystallisation process, refer to aforesaid processes.

For example, a compound that binds to GK protein is selected from the compound group represented by aforesaid formula (I).

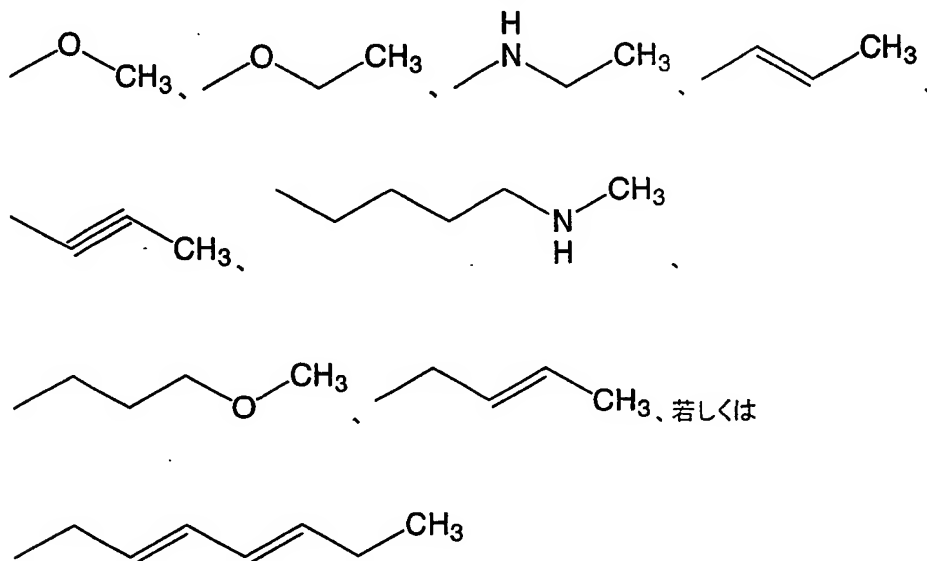
Wherein, as halogen atom of aforesaid formula (I), fluorine atom, chlorine atom, bromine atom, iodine atom or the like are exemplified, and among these, chlorine atom is preferred.

Moreover, as far as substituents in heteroaryl group of A, B of aforesaid formula (1) and formula (II) are concerned, amino group, carbamoyl group, carbamoyl amino group, carbamoyloxy group, carboxyl group, cyano group, sulphamoyl group, trifluoromethyl group, halogen atom, hydroxy group, formyl group, straight chained C1-C6 alkyl group, cyclic C3-C6 hydrocarbon group, aralkyl group, N-aralkyl amino group, N,N-diaralkyl amino group, aralkyloxy group, aralkyl carbonyl group, N-aralkyl carbamoyl group, aryl group, arylthio group, N-arylamino group, aryloxy group, aryl sulphonyl group, aryl sulphonyloxy group, N-arylsulfonylamino group, aryl sulphamoyl group, N-aryl carbamoyl group, aroyl group, aroxy group, C2-C6 alkanoyl group, N-C2-C6 alkanoyl amino group, C1-C6 alkylthio group, N-C1-C6 alkyl sulphamoyl group, N,N-di-C1-C6 alkyl sulphamoyl group, C1-C6 alkyl sulfinyl group, C1-

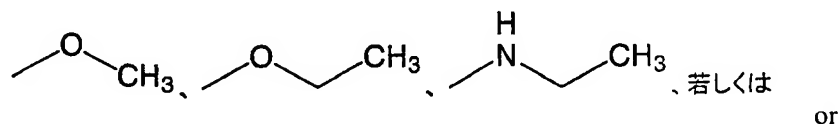
C6 alkylsulfonyl group, N-C1-C6 alkylsulfonyl amino group, C1-C6 alkoxy group, C1-C6 alkoxycarbonyl group or C1-C6 alkylamino group are denoted), or the like is nominated. Wherein, as for the preferably used substituent, amino group, carbamoyl group, carbamoyl amino group, carbamoyloxy group, carboxyl group, cyano group, sulphamoyl group, trifluoromethyl group, halogen atom, hydroxy group, formyl group, straight chained C1-C6 alkyl group or the like are exemplified.

Wherein, "hydrocarbon group" denotes 1-6 C straight chained alkyl group, or, among carbon atom constituting said alkyl group, a group in which 1 or 2, preferably 1 carbon atom may be substituted with nitrogen atom, sulfur atom or oxygen atom and/or carbon atom themselves in the said 1-6 C straight chain alkyl group may be bonded with double bond or triple bond. Number of said double bond or triple bond is preferably 1 or 2 and 1 is more preferred.

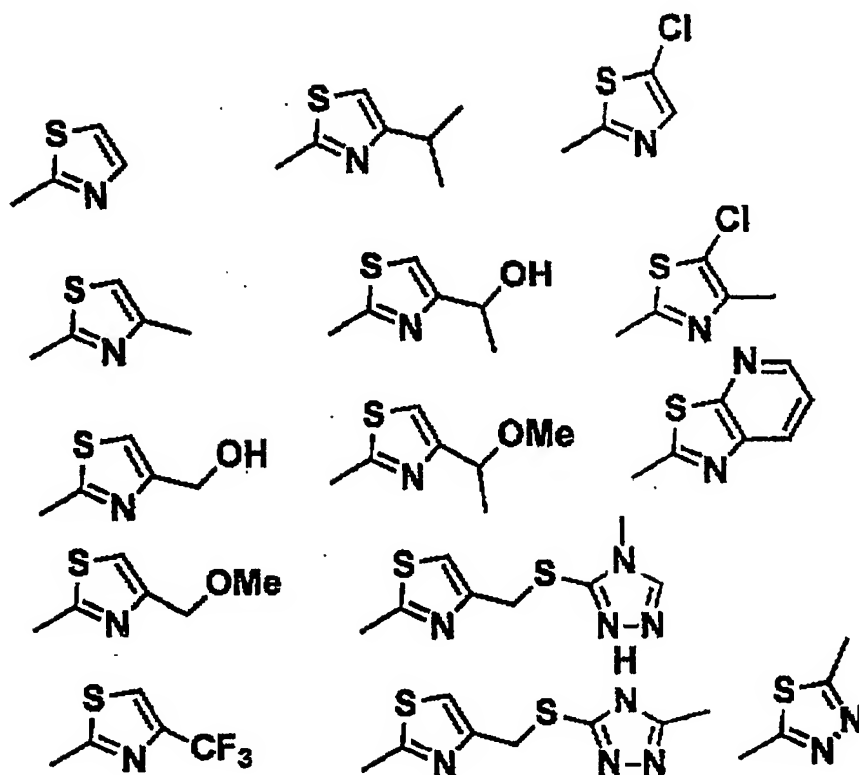
As said hydrocarbon group, in an embodiment, it is preferred to be methyl group, ethyl group, propyl group or isopropyl group, butyl group or a group represented by following formulae



More preferred hydrocarbon group is methyl group, ethyl group, propyl group, isopropyl group or a group represented by following formulae



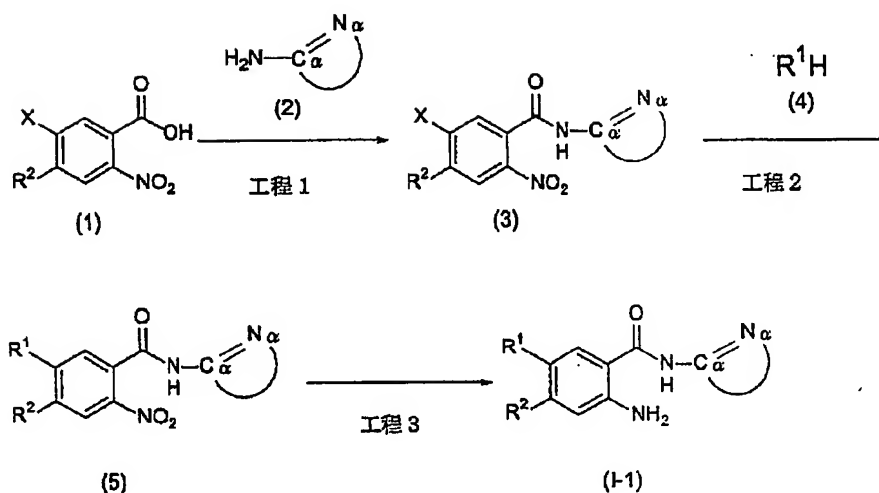




Moreover, particularly preferred compounds are any of the compound represented by aforesaid formulae (IIIa)-(IIIc).

The compound of this invention (1) can be readily produced by using well known reaction means or according to well known method. Moreover, the compound of general formula (I) of this invention can be produced not only by synthesis in ordinary liquid phase, but also by synthesis using solid phase developed remarkably in recent years such as combinatorial synthesis method, parallel synthesis method or the like. Preferably, it can be produced for example using the following process.

Step 1 to Step 2 to Step 3



(wherein, each symbol is the same as in the aforesaid definition)

#### Step 1

This step is a process to produce compound (3) by reacting carboxylic acid compound (1) or reactive derivative thereof and amino compound containing optionally substituted monocyclic or bicyclic heteroaryl group represented by aforesaid formula (2) or salts thereof. In this reaction, ordinary amide formation reaction may be carried out by a method described in literature (for example Base and experiment of peptide synthesis, Shinya Izumiya et al., Maruzen, 1983, Comprehensive Organic Synthesis, vol 6, Pergamon Press Co. 1991 and the like) or in accordance with these, or by combining these and conventional method, in other word, it can be carried out by using condensing agent well-known for a person skilled in the art or by ester activation method, mixed acid anhydride method, acid chloride method, carbodiimide method and the like which can be used by a person skilled in the art. As such amide forming reagent, for example thionyl chloride, N,N-dicyclohexylcarbodiimide, 1-methyl-2-bromo pyridinium iodide, N,N'-carbonyldiimidazole, diphenyl phosphoryl chloride, diphenyl phosphoryl azide, N,N'-disuccinimidyl carbonate, N,N'-disuccinimidyl oxalato, 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride, ethylchloroformate, chloro formic acid isobutyl ester or benzo triazol-1-yl-oxy-tris (dimethylamino) phosphonium hexafluoro phosphate and the like are proposed, and wherein, for example thionyl chloride, N,N-dicyclohexylcarbodiimide or benzo triazol-1-yl-oxy-tris (dimethylamino) phosphonium hexafluoro phosphate and the like are suitable. Moreover, in amide forming reaction, a base, a condensation assistant may be used with the aforesaid amide forming reagent.

As base used, for example tertiary aliphatic amine such as trimethylamine, triethylamine, N,N-diisopropyl ethylamine, N-methylmorpholine, N-methylpyrrolidine, N-methylpiperidine, N,N-dimethylaniline, 1,8-diazabicyclo[5.4.0] undec-7-ene (DBU), 1,5-azabicyclo[4.3.0] non-5-ene (DBN) or the like, for example aromatic amine such as pyridine, 4-dimethylaminopyridine, picoline, lutidine, quinoline, isoquinoline and the like are proposed, and wherein, for example tertiary aliphatic amine and the like is preferred, and in particular, for example triethylamine or N,N-diisopropyl ethylamine and the like is suitable.

As condensation assistant used, for example N-hydroxybenzotriazole hydrate, N-hydroxy succinimide, N-hydroxy-5-norbornene-2,3-dicarboximide or 3-hydroxy-3,4-dihydro-4-oxo-1,2,3-benzotriazole and the like are proposed, and among these, for example N-hydroxybenzotriazole and the like are suitable.

The amount of amino compound (2) used differs depending on the kind of compound and solvent used and other reaction conditions, however, usually, 0.02 to 50 equivalents, preferably 0.2 to 2 equivalents with respect to 1 equivalent of carboxylic acid compound (1) or reactive derivative thereof. Herein, as reactive derivative, for example active ester derivative, active amide derivative and the like which are used in the sphere of usual organic chemistry are nominated.

The amount of used amide forming reagent differs depending on the kind of compound and solvent used and other reaction conditions, however, usually 1-50 equivalents, preferably 1-5 equivalents with respect to 1 equivalent of carboxylic acid compound (1) or reactive derivative thereof.

The amount of used condensation assistant differs depending on the kind of compound and solvent used and other reaction conditions, however, usually it is 1-50 equivalents, preferably 1-5 equivalents with respect to 1 equivalent of carboxylic acid compound (1) or reactive derivative thereof.

The amount of used base differs depending on the kind of compound and solvent used and other reaction conditions, however, usually 1 to 50 equivalents, preferably 3 to 5 equivalents.

The reaction solvent used in this step, is for example inert organic solvent, and it is not restricted in



particular so long as it does not hinder the reaction. However, in an embodiment, for example methylene chloride, chloroform, 1,2-dichloroethane, trichloroethane, N,N-dimethylformamide, acetic acid ethylester, acetic acid methylester, acetonitrile, benzene, xylene, toluene, 1,4-dioxane, tetrahydrofuran, dimethoxyethane or a mixed solvent thereof are proposed, however, in particular for example methylene chloride, chloroform, 1,2-dichloroethane, acetonitrile, N,N-dimethylformamide or the like are suitable in term of securing a suitable reaction temperature.

The reaction temperature is -100°C to boiling point of solvent, preferably 0 to 30°C.

The reaction time is 0.5 to 96 hours, preferably 3 to 24 hours.

The base, amide formation reagent, condensation assistant used in this step 1 can be used as a single species or in combination of two or more.

When the compound (3) contains protecting group, said protecting group can be suitably eliminated. Elimination of aforesaid protecting group can be carried out by method described in literature (Protective Groups in Organic Synthesis, written by T.W. Green, the second edition, John Wiley & Sons Co, 1991, or the like) or method in accordance with this or by combining these and conventional method.

Compound (3) obtained in this way can be provided for the next step by isolating and purifying with well known separation and refinement means, for example concentration, vacuum concentration, crystallisation, solvent extraction, re-precipitation, chromatography and the like or without isolating and purifying.

## Step 2

This step comprises a process to produce compound (5) by reacting amide compound (3) obtained in aforesaid step 1 and compound (4).

In this reaction, a base may be added to the reaction system in accordance with requirements. As used compound (4), preferably phenol derivative or thiol derivative is preferred. As said phenol derivative or thiol derivative, for example phenol, thiophenol, thio imidazole, thio triazole and the like are

nominated. The amount of compound (4) used differs depending on the kind of compound and solvent used or other reaction conditions, however, usually it is 2-50 equivalents, preferably 2-5 equivalents with respect to 1 equivalent of amino derivative (3). As used base, for example tertiary aliphatic amine such as trimethylamine, triethylamine, N,N-diisopropyl ethylamine, N-methylmorpholine, N-methylpyrrolidine, N-methylpiperidine, N,N-dimethylaniline, 1,8-diazabicyclo[5.4.0] undec-7-ene (DBU), 1,5-azabicyclo[4.3.0] non-5-ene (DBN) or the like, for example aromatic amine such as pyridine, 4-dimethylaminopyridine, picoline, lutidine, quinoline, isoquinoline and the like, alkali metal such as metallic potassium, metallic sodium, metallic lithium and the like, alkali metal hydride such as sodium hydride, potassium hydride and the like, alkali metal alkylate such as butyl lithium and the like, alkali metal alkoxide such as potassium-tert-butyrate, sodium ethylate or sodium methylate and the like, alkali metal hydroxide such as potassium hydroxide, sodium hydroxide and the like, alkali metal carbonate such as potassium carbonate and the like are nominated, among these for example tertiary aliphatic amine, alkali metal hydride or alkali metal carbonate are preferred, and in particular, for example triethylamine, N,N-diisopropyl ethylamine, sodium hydride or potassium carbonate are suitable.

The amount of aforesaid base used differs depending on the kind of compound and solvent used and other reaction conditions, however, it is usually 0 to 50 equivalents, preferably 2-10 equivalents with respect to 1 equivalent of amide compound (3). Said base can be used as a single species or two or more species in accordance with requirements.

As used inert organic solvent, there are no restrictions in particular so long as the reaction is not hindered. However, in an embodiment, for example methylene chloride, chloroform, 1,2-dichloroethane, trichloroethane, N,N-dimethylformamide, N,N-dimethyl acetamide, acetic acid ethylester, acetic acid methylester, acetonitrile, benzene, xylene, water, toluene, 1,4-dioxane, tetrahydrofuran, or a mixed solvent thereof are proposed.

Compound (5) obtained in this way can be isolated and purified with well known separation and refinement means, for example concentration, vacuum concentration, crystallisation, solvent extraction, re-precipitation, chromatography and the like.

### Step 3

This step is a process to produce compound (I) used in this invention by reduction of compound (5). As for reductive reaction used in this step, well-known processes to a person skilled in the art are used. As the reductive reaction used in this step, in an embodiment, for example (1) catalytic reduction method using hydrogen, formic acid, ammonium formate, hydrazine hydrate and palladium, platinum, nickel catalyst, (2) reduction method using hydrochloric acid, ammonium chloride and iron, (3) reduction method using methanol and tin chloride are nominated.

The amount of reducing agent used in the aforesaid reductive reaction differs depending on the kind of compound and solvent to be used and other reaction conditions, however, it is usually 1-50 equivalents, preferably 2-20 equivalents with respect to 1 equivalent of compound (5).

The reaction solvent used is not restricted in particular so long as the reaction is not hindered. However, for example halogenated hydrocarbons such as dichloromethane, chloroform and the like, ethers such as diethyl ether, tert-butyl methyl ether, tetrahydrofuran and the like, amides such as N,N-dimethylformamide, N,N-dimethylacetamide and the like, sulfoxides such as dimethylsulfoxide and the like, nitriles such as acetonitrile and the like, an alcohol such as methanol, ethanol, propanol and the like, aromatic hydrocarbons such as benzene, toluene, xylene and the like, water or mixed solvent thereof can be used.

Reaction temperature and the reaction time are not restricted in particular. However, the reaction is carried out for 1-20 hours approx. and preferably 1 to 5 hours approx. at a reaction temperature of -10 to 100°C approx. and preferably 0 to 50°C approx.

Compound (1) used in this invention obtained in this way can be provided for the next step by isolating and purifying with well known separation and refinement means, for example concentration, vacuum concentration, crystallisation, solvent extraction, re-precipitation, chromatography and the like or without isolating and purifying.

Compound of aforesaid each step may contain protecting group on each substituent. Aforesaid protecting group can be suitably eliminated in each step using well known method, method in accordance with that or method combined these and the conventional method. As for the embodiment of

elimination, suitable elimination reaction is possible depending on the kind of compound, reaction and other reaction conditions. However, it is considered the case in which each protecting group is eliminated individually and the case in which each protecting group is simultaneously eliminated and the like, and it can be suitably selected by a person skilled in the art. As aforesaid protecting group, for example protecting group of hydroxy group, protecting group of amino group, protecting group of carboxyl group, protecting group of aldehyde, protecting group of keto group and the like are nominated. Moreover, the order of elimination aforesaid protecting groups is not limited in particular.

As protecting group of hydroxy group, for example lower alkyl silyl group such as tert-butyldimethylsilyl group, tert-butyl diphenyl silyl group and the like, for example lower alkoxymethyl group such as methoxy methyl group, 2-methoxyethoxymethyl group and the like, for example aralkyl group such as benzyl group, p-methoxybenzyl group and the like, for example acyl group such as formyl group, acetyl group and the like are proposed, and among these, tert-butyldimethylsilyl group, acetyl group and the like are in particular preferred.

As protecting group of amino group, for example aralkyl group such as benzyl group, p-nitrobenzyl and the like, for example acyl group such as formyl group, acetyl group and the like, for example lower alkoxycarbonyl group such as ethoxycarbonyl group, tert-butoxycarbonyl group and the like, for example aralkyloxy carbonyl group such as benzyloxycarbonyl group, p-nitrobenzyl oxycarbonyl group and the like are proposed, and among these, nitrobenzyl group, tert-butoxy carbonyl group, benzyloxycarbonyl group and the like are particularly preferred.

As protecting group of carboxyl group, for example lower alkyl group such as methyl group, ethyl group, tert-butyl group and the like, for example aralkyl group such as benzyl group, p-methoxybenzyl group and the like are nominated, and among these, methyl group, ethyl group, tert-butyl group, benzyl group and the like are particularly preferred.

As protecting group of keto group, for example dimethyl ketal group, 1,3-dioxirane group, 1,3-dioxolane group, 1,3-dithiane group, 1,3-dithiorane group and the like are proposed, and among these, dimethyl ketal group, 1,3-dioxolane group and the like are more preferred.

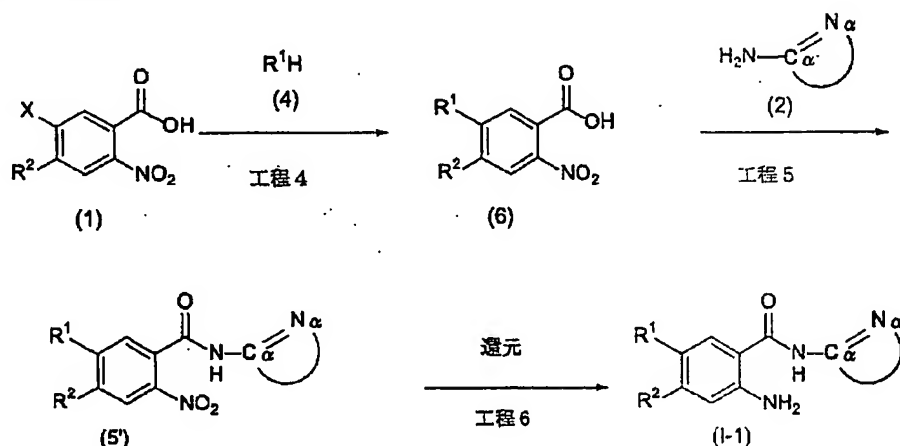
As protecting group of aldehyde group, for example, dimethylacetal group, 1,3-dioxirane group, 1,3-dioxolane group, 1,3-dithiane group, 1,3-dithiorane group and the like are proposed, and among these, dimethylacetal group, 1,3-dioxolane group and the like are more preferred.

In the production of compound used in this invention, there is a case that the protecting group is introduced to functional group in order to proceed reaction with good efficiency. The introduction of these protecting groups can be suitably selected by a person skilled in the art, and elimination of aforesaid protecting groups can be carried out by a method described in aforesaid Protective Groups In Organic Synthesis and the like, a method in accordance with that or by combining that and conventional method. Moreover, the order of elimination of protecting groups can be suitably selected by a person skilled in the art.

Compound (1) obtained in this way can be subjected to the next step after isolating and purifying with well known separation and refinement means, for example concentration, vacuum concentration, crystallisation, solvent extraction, re-precipitation, chromatography and the like or without isolating and purifying.

Moreover, the compound used in this invention (I) can be also produced by the following step.

Step 4 to Step 5 to Step 6



(wherein, each symbol has same aforesaid definition).

As far as the aforesaid Step 4, Step 5 and Step 6 are concerned, it can be carried out using the same amount of reagent, reaction solvent, reaction temperature and other reaction conditions as in aforesaid Step 1, Step 2 and Step 3.

When a protecting group is necessary for R2, it can be carried out by a person skilled in the art suitably selecting a process from a method described in aforesaid Protective Groups In Organic Synthesis and the like, a method in accordance with that or by combining that and conventional method.

Compounds (6) and (5') obtained in this way can be provided for the next step after isolating and purifying with well known separation and refinement means, for example concentration, vacuum concentration, crystallisation, re-precipitation, solvent extraction and the like or without isolating and purifying.

Compound (1) used in this invention can be isolated and purified by well known separation and refinement means, for example concentration, vacuum concentration, crystallisation, re-precipitation, solvent extraction and the like.

In aforesaid step 1 to 6, the elimination of protecting groups differ depending on the kind of aforesaid protecting group and stability of compound, however, it can be carried out by aforesaid method described in Protective Groups in Organic Synthesis, written by T.W. Green, the second edition, John Wiley & Sons Co, 1991, or the like or a method in accordance with this or by combining these and conventional method. For example, it can be carried out by solvolysis using acid or base, chemical reduction using hydrogenated metallic complex and the like or catalytic reductions using palladium carbon catalyst, Raney nickel and the like.

The benzamide compound put forward by this invention can exist as pharmacologically acceptable salt. Aforesaid salt can be produced in accordance with conventional methods. In an embodiment, when aforesaid compound (1) contains basic group derived from for example amino group, pyridyl group within the molecule, it can be converted to corresponding pharmacologically acceptable salt by treating aforesaid compound with an acid.

As aforesaid acid addition salt, for example the acid addition salt of halide acid salt such as hydrochloride, hydrofluoric acid salt, hydrobromic acid salt, hydroiodic acid salt or the like, inorganic acid salt such as nitrate, perchlorate, sulfate, phosphate, carbonate or the like, lower alkyl sulfonate such as methanesulfonate, trifluoromethanesulfonate, ethanesulfonic acid salt or the like, aryl sulfonate such as benzensulphonate, p-toluenesulfonate or the like, organic salt such as fumarate, succinate, citrate, tartrate, oxalate, maleate or the like and organic acid of amino acid or the like such as glutamic acid salt, aspartate or the like are nominated. Moreover, when the compound of this invention is containing acidic group in aforesaid group, for example when containing carboxyl groups, it can be converted to corresponding pharmacologically acceptable salt by treating aforesaid compound with a base. As aforesaid base addition salt, for example salt of alkali metal salt such as sodium, potassium and the like, alkaline earth metal salt such as calcium, magnesium and the like, organic base such as ammonium salt, guanidine, triethylamine, dicyclohexylamine and the like are nominated. Furthermore, the compound of this invention may exist as free compound or arbitrary hydrate or solvate of salts thereof.

In accordance with this invention, as explained in detail in the description of Examples, crystal of complex of GK protein containing amino acid sequence shown in Sequence Number 5 and compounds of aforesaid formula (IIIa)-formula (IIIc) are obtained. In GK protein shown in Sequence Number 5, it has been elucidated that compound binding site is constituted from the amino acid residue of tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459 by analysing these crystal three - dimensional structure coordinates.

Moreover, according to another embodiment of this invention, a process for the production of crystal containing a complex of protein and a compound that binds to the protein, wherein a protein production step to produce a protein containing amino acids sequence in which prescribed number of amino acid residues at N terminal side and/or C terminal side are deleted as described above from the protein containing amino acid sequence in accordance with Sequence Number 2 and a step to cause reaction of a compound which binds to the protein obtained in aforesaid protein production step with the protein obtained in said protein production step are included, is put forward.

As protein to be produced in the aforesaid protein production step, the number thereof is not restricted as long as it is within a range that steric hindrance between adjacent GK proteins in the crystal is eliminated. In an embodiment, for example, in the amino acids sequence shown in Sequence Number 2, the amino acids sequences in which amino acid residues at N terminal side are deleted in numbers of 1-50, preferably 3-30, more preferably 5-25, still more preferably 8-18, even more preferably 11-15 or the like are nominated. Moreover, the amino acid sequences in which amino acid residues at C terminal side of 1-8, preferably 1-7, more preferably 2-6 or the like are deleted, are nominated.

(The drug design process using three-dimensional structural coordinate).

Three-dimensional structure of GK protein of this invention obtained as above provides important information for drug creation system using CARDD (Computer Aided Rational Drug Design). It is an important step of the target drug creation and development to elucidate the active center and allosteric site of this GK protein and to search for a compound which is compatible to said site, interacts with the GK protein and thereby activates to inhibits the GK protein.

In other words, according to another embodiment of this invention, a drug design process of the kind to design structure of compound that binds to said protein based on stereostructure information of protein, characterised in that the stereostructure information of said protein comprises information to be obtained by analysing the crystal obtained as described above, is put forward. As such drug design process, there are techniques to make drug design using energy calculation, activity prediction value analogous to this or pharmacophore and a technique to visually design drug using computer graphics technique.

As process by technique using energy calculation, activity prediction value analogous to this or pharmacophore, (1) a drug design process including a binding site deduction step to deduce compound binding site of said protein based on stereostructural information obtained as above and a selection step to select a compound compatible to the compound binding site deduced in aforesaid binding site deduction step from the compound library, (2) a drug design process including a binding site deduction step to deduce compound binding site of said protein based on aforesaid stereostructural information and a compound structure assembly step to construct a structure of compound compatible to the compound binding site deduced in aforesaid binding site deduction step, or the like are exemplified.



As process to deduce compound binding site of aforesaid protein, for example, a process wherein the ligand bonded site in the co-crystal of compound is identified by confirming with visual observation on display of computer, and in addition to that, a process wherein the site to which ligand is likely to bind is identified with respect to the protein crystal structure solved under the condition that ligand is not bound, are nominated. In any processes, well-known method and commercial computer soft wear can be used. In former process, for example, it is possible to use software such as Insight II (Accelrys Inc.), SYBYL (Tripos Inc.), MOE (Chemical Computing Group) or the like. On the other hand, For example, in latter process, well known technique such as Cavity search: an algorithm for the isolation and display of cavity-like binding regions, (Journal of Computer-Aided Molecular Design. 4(4): 337-54, 1990) or the like can be used, and it can be carried out using software such as SiteID (Tripos Inc.) or the like.

Once the binding site of compound in protein was able to be deduced, a compound which can be compatible to the deduced binding site is selected. As process to select this candidate compound, structural information of the compound is acquired from existing compound library, and bindable candidate compound is selected by comparing the structural information of compound in the library and structural information of the binding site deduced as above.

In a further embodiment, 1 or more residues of amino acid residues of amino acid sequence shown in Sequence Number 5 (tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459) or pharmacophore of hydrogen bonding or hydrophobic properties or the like formed from the functional group of ligand in the complex, and also the protein surface produced from the protein structure or a structure in which the orientation of a part of the side chain thereof is modified, are used as search condition, and the conformation and orientation of each compound is systematically searched from the compound library, and whether the conditions are satisfied or not is judged and it is selected.

As an alternative process, while systematically searching the conformation and orientation of each compound from the compound library, the candidate compound is virtually docked with respect to the structure of ligand binding site constructed from the amino acid residues (tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459) or a structure in which the orientation

of a part of the side chain thereof is modified, the species that formed interaction of close proximity of 4 Å or less with 1 or more residues of amino acid residues of amino acid sequence (tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459) is selected, or selection is carried out using energy evaluation function.

On the other hand, the candidate compound can also be selected by designing a bindable compound based on the structural information of the binding site deduced as above. In a further embodiment, each atomic species and functional groups are connected so that interactions are possible with respect to the structure of ligand binding site constructed from the amino acid residues (tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459) or a structure in which the orientation of a part of the side chain thereof is modified, and thereby a chemical structure is constructed. As this process, a process wherein chemical groups such as methyl, ethyl and the like are arranged in the active site and a compatible compound is searched, and a process wherein atoms are bonded at active site using a computer program.

Moreover, with the process by energy evaluation using computer, for example a process to determine the bond energy of a compound and GK protein using molecular force field calculation is nominated. The calculation thereof is applied to each compound in database, and candidate compounds which can form stable binding are selected from the library compound. With some computer programs, such as Ludi of Insight II, when three-dimensional structural coordinates of interacting amino acid residues in the protein molecule are input, candidate of bindable compounds are automatically selected and output, and it can be suitably used.

Moreover, as far as the drug design on the basis of three-dimensional structure of molecule is concerned, many literature are known including development of pharmaceutical Vol. 7 "molecular design" (Hirokawa Shoten). In an embodiment, first, using flexible ligand binding simulation software such as for example FlexiDock, FlexX or the like, a library of low molecular (molecular weight 1000 or less) compounds (for example about 150000 species) can be screened with computer. For chemical compounds in this library, three-dimensional structure is built using a program such as CONCORD or the

like, and compounds compatible to the active site can be selected.

On the other hand, as a process of visual drug design, a drug design process characterised in including a binding site deduction step to deduce compound binding site of said protein based on aforesaid stereostructural information and a design step wherein the structure of the compound is visually designed so that aforesaid compound binding site deduced in aforesaid binding site deduction step and a compound compatible to said compound binding site can interact, is nominated. For example, structure assembly or structure modification is carried out with respect to the structure of ligand binding site constructed from the amino acid residues (tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459) or a structure in which the orientation of a part of the side chain thereof is modified, so that it can interact with 1 or 2 or more residues among these residues.

In an embodiment, with visual process, first, crystal structure of the complex of GK protein and a compound bound to this is displayed on a computer screen according to the obtained structural coordinates. And, while considering the chemical interaction, the binding possibilities of the compounds in the library and GK protein are successively examined on computer. Wherein, the chemical interactions to be considered are electrostatic interaction, hydrophobic interaction, hydrogen bonding, van der Waals interaction or the like. In other words, the structure in three dimensional space of said compound is generally considered whether a structure favourable for the interaction is formed or not, so that among the functional groups thereof, the groups likely to be negatively charged such as carboxyl group, nitro group, halogen group or the like interact with amino acid residues having positive charge such as lysine, arginine, histidine of GK protein, the groups likely to be positively charged such as amino group, imino group, guanidyl group or the like interact with amino acid residues having negative positive charge such as glutamic acid, aspartic acid of GK protein, hydrophobic functional groups such as aliphatic group and aromatic group interact with hydrophobic amino acid residues such as alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine, the groups which participate in hydrogen bond such as hydroxy group, amide group or the like can for hydrogen bonding with the main chain or side chain part of the GK protein, furthermore steric hindrance is not caused by the binding of said compound and GK protein, moreover, furthermore, the void part is filled so that the void part is eliminated as much as possible so that the van der Waals interaction is increased, or the like. In this way,

the factors such as electrostatic interaction, hydrophobic interaction, van der Waals interaction, hydrogen bond or the like are comprehensively considered visually on the computer screen, and finally, whether the candidate compound can bind to the GK protein or not is determined.

As program for selecting compound candidate by visual observation in this way, simulation programs such as Insight II and MOE or the like are exemplified. In order to generate promising candidate compounds that interact with GK protein, the candidate compounds are contacted with GK protein, and activity of GK protein is measured. In practice, the promising candidate compound is mixed with GK protein, crystallised, and whether it is compatible or not is evaluated. Further, more desirable structure is formed by modifying the compatible complex using organic synthesis.

Moreover, the visual technique and the technique that considers energy may be suitably combined, and used. As such computer software, flexiDock (Tripos Inc.), FlexX (Tripos Inc.), SYBYL (Tripos Inc.), Insight II (Accelrys Inc.), MOE (Chemical Computing Group Inc.) or the like are nominated.

Moreover, in accordance with this invention, the compounds selected by aforesaid drug design process are synthesized, and these compound groups can be provided as compound array (compound library). Because a large quantity of candidate compounds can be assayed at one time using a technique such as high through-put screening or the like, the inhibitor or activator of glucokinase can be screened with good efficiency.

(Compounds obtained by process of this invention and therapeutic agent including these)

The compounds designed by aforesaid drug design process have has ability to bind to glucokinase, therefore they can be used as activators of glucokinase or glucokinase inhibitors. Moreover, the therapeutic agent or medicinal composition containing such compound can be effectively used as therapeutic agent of disease involving glucokinase activity (for example diabetes mellitus therapeutic agent).

Aforesaid medicinal composition contains a compound that binds to glucokinase of this invention as effective ingredient in pharmacologically effective dose thereof together with suitable pharmacologically permitted support or diluent. As the pharmacologically acceptable support which can be used in aforesaid

medicinal composition (drug formulation), diluent such as filler, extender, binding agent, humectant, disintegrating agent, surface active agent, lubricant or the like which are conventionally used corresponding to the form of the formulation or excipient or the like are exemplified. These carriers can be suitably selected and used corresponding to administration unit form of the obtained formulation.

As administration unit form of medicinal composition of this invention, various forms can be selected according to therapeutic purpose, and, as representative examples thereof, solid administrative form such as tablet, pill, powder, powder agent, granule, encapsulated formulation or the like and liquid agent administrative form such as solution, suspending agent, emulsion, syrup, elixir or the like are included. Further these are classified into orally administered agent, aoral drug, transnasal agent, vaginal agent, suppository, sublingual agent, ointment or the like according to administration route, and it can be formulated, molded and prepared each according to conventional process. For example, when it is formed to a tablet form, excipient such as lactose, lactose, refined sugar, sodium chloride, glucose, urea, starch, calcium carbonate, kaolin, crystalline cellulose, silicic acid, potassium phosphate or the like, binding agent such as water, ethanol, propanol, simple syrup, glucose syrup, starch solution, gelatin solution, carboxymethylcellulose, hydroxypropylcellulose, methylcellulose, polyvinylpyrrolidone or the like, disintegrating agent such as carboxymethylcellulose sodium, carboxymethylcellulose calcium, low degree of substitution hydroxypropylcellulose, dried starch, sodium alginate, agar powder, laminaran powder, sodium bicarbonate, calcium carbonate or the like, surface active agent such as polyoxyethylene sorbitan fatty acid ester species, lauryl sodium sulfate, stearic acid monoglyceride or the like, disintegration inhibitor such as refined sugar, stearin, cacao butter, hydrogenation oil or the like, absorption accelerating agent such as quaternary ammonium base, sodium lauryl sulfate or the like, humectant such as glycerol, starch or the like, adsorbent such as starch, lactose, kaolin, bentonite, colloidal silica or the like, lubricant or the like such as purified talc, stearate, boric acid powder, polyethyleneglycol or the like can be used. Further, the tablet can be formed into a tablet coated with ordinary agent coating in accordance with requirements, for example sugar coated tablet, gelatin encapsulation tablet, enteric coated tablet, film coatings tablet and moreover can be made into double layer tablet or multilayer tablet.

When a form of pill is formed, as formulation carrier, for example, excipient such as glucose, lactose, starch, cacao butter, hardened vegetable oil, kaolin, talc or the like, binding agent such as powdered gum

arabic, tragacanth powder, gelatin, ethanol or the like, disintegrating agent or the like such as laminaran, agar or the like can be used.

For encapsulated formulation, effective ingredient of this invention is mixed with the various formulation carrier exemplified as above according to normal method, and it is prepared by being packed into hard gelatin capsule, soft capsule or the like.

The liquid administration form for oral administration includes pharmacologically permitted solution, emulsion, suspension, syrup, elixir or the like containing generally used inert diluent, for example water, and furthermore, auxiliary such as wetting agent, emulsion, suspending agent or the like can be contained, and these are prepared according to normal method.

For the preparation of liquid administrative form for aoral administration, for example, sterile aqueous or non-aqueous solution, emulsion, suspension or the like, as diluent, for example water, ethanol, propylene glycol, polyethyleneglycol, ethoxylation isostearyl alcohol, polyoxyisostearyl alcohol, polyoxyethylene sorbitan fatty acid ester and vegetable oil or the like such as olive oil or the like can be used, and moreover, injectable organic ester species, for example, ethyl oleate or the like can be formulated. Further, ordinary solubiliser, buffer agent, wetting agent, emulsifier, suspending agent, preservative, dispersant or the like can be added to these. Sterilisation can be carried out for example by filtration operation through bacteria retaining filter, formulation of fungicide, irradiation treatment and heat treatment or the like. Moreover, these can be prepared as sterile solid composition which can be dissolved in sterile water or suitable sterilisable vehicle immediately before the use.

When forming into a form of suppository or vaginal administration, as formulation carrier, for example polyethyleneglycol, cacao butter, higher alcohol, higher alcohol ester, gelatin and semi-synthetic glyceride or the like can be used.

When forming into a form ointment such as paste, cream, gel or the like, as diluent, for example white petrolatum, paraffin, glycerol, cellulose derivative, propylene glycol, polyethyleneglycol, silicon, bentonite and vegetable oil or the like such as olive oil or the like can be used.

A composition for transnasal or sublingual administration can be prepared according to conventional method using standard excipient.

Moreover, in agent of this invention, colorant, preservative, flavor, flavor agent, sweetener or the like or other pharmaceutical or the like can be contained in accordance with requirements.

The amount of the effective ingredient to be contained in the aforesaid drug formulation and dose thereof are not restricted in particular, and it is suitably selected from a wide range corresponding to the desired therapy effect, administration method, therapy period, age, sex of patient, other conditions or the like. In general, the dose is about 0.01 mg - 1000 mg, preferably about 1 mg - 100 mg per 60 kg in weight per day usually, and it can be administered once or divided into several times per day.

Sequence number of sequence table of this specification shows following sequence.

(Sequence number: 1).

Base sequence of DNA encoding human derived liver type glucokinase is shown.

(Sequence number: 2).

Amino acid sequence of human derived liver type glucokinase is shown.

(Sequence number: 3).

Amino acid sequence of human derived beta cell glucokinase is shown.

(Sequence number: 4).

Base sequence of DNA encoding the protein in which 11 amino acid residues at N terminal side of human derived liver type glucokinase are deleted, is shown.

(Sequence number: 5).

Amino acid sequence of the protein in which 11 amino acid residues at N terminal side of human derived liver type glucokinase are deleted, is shown.

(Sequence number: 6).

Base sequence of primer-1 used in PCR reaction in the following Example 1 is shown.

(Sequence number: 7).

Base sequence of primer-2 used in PCR reaction in the following Example 1 is shown.

(Sequence number: 8).

Amino acid sequence of the protein in which 15 amino acid residues at N terminal side of human derived liver type glucokinase are deleted, is shown.

(Sequence number: 9).

Base sequence of the primer used in PCR reaction in the following Example 6 is shown.

(Sequence number: 10).

Base sequence of the primer used in PCR reaction in the following Example 6 is shown.

### Examples

Hereinafter, this invention will be described in concrete terms using Examples.

#### A process for purification of mutant type enzyme

In human glucokinase, there are liver type and pancreas type depending on the difference of promoter, and 15 residues at N terminal are different. In order to carry out crystallisation for the purpose of three-dimensional structure analysis, a mutant type enzyme which lacked a part or a whole of this region was made by the following process.

PCR reaction was carried out using cDNA of human liver type glucokinase cloned on pCR2.1 (made by INTROGEN Co.) and two kinds of primer sets, comprising

- a combination of 5'-gtcacaaggagccagaagcttatggccttgactctgtag-3' (sequence number 6) and  
5'-gaagccccacgacattgttccttctgc-3 (sequence number 7), and  
a combination of 5'-ccaggcccagacagccaagcttatgtagagcagatcc-3' (sequence number 9) and  
5'-gaagccccacgacattgttccttctgc 3' (sequence number 10).



The Hind III, Cla I fragment of the obtained PCR product was substituted with Hind III-Cla I region of liver type GK cloned at Hind III, Eco RI site of pFLAG/CTC vector (Eastman Kodak), and thereby cDNAs encoding mutant type GK ( $\Delta 1-11$ ) which lacked 1-11 residues of liver type GK and mutant type GK ( $\Delta 1-15$ ) which lacked 1-15 residues were obtained. The sequence of the obtained DNA was confirmed, and thereafter, these vectors were made as expression vectors, and Escherichia coli DH alpha strain (made by Takara Shuzo company) was transformed.

Transformant was cultured in LB medium at 37°C till the absorption at 600 nm became 0.8, and thereafter, isopropyl-1-thio-beta-D-galactoside (made by Wako Pure Chemicals Co.) was added so as to become the final concentration of 0.4 mM, and the protein production was induced at 25°C for 16 hours.

Cultured Escherichia coli was collected using centrifuge, and it was suspended in a buffer containing the following components (50 mM potassium phosphate (Potassium Phosphate) pH 7.5, 50 mM NaCl, 2 mM DTT, 0.5 mM Pefabloc SC (made by Kanto Chemicals Company), a proteinase inhibitor mixture (made by Roche Co.)) .

Collected Escherichia coli was pulverised by ultrasonic pulverisation method, and soluble fraction was dialysed against aforesaid buffer, and thereafter, it was purified using HiTrapQ column (made by Amersham Corp.). The GK fraction eluted from HiTrapQ column by potassium chloride gradient was diluted to a salt concentration of 50 mM by dilution.

The diluted GK fraction was purified by Glucosamin Sepharose column produced by a process demonstrated in the paper (Preparative Biochemistry, 20(2), 163-178 (1990)). The GK fraction was adsorbed onto Glucosamin Sepharose column, and impurity was eliminated with 100 mM sodium chloride, and thereafter, it was eluted by glucose of 1 M.

The eluted GK fraction was refined by MonoQ10/10 column. The GK fraction eluted from the MonoQ10/10 column (made by Amersham Corp.) by sodium chloride gradient was purified by Superdex 200 column (made by Amersham Corp.) using 50 mM Tris-Cl pH 7.2, 50 mM NaCl buffer as mobile layer.

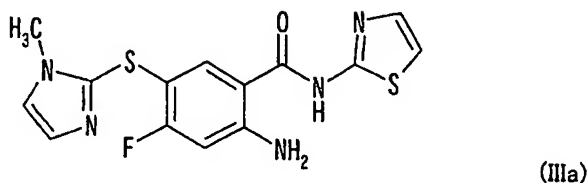
Crystallisation processCrystal of mutant type GK [ $\Delta$ 1-11] / glucose / compound complex

The crystal of mutant type GK ( $\Delta$ 1-11) / glucose / compound complex was obtained using a technique of the following vapor diffusion. Moreover, mutant type GK ( $\Delta$ 1-11) denotes a glucokinase containing amino acid sequence represented by Sequence Number 5.

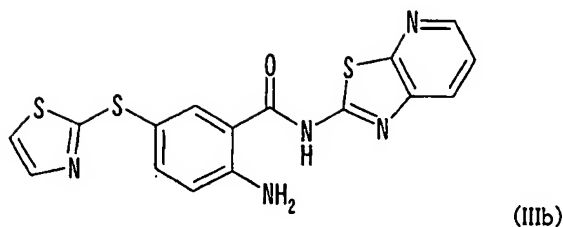
In other words, mutant type GK purified to a high purity was concentrated, and finally a solution of mutant type GK of about 10 mg/ml (25 mM Tris-Cl, 50 mM NaCl, 5 mM TCEP) was formed. Thereto were added glucose of final concentration 20 mM and following compound 1 (compound of formula IIIa) which activates GK of final concentration 0.3 mM, and this was used for crystallisation. To protein solution 1-5  $\mu$ l was added as crystallisation solution, an equal quantity of 28-30 % PEG 1500 and 0.1 M Hepes-NaOH (pH 6.6), and this solution formed by admixing was placed in a closed container containing 0.5-1 ml of crystallisation solution as that both solutions did not form contact, and the container was left to stand at 20°C. After standing for about 3 days - 1 months, crystals with maximum size of about 0.4 mm x 0.4 mm x 0.7 mm was obtained in the sample solution (Example 1).

Furthermore, the crystals obtained by aforesaid method were immersed for about 3-7 days in 28-80 % PEG 1500, 0.1 M HePes-NaOH (pH 6.6) solution so that the following compound 2 (compound represented by formula IIIb) was contained in a concentration of 0.3 mM, and thereby a complex crystals of the following compound 2 and aforesaid mutant type GK were obtained.

## Compound 1



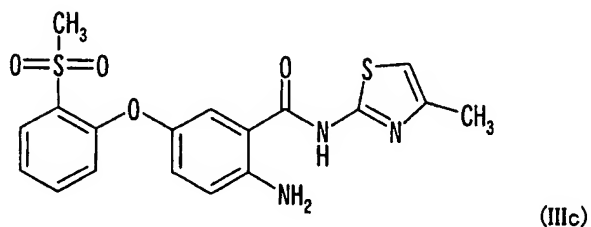
## Compound 2



(IIIb)

Moreover, crystallisation was carried out in the same way as in Example 1 except that compound 3 (compound represented by formula IIIc) was used in stead of aforesaid compound 1, and as a result, crystals were respectively obtained in the same way as in Example 1 (Example 3).

#### Compound 3



(IIIc)

The obtained crystals were immersed into a crystallisation solution added with 10 % glycerol, thereafter it was rapidly frozen in liquid nitrogen. The X-ray diffraction data of the frozen crystal was collected in 100 K nitrogen gas stream by oscillation method at BL6B of synchrotron institution KEK-PF. From the obtained diffraction pattern, diffraction intensity was numerised using DENZO/SCALEPACK (made by HKL Co.), and crystal structure factor was determined. At this step, the crystal was found to be hexagonal system and had a space group of  $P6_522$  or  $P6_122$ , and crystalline unit lattice was  $a = b = 79.9$  angstrom,  $c = 322.2$  angstrom,  $\alpha = \beta = 90^\circ$ ,  $\gamma = 120^\circ$ .

Using the obtained structure factor and three-dimensional structural coordinates of Human hexokinase type 1, the structure was analysed by molecular replacement method. Data with the resolution of 8 angstrom to 4 angstrom was used for the calculation, and it was performed by Amore program of CCP4 (Council for the Central laboratory of the Research Councils). The R factor of structure obtained by calculation was 53.7 %, and it was found that the space group of the crystal was  $P6_522$  and a single molecule of mutant type GK was contained in asymmetrical unit. Electron density map was obtained

from this structure and structure factor, and the structure of mutant type glucokinase was determined using a program O (made by Dat-ONO Company).

Thereafter, refinement of the position of amino acid was carried out using CNX (Accelrys Inc.) and identification of amino acid residue was carried out using program O. This operation was repeated, and the structural coordinate of 448 amino acid residues from threonine 14 of the mutant type glucokinase to cysteine 461, 1 molecule of glucose molecule, 1 molecule of compound A, 1 sodium ion and 149 water molecules were identified, and the structural coordinates were determined. The R factor which is used as index of accuracy of finally determined structure was  $R = 23.2\%$  with respect to the data of resolution from 30 angstrom to 2.3 angstrom, and the R factor ( $R_{\text{free}}$ ) with respect to the data which was not used for the calculation in the refinement step of the structure was 27.4 %. There was no amino acid residue having the unacceptable structure by confirmation with Ramachandran plot.

The structure of the determined mutant type glucokinase was similar to the structure of the hexokinase which was isozyme, but the structure of the binding site of compound 1 (compound of formula IIIa) which activates glucokinase was different. This structural difference could not be expected with the ability of current computational chemistry and it became clear for the first time by this structural analysis that this site was the binding site of activator and its detailed stereostructure. Figure 1a is ribbon diagram showing three-dimensional structure of the glucokinase elucidated here. As shown in Figure 1a, the newly found activator binding site was located between large domain and small domain, and it was about 20 angstrom away from the active center wherein glucokinase bonded with the substrate, glucose. The amino acid residue of glucokinase constituting the activator binding site was as follows. Tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459.

Moreover, the binding scheme of compound 1 (compound of formula IIIa) with respect to this binding site is shown in Figure 2 and the structure of binding site of glucokinase is shown in Figure 3. The thiazole ring formed van der Waals contact with each amino acid side chain molecule of valine 62, valine 452, valine 455, and moreover the nitrogen atom on thiazole ring was hydrogen bonded with nitrogen atom of main chain of arginine 63. The nitrogen atom of amide on compound 1 was hydrogen bonded with oxygen atom of main chain of arginine 63. Benzene ring part of compound 1 was formed van der

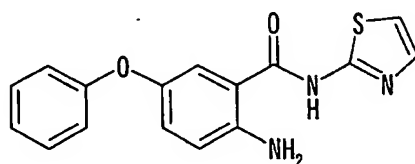
Waals contact with isoleucine 211, and the fluorine atom substituted to benzene ring formed van der Waals contacted with side chain of tyrosine 214. Aniline structure of compound 1 formed hydrogen bond with oxygen atom of side chain of tyrosine 215. Imidazole ring part bonded to the benzene ring via sulfur formed van der Waals contacted with amino acid side chain part of methionine 210, methionine 235, tyrosine 214. The serine 64-serine 69 part connecting the small domain and the large domain had a structure exposed to the solution, and compound 1 was bonded to the lower part of the arc-form structure formed by this part (Figure 3).

#### Example 4

##### Example of drug design

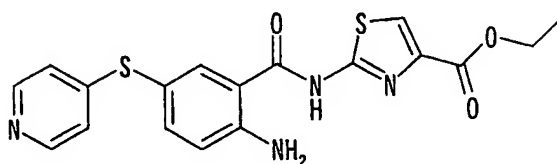
Using software UNITY (made by Tripos Company), pharmacophore of hydrogen bond acceptor and the hydrogen bond donor respectively generated from the main chain NH, CO of Arg 63, hydrophobic pharmacophore formed in the space corresponding to the phenyl group of aniline part of the ligand which formed the complex, and the protein surface formed on the basis of structure of the protein were used as search conditions, and Library compounds were screened, and the following compound 4 and compound 5 were obtained, and assay was carried out. As a result, activity of 780 % and 560 % was respectively observed. Wherein, the activity of 780 % denotes that the activity was enhanced upto 780 % by these compound when the activity of glucokinase of the control was 100 % (using glucose 2.5 M and ligand 10  $\mu$ M).

Compound 4



Activity: 780 %

Compound 5



Activity: 560 %

**Example 5**Crystal of mutant type GK ( $\Delta$ 1-15)

The crystal of simple substance of mutant type GK ( $\Delta$ 1-15) (glucokinase containing amino acid sequence represented by Sequence Number 8) was obtained using the following vapor diffusion technique.

In other words, mutant type GK purified to a high purity was concentrated, and finally a solution of mutant type GK of about 10 mg/ml (25 mM Tris-Cl pH 7.2, 50 mM NaCl, 5 mM TCEP) was formed. To protein solution 1-5  $\mu$ l was added an equal quantity of crystallisation solution (1.5-1.6 M ammonium sulfate, 50 mM NaCl, 0.1 M Bicine NaOH (pH 8.7)), and this solution formed by admixing was placed in a closed container containing 0.5-1 ml of crystallisation solution as that both solutions did not form contact, and the container was left to stand at 20°C. After standing for about 3 days - 1 months, crystals with maximum size of about 0.07 mm x 0.07 mm x 0.5 mm was obtained in the sample solution.

The obtained crystals were immersed into the crystallisation solution added with 20 % glycerol, and continuing it was frozen rapidly in liquid nitrogen. The X-ray diffraction data of the frozen crystal were collected by oscillation method in 100K nitrogen gas stream at BL32B2 of synchrotron institution Spring-8. From the obtained diffraction image, the diffraction intensity was numerised using Mosflm, and crystal structure factor was determined. At this step, it became clear that the crystal was hexagonal system and had space group of  $P6_322$  or  $P6_122$ , and crystal unit lattice was  $a = b = 103.2$  angstrom,  $c = 281.0$  angstrom,  $\alpha = \beta = 90^\circ$ ,  $\gamma = 120^\circ$ .

Next, molecular replacement method was carried out using the obtained structure factor and structure was analyzed. As model of stereostructure, three-dimensional structural coordinates of each domain of glucokinase determined from the mutant type GK ( $\Delta$ 1-11) / glucose / compound complex crystal was separately used. The calculation was performed by Amore program of CCP4 (Council for the Central laboratory of the Research Councils) using data of resolution of 8-4 angstrom. It was found that the space group of the crystal was  $P6_322$ , and a single molecule of mutant type GK ( $\Delta$ 1-15) was contained in the asymmetrical unit. Electron density map was obtained from this structure and structure factor, and the structure of mutant type GK ( $\Delta$ 1-15) simple substance was determined using program O (made by Dat-ONO Company).

Next, refinement of position of amino acid was carried out using CNX (made by Molecular Simulation Company) and identification of amino acid residue was carried out using program O. This operation was carried out repeatedly, and the structure coordinate of 424 amino acid residues from asparagine 180 to cysteine 461 and from methionine 15 to histidine 156 of mutant type glucokinase, and 2 molecules of sulfate ions, 1 sodium ion and 7 water molecules were identified, and the structural coordinates were determined. The R factor which is used as index of accuracy of finally determined structure was  $R = 23.8\%$  with respect to data of resolution of 50-3.4 angstrom, and the R factor ( $R_{\text{free}}$ ) with respect to the data which was not used for the calculation in the refinement step of structure was 30.6 %. There was no amino acid residue having the unacceptable structure by confirmation with Ramachandran plot.

The ribbon diagram showing the structure of glucokinase ( $\Delta 1-11$ ) / glucose / compound 1 and the ribbon diagram showing the structure of glucokinase ( $\Delta 1-15$ ) simple substance are respectively shown in Figure 1a and Figure 1b. Moreover, the figure on the right is a rotated figure of the figure on the left. In the structure of determined mutant type GK ( $\Delta 1-15$ ) simple substance, the structures of main parts of the large domain and the small domain were similar to the respective structures of glucokinase determined by mutant type GK ( $\Delta 1-11$ ) / glucose / compound complex crystal, but relative position of two domains was greatly different. In mutant type GK ( $\Delta 1-15$ ) simple substance structure, the main part of the small domain was rotated by about 99 degrees from position of small domain in mutant type GK ( $\Delta 1-11$ ) / glucose / compound complex structure. Moreover, alpha 13 helix located at C terminal region of glucokinase which constituted the small domain in the mutant type GK ( $\Delta 1-11$ ) / glucose / compound complex structure no longer constituted the small domain in the mutant type GK ( $\Delta 1-15$ ) simple substance structure, and it was located at between two domains. Moreover, because both the activator binding site and binding site of substrate, glucose were present between two domains in the mutant type GK ( $\Delta 1-11$ ) / glucose / compound complex structure, the structures of their sites were greatly changed in the newly determined structure. The amino acid residues that play an important role in enzyme activity did not form active site in the mutant type GK ( $\Delta 1-15$ ) simple substance structure, and the structure of mutant type GK ( $\Delta 1-15$ ) simple substance analysed here was a structure of inactive state of glucokinase. Moreover, the activator binding site had completely disappeared in the structure of mutant type GK ( $\Delta 1-15$ ) simple substance. The structural change of glucokinase (rotation of domains about 99°) observed by the mutant type GK ( $\Delta 1-11$ ) / glucose / compound complex structure and the mutant type GK ( $\Delta 1-15$ )

simple substance structure was far greater compared with the previously known structural change of hexokinase (rotation of domains about 12°), and it could not be expected with the ability of current computational chemistry and it became clear from this structure analysis for the first time.

Moreover, in order to hinder the structural change to the inactive form mutant type GK ( $\Delta$ 1-15) simple substance structure, by designing a compound that binds to the compound binding site indicated by the mutant type GK ( $\Delta$ 1-11) / glucose / compound complex structure, it became clear that activator of glucokinase could be designed.

#### Possible Applications in Industry

As described above, in accordance with this invention, crystal of the glucokinase protein which was difficult to crystallise in the prior art was obtained. The three-dimensional structural coordinates obtained by analysing this crystal structure can be suitably used in order to design compounds that bind to glucokinase. Moreover, because the compounds designed in this way bind to glucokinase, they can be used as therapeutic agent of disease involving the glucokinase activity (for example diabetes mellitus therapeutic agent) as glucokinase activator or inhibitor.

#### **Patent Claims**

1. A glucokinase protein characterised in being used for crystallisation.
2. A protein in accordance with Claim 1 comprising amino acid sequence in accordance with Sequence Number 5.
3. A crystal of protein comprising amino acid sequence in accordance with Sequence Number 5 or amino acid sequence substantially the same amino acid sequence thereof.
4. A crystal in accordance with Claim 3, wherein the said protein is glucokinase protein.
5. A crystal in accordance with Claim 3 comprising crystals of protein containing amino acid sequence in accordance with Sequence Number 5.



6. A crystal in accordance with Claim 3, wherein the lattice constant satisfies the following equations (1)-(4)

$$a = b = 79.9 \pm 4 \text{ \AA} \quad (1)$$

$$c = 322.2 \pm 15 \text{ \AA} \quad (2)$$

$$\alpha = \beta = 90^\circ \quad (3)$$

$$\gamma = 120^\circ \quad (4)$$

7. A crystal in accordance with Claim 6, wherein the space group is  $P6_522$ .

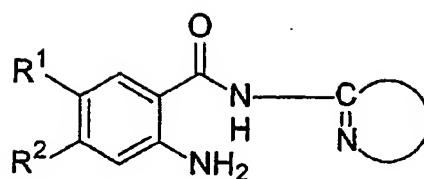
8. A crystal of protein specified by three-dimensional structure coordinates data in accordance with Table 1.

9. A crystal wherein in three-dimensional structure coordinates data changed in at least one data of three-dimensional structure coordinates data in accordance with Table 1, the mean square error between atoms of main chain of amino acid represented by three-dimensional structure coordinates data in accordance with Table 1 (C alpha atom) and C alpha atoms represented by the said changed three-dimensional structure coordinates data corresponding to aforesaid C alpha atoms is 0.6 Å or less.

10. A crystal in accordance with any of Claims 3-9, wherein the compound binding site is constructed by at least one of amino acid residues of tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459 in amino acid sequence shown in sequence Number 5.

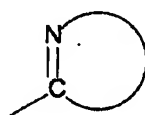
11. A crystal including a complex of the protein comprising amino acid sequence in accordance with Sequence Number 5 or amino acid sequence substantially the same amino acid sequence thereof and a compound which can bind to the said protein.

12. A crystal in accordance with Claim 11, wherein aforesaid compound is represented by formula (1).



(I)

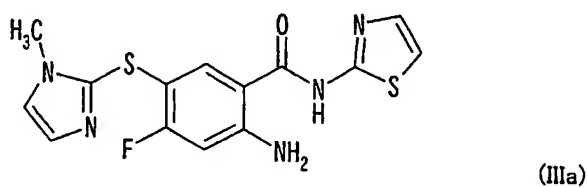
[wherein, R1 shows halogen atom, -S-(O)<sub>p</sub>-A, -S-(O)<sub>q</sub>-B or -O-B (wherein, p and q are the same or different and denote an integer of 0-2, A denotes C1-C6 alkyl group of optionally substituted straight chain, B denotes optionally substituted five-membered or six-membered ring aryl group or heteroaryl group, R2 denotes a hydrogen atom or halogen atom, and



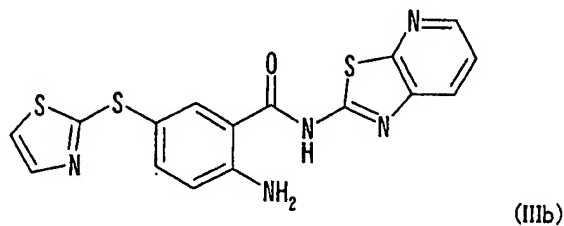
(II)

denotes an optionally substituted monocyclic or bicyclic heteroaryl group having a nitrogen atom adjacent to the carbon atom bonded to amide group].

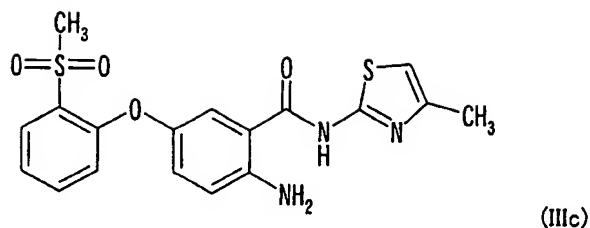
13. A crystal in accordance with Claim 12, wherein aforesaid compound is any of the compound represented by formula (IIIa)-(IIIc).



(IIIa)



(IIIb)



14. A protein in accordance with Claim 1 comprising amino acid sequence in accordance with Sequence Number 8.

15. A crystal of protein comprising amino acid sequence in accordance with Sequence Number 8 or amino acid sequence substantially the same amino acid sequence thereof.

16. A crystal in accordance with Claim 15, wherein the said protein is glucokinase protein.

17. A crystal in accordance with Claim 15 comprising crystals of protein containing amino acid sequence in accordance with Sequence Number 8.

18. A crystal in accordance with Claim 15, wherein the lattice constant satisfies the following equations

$$a = b = 103.2 \pm 5 \text{ \AA} \quad (5)$$

$$c = 281.0 \pm 7 \text{ \AA} \quad (6)$$

$$\alpha = \beta = 90^\circ \quad (7)$$

$$\gamma = 120^\circ \quad (8)$$

19. A crystal in accordance with Claim 18, wherein the space group is  $P6_522$ .

20. A crystal of protein specified by three-dimensional structure coordinates data in accordance with Table 2.

21. A crystal wherein in three-dimensional structure coordinates data changed at least one data of three-dimensional structure coordinates data in accordance with Table 2, the mean square error between atoms of main chain of amino acid represented by three-dimensional structure coordinates data in accordance

with Table 2 (C alpha atom) and C alpha atoms represented by the said changed three-dimensional structure coordinates data corresponding to aforesaid C alpha atoms is 0.6 Å or less.

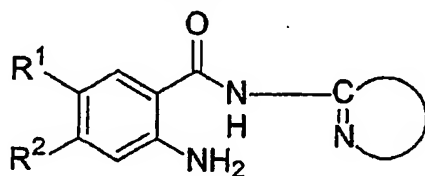
22. A process for the production of crystal containing a complex of protein and a compound that binds to the protein thereof, including

a protein production step wherein a protein containing the amino acid sequence having deletion of 1-50 amino acid residues from either or both of N terminal and C terminal of the protein containing amino acid sequence in accordance with Sequence Number 2 is produced, and

a protein reaction step wherein a compound that binds to the protein obtained in the said protein production step and the protein obtained in the said protein production step are reacted.

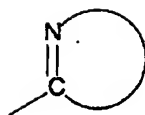
23. A process to produce crystal of the kind wherein a crystal of a protein is produced, characterised in that a protein including amino acid sequence in accordance with Sequence Number 5 or amino acid sequence substantially the same amino acid sequence thereof and having glucokinase activity and a compound which can bind to the said protein are used.

24. A process for the production of crystalline protein in accordance with Claim 23, wherein the compound which can bind to said protein is a compound represented by formula (1).



(I)

[wherein, R1 shows halogen atom, -S-(O)p-A, -S-(O)q-B or -O-B (wherein, p and q are the same or different and denote an integer of 0-2, A denotes C1-C6 alkyl group of optionally substituted straight chain, B denotes optionally substituted five-membered or six-membered ring aryl group or heteroaryl group, R2 denotes a hydrogen atom or halogen atom, and



(II)

denotes an optionally substituted monocyclic or bicyclic heteroaryl group containing nitrogen atom adjacent to the carbon atom bonded to amide group].

25. A process for the production of crystal in accordance with Claim 23 or 24 using co-crystallisation or soaking method

26. A drug design method of the kind wherein based on stereostructural information of a protein, the structure of compound that binds to said protein is designed, characterised in that the stereostructure information of said protein is the information obtained by analysing crystal in accordance with any of Claims 3-13 or 15-21.

27. A drug design method in accordance with Claim 26 characterised in that  
a binding site deduction step wherein the compound binding site of said protein is deduced based on aforesaid stereostructure information, and  
a selection step wherein a compound compatible to the compound binding site deduced in aforesaid binding site deduction step is selected from compound library,  
are included.

28. A drug design method in accordance with Claim 26 characterised in that  
a binding site deduction step wherein the compound binding site of said protein is deduced based on aforesaid stereostructure information, and  
a compound structure assembly step wherein the structure of compound compatible to compound binding site deduced in aforesaid binding site deduction step is constructed,  
are included.

29. A drug design method in accordance with Claim 26 characterised in that

a binding site deduction step wherein the compound binding site of said protein is deduced based on aforesaid stereostructure information, and

a design step wherein the structure of compound is designed by visual observation so that the compound binding site deduced in aforesaid binding site deduction step and a compound compatible to said compound binding site interact,  
are included.

30. A drug design method in accordance with any of Claims 26-29, wherein aforesaid compound binding site is constituted by at least one of amino acid residue of tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459 in amino acid sequence shown in sequence Number 5.

31. A drug design method in accordance with any of Claims 26-30 further including a step to measure physiological activity of the candidate compound predicted to be compatible to aforesaid compound binding site.

32. A drug design method in accordance with any of Claims 26-30 further including a binding determination step wherein the candidate compound predicted to be compatible to aforesaid compound binding site and a protein including amino acid sequence in accordance with and Sequence Number 5 or amino acid sequence which is substantially the same amino acid sequence thereof are contacted, and whether the candidate compound binds to the said protein or not is assessed.

33. A process for the production of compound array including the compound group selected by drug design method in accordance with any of Claims 26-30 is combined as compound array.

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